

STIC-Biotech/ChemLib

166285

From: Dunston, Jennifer
Sent: Tuesday, September 20, 2005 11:49 AM
To: STIC-Biotech/ChemLib
Subject: Sequence Search 10/705757

Please do a sequence search for SEQ ID NOS: 1, 3 and 5 against the commercial protein databases.
SEQ ID NOS: 1, 3 and 5 are 2623, 1302 and 942 nt in length, respectively.

Thank you.

Jennifer Dunston, Ph.D.
USPTO Art Unit 1636
REM 2B76
Mailbox: REM 2C70
(571) 272-2916

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 9/23
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 16:20:36 : Search time 68.9838 Seconds
(without alignments)
5676.828 Million cell updates/sec

Title: US-10-705-757-1

Perfect score: 4789
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DELEXT=7

Database :

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5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1670	34.9	313	3	US-09-237-543-9
2	1670	34.9	313	3	US-09-644-450-9
3	1670	34.6	313	2	US-08-463-0818-26
4	1657	34.6	313	2	US-08-463-379A-26
5	1657	34.6	313	2	US-08-463-390B-26
6	1657	34.6	313	3	US-08-463-074B-26
7	1657	34.6	313	3	US-08-465-585C-26
8	1657	34.6	313	3	US-08-652-446-26
9	1636	34.2	313	3	US-09-237-543-8
10	1636	34.2	313	3	US-09-644-450-8
11	1582	33.0	313	3	US-09-237-543-7
12	1582	33.0	313	3	US-09-644-450-7

13	1296.5	27.1	257	2	US-07-857-224B-41	Sequence 41, Appl
14	1149.5	24.0	455	3	US-09-237-543-5	Sequence 5, Appl
15	1149.5	24.0	455	3	US-09-644-450-5	Sequence 5, Appl
16	1133	23.7	326	3	US-09-237-543-2	Sequence 2, Appl
17	1133	23.7	326	3	US-09-644-450-2	Sequence 2, Appl
18	1105	23.1	323	3	US-09-237-543-6	Sequence 6, Appl
19	1105	23.1	323	3	US-09-644-450-6	Sequence 6, Appl
20	1079.5	22.5	254	3	US-09-237-543-4	Sequence 4, Appl
21	1079.5	22.5	254	3	US-09-644-450-4	Sequence 4, Appl
22	903.5	18.9	372	4	US-09-949-016-7140	Sequence 7140, Ap
23	390	8.1	1323	3	US-09-770-170-2	Sequence 2, Appl
24	384.5	8.0	630	4	US-10-355-975A-38	Sequence 38, Appl
25	384.5	8.0	631	4	US-09-579-664B-11	Sequence 11, Appl
26	384.5	8.0	631	4	US-10-355-975A-11	Sequence 11, Appl
27	383	8.0	776	4	US-09-523-849-34	Sequence 34, Appl
28	376	7.9	1101	3	US-09-770-170-8	Sequence 8, Appl
29	371.5	7.8	778	4	US-10-116-326-2	Sequence 2, Appl
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33	364.5	7.6	511	4	US-09-633-328B-4	Sequence 4, Appl
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36	356	7.4	602	4	US-09-949-016-7417	Sequence 7417, Ap
37	356	7.4	602	4	US-09-949-016-7418	Sequence 7418, Ap
38	354.5	7.4	722	4	US-08-817-832B-32	Sequence 32, Appl
39	354	7.4	504	4	US-09-554-726A-10	Sequence 10, Appl
40	353.5	7.4	722	4	US-09-984-890-4	Sequence 4, Appl
41	353.5	7.4	724	4	US-10-274-194-4	Sequence 4, Appl
42	352.5	7.4	724	4	US-09-984-890-2	Sequence 2, Appl
43	352.5	7.4	724	4	US-10-274-194-2	Sequence 2, Appl
44	352.5	7.4	1005	3	US-09-770-170-4	Sequence 4, Appl
45	348	7.3	418	4	US-09-248-796A-18441	Sequence 18441, A

ALIGNMENTS

RESULT 1
US-09-237-543-9
Sequence 9, Application US/09237543A
Patent No. 6143540
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
NUMBER OF FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-09-237-543-9

Alignment Scores:

Pred. No.: 3.94E-117
Score: 1670.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 34.87%
DB: 3
Gaps: 0

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DB 1 MetLeuLeuSerYsIleLeuSerLeuAlaHisLeuArgAlaIaProCysaenApLeu 20
QY 411 CAGCGACCAAGCTGCGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 470
DB 21 HisAlaThrIleuAlaProGlyIleGluIleGluProLeuIleuSerGlnIleVal 40

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DB 41 G1YProleuLeuLysSerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
QY 531 AACTTGGCCGGTGGCCATCAAAACAGTGAAGAGACCGGATTTCCGACTGGAGAGACTG 590
DB 61 AsnLeuProValAlaIleuYshIleValGluLysAspArgIleSerAspTrpGlyGluLeu 80
QY 591 CCTAATGGCACTCGAGTGGCCCATGGAAGTGGTCTCTGCTGAAGAAAGGTAGCTGGGTTTC 650
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QY 711 GAGAGGCCGAGCCGAGTGAAGATCTCTTGCATTCATCAGGAAAGGGAGCCCTGCA 770
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DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValIleuGlnAlaValArgHisCyshIAsn 160
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US-09-644-450-9
; Sequence 9, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
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! ORGANISM: Homo sapiens
US-09-644-450-9
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Pred. No.: 3,94e-117 Length: 313
Score: 1670.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.87% Indels: 0
DB: 3 Gaps: 0
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QY 531 AACTTGGCCGGTGGCCATCAAAACAGTGAAGAGACCGGATTTCCGACTGGAGAGACTG 590
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QY 1251 GAGATCCAGCTCCAGACGCTGTGCGCGGCGCCAGCAAA 1289
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerIys 313

RESULT 3
 US-08-463-081B-26
 Sequence 26, Application US/08463081B
 Patent No. 5871960 5837487
 Patent No. 5871960 5837487
 GENERAL INFORMATION:
 APPLICANT: Smith, Kendall A. & Beadling, Carol
 TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
 TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESSES:
 ADDRESSES: PRETTY, SCHROEDER & POPLAWSKI
 STREET: 444 South Flower St. - Suite 1900
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90071

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Version #1.0,
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/463,081B
 FILING DATE: 5-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/104,736
 FILING DATE: 10-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/796,066
 FILING DATE: 20-NOV-91
 ATTORNEY/AGENT INFORMATION:
 NAME: Viviana Amzel, Ph. D.
 REGISTRATION NUMBER: 30,930
 REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 622-7700
 TELEFAX: (213) 489-4210
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 313 amino acids
 TYPE: amino acid
 STRANDEDNESS: n.a.
 TOPOLOGY: n.a.
 MOLECULAR TYPE: peptide
 US-08-463-081B-26

Alignment Scores:
 Pred. No.: 3 72e-116 length: 313
 Score: 1657.00 Matches: 311
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 Best Local Similarity: 99.36% Mismatches: 2
 Query Match: 34.60% Indels: 0
 DB: 2 Gaps: 0

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QY 471 GGCCTGCTACTGAGGCAAGCGGCTTGCCTGCTGCTACTCAGGACATCCGCTCCGAC 530
 DB 41 GlyProLeuLeuGlnIysSerGlyGlyPheGlySerValIyrSerGlyIleArgValSerAsp 60

QY 531 AACTTCCCGGTGGCCATCAAACTGTGAGAGAGACCGGATTTCCGACTGGGGAGACTG 590
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QY 591 CCTAATGGGACCTGAGTGGCCATGAGAGTGGTCTCTGAAAGAGGTGAGCTCGGTTTC 650
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QY 651 TCCGGCGTCAATTAAGCTCTGGAAGTGGTTCGAGAGGCGCCGACAGTTTCCTGATCTG 710
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGlnArgProAspSerPheValIleLeu 120

QY 711 GAGAGCCCGAGCGCGGTGCAAGATCTTCTGACTTATCAAGGAAAGGGAGCCCTTGCA 770
 DB 121 GluArgProGlnProValGlnAspLeuPheAspPheIleThrGlnArgGlyAlaLeuGln 140

QY 771 GAGGAGCTGGCCCGGCTTCTTCTGAGAGGTGTCGAGGCGGTGCGGCACTGCAAC 830
 DB 141 GluGlnLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160

QY 831 TCGGGGCTGCTACCCGCGCATCAAGACGAAACATCTTATCGACTCAATCGCGC 890
 DB 161 CysGlyValLeuHisArgAspIleLysAspGlnAsnIleLeuIleAspLeuAsnArgGly 180

QY 891 GAGCTCAAGCTCATGCACTTTCGGGTGCGGCGCTCTCAAGACACCGCTTACAGGAC 950
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QY 951 TTGATGGGACCGGAGTGTATGCGCTCCAGAGTGTATCGGCTACATGCTACATGGC 1010
 DB 201 PheAspGlyThrArgValIyrSerProGlnIrrpIleArgIyrHisArgIyrHisGly 220

QY 1011 AGCTCGGCGCACTGTGCTCCCTGGGATCTCTGTATGATATGCTGTGTGAGATATT 1070
 DB 221 ArgSerAlaIleValIrrpSerLeuGlyIleLeuLeuIyrAspMetValCysGlyAspIle 240

QY 1071 CTTTTCAGCATGACGAAGATCATCAGAGGCGCAGTTTCTTTCAGGACGAGGCTCTC 1130
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QY 1131 TCGAATGTCAGACTCATTTAGTGGTGGCCCTGAGACCATCAGATAGCCCAACC 1190
 DB 261 SerGlnCysGlnHisLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280

QY 1191 TTCGAAGAATCCGAACCATCATGATGATGATGATGATGATGATGATGATGATGAT 1250
 DB 281 PheGlnGlnIleGlnHisHisProTrpMetGlnAspValLeuLeuProGlnGlnIrrpAla 300

QY 1251 GAGATCCAGCTCCAGACGCTGTGCGCGGCGCCAGCAAA 1289
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerIys 313

RESULT 4
 US-08-461-379A-26
 Sequence 26, Application US/08461379A
 Patent No. 5871961
 GENERAL INFORMATION:
 APPLICANT: Smith, Kendall A. & Beadling, Carol
 TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
 TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESSES:
 ADDRESSES: Ratner & Prestia
 CITY: Valley Forge
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19482

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

Alignment Scores:

Pred. No.: 3,72e-116 Length: 313
 Score: 1657.00 Matches: 311
 Percent Similarity: 99.36% Conservative: 0
 Best Local Similarity: 99.36% Mismatches: 2
 Query Match: 34.60% Indels: 0
 DB: 2 Gaps: 0

US-10-705-757-1 (1-2623) x US-08-463-390B-26 (1-313)

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 QY 411 CAGCCCAACCAAGCTGGCGCGCGCGCAAGAGAGAGAGCCCTGAGTGCAGTACCAAGTG 470
 Db 21 HisAlaThrlyLeuAlaProGlyLyseGlyuyluProleuGluSerGlnTyrglnVal 40
 QY 471 GGGCGGCTACTGGGCGAGCGGGGCTTGGGCTCGGCTTACTAGGCAATCCGGCTCTCCGAC 530
 Db 41 GlyProleuLeuGlySerGlyGlyPheGlySerValTySerGlyIleArgValSerAap 60
 QY 531 AACTTGGCGGTGCGCATCAACACGTGGAGAGAGACCGGATTTCCGACTGGGAGAGACTG 590
 Db 61 AsnleuProValAlaIlelyshIleValGlylyAapArgIleSerAapTrpGlyGlnleu 80
 QY 591 CTTAATGCACTCGAGTGCCTCCATGGAAGTGTCTCTGTAAGAAAGTGAAGCTCGGATTTC 650
 Db 81 ProAenGlyThrArgValAlPrometGlyValValleuLeuLylyValSerSerGlyPhe 100
 QY 651 TCCGGCGCTCATTAAGCTCTCGGACTGTTGAGAGGCGCCGACAGTTTCCTGATCTGTG 710
 Db 101 SerGlyValIleArgLeuLeuAapTrpPheGlyArgProAapSerPheValIleuIleleu 120
 QY 711 GAGAGGCGCGAGCGGTGCAAGATCTCTGCACTTCAACGAGAAAGGGAGCGCTTCAAA 770
 Db 121 GlnArgProGluProValGlnAapPheAapPheAapIleThrGlyuyluValAlaGln 140
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 QY 951 TTCAGTGGAGCCGAGTGTATAGCCCTCAAGAGTGAATCCGCTACATCCGCTACATGAGC 1010
 Db 201 PheAapGlyThrArgValTySerProProGluTrpIleArgTyHisAlaGlyuyluSerGly 220
 QY 1011 AGGTGGCGGAGTCTGTGCTCCCTGGAGATCTGTGTATGATATGATGTGTGTGAGATATT 1070
 Db 221 ArgSerIleAlaValAlaTrpSerleuGlyIleleuLeuTyArgPheMetValCyseGlyAapIle 240
 QY 1071 CCTTTCAGAGTGAAGAGATCATGAGGGGCGAGGTTTCTTCAAGAGAGGGGTCTT 1130
 Db 241 ProPheGlnIleAapArgIleuGlnIleIleArgGlyGlnAlaPhePheAapGlnAlaGlyValSer 260
 QY 1131 TCAGAAATGTCAAGATCTCATTAAGTGTGTGAGCCCTGAGACCATGAGATAGAGCAACC 1190
 Db 261 SerGlnCyseGlnIleleuIleArgTrpCyseuAlaIleuArgProSerAapArgProThr 280
 QY 1191 TTGCAAGAAATCCGAACCATCATGAGATGAGATGTTCTCTGCGCCCAAGAAATCTGCT 1250
 Db 281 PheGlnIleuIleGlnAenAlaProTrpMetGlnAapValIleuLeuProGlnIleuAla 300
 QY 1251 GAGATCCAGCTCCAGAGCTGTGCGCGGGCGCCAGCAA 1289

Db 301 GlnIleHisleuHisSerleuSerProGlyProSerLyS 313

RESULT 6
 US-08-463-074B-26
 Sequence 26, Application US/08463074B
 Patent No. 6020155
 GENERAL INFORMATION:
 APPLICANT: Smith, Kendall A. & Beadling, Carol
 TITLE OF INVENTION: Nucleic Acids Encoding CRI Fusion Protein, Vector an
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
 ADDRESS: (B) STREET:
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0,
 SOFTWARE: Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/463,074B
 FILING DATE: 5-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/104,736
 FILING DATE: 10-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/796,066
 FILING DATE: 20-NOV-91
 ATTORNEY/AGENT INFORMATION:
 NAME: Viviana Amzel, Ph. D.
 REGISTRATION NUMBER: 30,930
 REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 622-7700
 TELEFAX: (213) 489-4210
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 313 amino acids
 TYPE: peptide
 STRANDEDNESS: n.a.
 TOPOLOGY: n.a.
 MOLECULE TYPE: peptide
 US-08-463-074B-26

Alignment Scores:
 Pred. No.: 3,72e-116 Length: 313
 Score: 1657.00 Matches: 311
 Percent Similarity: 99.36% Conservative: 0
 Best Local Similarity: 99.36% Mismatches: 2
 Query Match: 34.60% Indels: 0
 DB: 3 Gaps: 0

US-10-705-757-1 (1-2623) x US-08-463-074B-26 (1-313)

QY 351 ATGCTCTTGTCCAAATCAACTCGCTTGCACCTGCGCGCGCCCTGCAAGCACTG 410
 Db 1 MetleuLeuSerlySileAenSerleuAlahisLeuArgAlaAArgAlaCyshAenApleu 20
 QY 411 CAGCCCAACCAAGCTGGCGCGCGCGCAAGAGAGAGAGCCCTGAGTGCAGTACCAAGTG 470
 Db 21 HisAlaThrlyLeuAlaProGlyLyseGlyuyluProleuGluSerGlnTyrglnVal 40
 QY 471 GGGCGGCTACTGGGCGAGCGGGGCTTGGGCTCGGCTTACTAGGCAATCCGGCTCTCCGAC 530
 Db 41 GlyProleuLeuGlySerGlyGlyPheGlySerValTySerGlyIleArgValSerAap 60
 QY 531 AACTTGGCGGTGCGCATCAACACGTGGAGAGAGACCGGATTTCCGACTGGGAGAGACTG 590
 Db 61 AsnleuProValAlaIlelyshIleValGlylyAapArgIleSerAapTrpGlyGlnleu 80

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QY 591 CCTAATGCACTGAGTGGCCCATGGAAGTGTCTGTGTAAGAAGGTGAGTCTGGGTTTC 650
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Db 81 ProhenglYThrArgValProMetGluValLeuLeuYsValSerSerGlyPhe 100
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QY 651 TCCGGGCTCATTAAGCTCTGTGACTGGTTTGAAGAGCCCGACAGTTTCTGTGATCTTG 710
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Db 101 SerGlyValIleArgLeuLeuAmpTrpPheGluArgProAspSerPheValLeuIleLeu 120
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|
QY 711 GAGAGGCCGAGCCGGGTGCAAGATCTCTTCACTTCACTCAAGAAAGGGAGCCCTTGCA 770
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Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
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QY 771 GAGAGCTGGCCCGGAGCTCTTCTGTGAGTGTGAGAGCCGCTGGGGCACTGGCCCAAC 830
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Db 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgIleCysHisAsn 160
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QY 831 TGGGGGTGCTACACCGGACATCAAGACGAAACATCTTATTCAGCTCAATCCGGC 890
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Db 161 CysGlyValLeuIleArgValIleArgValIleArgValIleArgValIleArgValIle 180
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|
QY 891 GAGCTCAAGCTCATCGACTTGGAGTGGGGGCGCTGCTCAAGACACCGTCAACGAGC 950
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Db 181 GluLeuLeuLeuIleAspPheGlySerGlyAlaLeuLeuYsAspThrValIleTrpAsp 200
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QY 951 TTGAGTGGGACCCGAGTGTATTAAGCCCTCCAGAGTGAATCCGCTACAGCTCAATGGC 1010
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Db 201 PheAspGlyThrArgValIleArgProGluTrpIleArgTrpHisArgTrpHisGly 220
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QY 1011 AGGTGGCGGACGTGTGTCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1070
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Db 221 ArgSerIleAlaValIleTrpSerIleGlyIleLeuLeuTrpAspMetValCysGlyAspIle 240
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QY 1071 CCTTTGAGAGCATGACGAAGATCATACAGGGGCGGAGTTTCTTCAAGGAGAGGTTCT 1130
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Db 241 ProPheGluIleHisArgGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
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QY 1131 TCAGAAATGAGCATCTCATTAAGTGTGTGCTGGCCCTGAGACCATCAATAGAGCAAC 1190
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Db 261 SerGluCysGlnHisLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProTrp 280
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QY 1191 TTCGAAGAAATCCAGAACATCCATGAGTGAAGATGTTTCTGCTGCCCGAGAACTGCT 1250
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Db 281 PheGluGluIleGlnIleAsnHisProTrpMetGlnAspValLeuLeuProGluGlnIleTrpAla 300
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QY 1251 GAGATCCACTCCACAGACTGTGCGCGGGGCCAGCAAA 1289
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Db 301 GluIleHisLeuHisSerLeuSerProGlyProSerIleYs 313
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RESULT 7
US-08-465-585C-26
Sequence 26, Application US/08465585C
Patent No. 6027914
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecro
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
CITY: Los Angeles (B) STREET:
STATE: California
COUNTRY: USA
ZIP: 900071
444South Flower St. - Suite 190
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-JUNE-1995

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/330,108
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: USSN 08/104,736
; FILING DATE: 10-AUG-1993
; APPLICATION NUMBER: USSN 07/796,066
; FILING DATE: 20-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 4894210
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-465-585C-26

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Alignment Scores:
Pred. No.: 3,72e-116 Length: 313
Score: 1657.00 Matches: 311
Percent Similarity: 99.36% Conservative: 0
Best Local Similarity: 99.36% Mismatches: 2
Query Match: 34.60% Indels: 0
Gaps: 0
US-10-705-757-1 (1-2623) x US-08-465-585C-26 (1-313)

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Db 1 MetLeuLeuSerLeuIleAsnSerLeuAlaHisLeuArgAlaCysAsnAspLeu 20
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QY 411 CACGCCACCAACTGGCGCGCCGCGCAAGAGAGAGCCCTGAGTGTGAGTGTGAGTGTG 470
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Db 21 HisAlaThrIleLeuAlaProGlyIleArgIleGluProLeuGluSerGlnIleVal 40
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QY 471 GGCCTGCTACTGAGCGCGGCTTGGCTGTCTACTCAAGCATCCGCTCTCCGAC 530
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Db 41 GlyProLeuLeuGlySerGlyIlePheGlySerValIleArgValSerAsp 60
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QY 531 AACTTGGCGGTGGCCATCAACAGTGAAGACCGGATTTCCGACTGGGGAGAGCTG 590
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Db 61 AsnLeuProValAlaIleIleHisIleValGluYsAspArgIleSerAspTrpGlyLeu 80
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|
QY 591 CCTAATGCACTGAGTGGCCCATGGAAGTGTCTGTGTAAGAAGGTGAGTCTGGGTTTC 650
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Db 81 ProhenglYThrArgValProMetGluValIleLeuLeuYsValSerSerGlyPhe 100
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QY 651 TCCGGGCTCATTAAGCTCTGTGACTGGTTTGAAGAGCCCGACAGTTTCTGTGATCTTG 710
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Db 101 SerGlyValIleArgLeuLeuAmpTrpPheGluArgProAspSerPheValLeuIleLeu 120
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QY 711 GAGAGGCCGAGCCGGGTGCAAGATCTCTTCACTTCACTCAAGAAAGGGAGCCCTTGCA 770
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Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
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QY 771 GAGAGCTGGCCCGGAGCTCTTCTGTGAGTGTGAGAGCCGCTGGGGCACTGGCCCAAC 830
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Db 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgIleCysHisAsn 160
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QY 831 TGGGGGTGCTACACCGGACATCAAGACGAAACATCTTATTCAGCTCAATCCGGC 890
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Db 161 CysGlyValIleLeuIleArgValIleArgValIleArgValIleArgValIleArgValIle 180
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QY 891 GAGCTCAAGCTCATCGACTTGGAGTGGGGGCGCTGCTCAAGACACCGTCAACGAGC 950
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Db 181 GluLeuLeuLeuIleAspPheGlySerGlyAlaLeuLeuYsAspThrValIleTrpAsp 200

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QY 951 TTGATGGGACCGGAGTGTATAGCCCTCGAAGTGGATCCGCTACCGTACCAATGCG 1010
 DB 201 PheAepGlyThrArgValItyrSerProGluThrIleArgIyThIaArgIyThIaGly 220
 QY 1011 AGGTGGCGGAGCTGTGCTCCCTGGGAGATCCCTGCTATGATATGCTGTGAGATATT 1070
 DB 221 ArgSerIaIaIaValItyrSerIeGlyIleIeuIeuIyThrAepMetValCySgIyAepIle 240
 QY 1071 CCTTCGAGCATGACGAAGAGATCATCAAGGGCCAGGCTTTCTTCAGCAGAGGGCTCT 1130
 DB 241 ProPheGluIuHIsaArgIuGluIleIleIaArgIyGluValIaPhePheArgGluArgValIser 260
 QY 1131 TCGAATGACGATCTCATTTAGATGTGCTGCTGGCCCTGAGACATGATGATGACCAACC 1190
 DB 261 SerGluCySgIuHIsaIleuIleIaArgIyCySgIeuaIaIeuArgProSerAaPArgProThr 280
 QY 1191 TTGCAAGAATCCGACGAACATCCATGATGATGACGAAGATGTTCTCTGCCCGGCAAACTGT 1250
 DB 281 PheGluGluIuIeGluIaHIsaHIsaProItyrMetGluAepValIleuIeuProGluIuThIa 300
 QY 1251 GAGATCCAGCTCCACAGCTGTGCGCGGCGCCGCAAA 1289
 DB 301 GluIeHIsaIeuHIsaSerIeuSerProGlyProSerIys 313
 RESULT 8
 US-08-652-446-26
 Sequence 26, Application US/08652446
 Patent No. 6057427
 GENERAL INFORMATION:
 APPLICANT: Smith, Kendall A. & Beadling, Carol
 TITLE OF INVENTION: Nucleic Acids Encoding CPS
 TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
 ADDRESS: 444 South Flower St. - Suite 1900
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0,
 SOFTWARE: Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/652,446
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP App. # 96921319.8
 FILING DATE: 5-JAN-1998
 APPLICATION NUMBER: PCT/US/96/09194
 FILING DATE: 5-JUN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/330,108
 FILING DATE: 27-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/463,074
 FILING DATE: 5-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/462,337
 FILING DATE: 5-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/462,390
 FILING DATE: 5-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/465,585
 FILING DATE: 5-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/463,081
 FILING DATE: 5-JUN-1995

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/461,379
 FILING DATE: 5-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/739,523
 FILING DATE: 29-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Viviana Knezel, Ph. D.
 REGISTRATION NUMBER: 30,930
 REFERENCE/DOCKET NUMBER: PP66 40035
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 622-7700
 TELEFAX: (213) 489-4210
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 313 amino acids
 TYPE: peptide
 STRANDEDNESS: n.a.
 TOPOLOGY: n.a.
 MOLECULE TYPE: peptide
 US-08-652-446-26
 Alignment Scores:
 Pred. No.: 3,72e-116
 Score: 1657.00
 Percent Similarity: 99.36%
 Best Local Similarity: 99.36%
 Query Match: 34,60%
 DB: 3 Gaps: 0
 US-10-705-757-1 (1-2623) x US-08-652-446-26 (1-313)
 QY 351 ATGCTTTGTCAAAATCAACTGCTTGCCACCTCGCGCGCCCTGCAACCACTG 410
 DB 1 MetIeuIeuSerIyIleIaHIsaSerIeuIaHIsaIeuArgIaArgIaIaCySaaAepIeu 20
 QY 411 GAGGCCAAGAGCTGCG 470
 DB 21 HIsaIaThIyIeuIaIaProGlyIySgIuIySgIuIySgIuIySgIuIySgIuIySgIuIy 40
 QY 471 GCGCGCTACTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 530
 DB 41 GlyProIeuIeuIySerIyIyGlyIyPheGlyIySerValIySerGlyIleArgValIserAep 60
 QY 531 AACTTCCGAGTGGCCATCAACAACGTGAGAAAGACCGGATTTCCGACTGGGAGAGCTG 590
 DB 61 AeuIeuProValaIaIleIyHIsaValaIyIySaaPArgIleIserAepItyrGlyIuIeu 80
 QY 591 CTAATGCGACTGAGTGGCCATGGAAGTGTCTCTGGAAGAGGTGAGCTGGGTTTC 650
 DB 81 ProAaGlyThrArgValIaProMetGluValaIleuIeuIySgIyValIserSerGlyPhe 100
 QY 651 TCCGGGCTGATTAGGCTCCGCGAGCTGTTGAGAGGCCCGGAGCGTTTCGCTGATCCTG 710
 DB 101 SerGlyValIleArgIeuIeuIySaaPArgIyIleIeuIeuIySgIyValIserSerGlyPhe 120
 QY 711 GAGAGGCCCGAGCGCGGTGCAAGATCTTTCGACTTCATCAAGAAAGGAGGAGCCCTGCA 770
 DB 121 GluArgProGluIuProValaGluAepIeuPheAepPheIleThrGluArgIyIaIeuGlu 140
 QY 771 GAGGAGCTGGCCCGGAGCTTTCTTTCGAGAGTGTGGAAGCCGCTGGGCGACTGCCCAAC 830
 DB 141 GluGluIeuIaIySerPhePheItyrGluIyValaIleuGluIaValaIyHIsaIySgIySaaA 160
 QY 831 TCGGGGCTGCTACACCGGACATCAAGACGAAGAAATCTTTCGACTTCGACTTCGCGGCG 890
 DB 161 CySgIyValIeuHIsaArgAepIleIySaaPArgIyIleuIeuIySgIySaaAArgGly 180
 QY 891 GAGCTCAAGCTCATGCACTTCGAGGTGCGGCGCGCTGCTCAAGACACCGTTCATCAAGAC 950
 DB 181 GluIeuIyIeuIleAepPheGlySerGlyIaIleuIeuIyAaPThrValIyThrAaP 200
 QY 951 TTGATGGGACCGGAGTGTATAGCCCTCGAAGTGGATCCGCTACCAATGCG 1010

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Db      201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
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Db      221 ArgSerAlaIaIaValTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
Qy      1071 CCTTGCAGCATGACGAAGAGATCATCAAGGGGCGAGGTTTCTTCCAGSCAGAGGTTCTCT 1130
Db      241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
Qy      1131 TCAGATGTGACGATCTCATTTAATGTGCTTGGCCCTGAGACCATCAATAGAGCCAAACC 1190
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Qy      1191 TTCGAAGAATCCAGAACCATCATCATGAGATGATGTTCTCTGCGCCCGCAAGAACTGCT 1250
Db      281 PheGluGluIleGlnHisAspHisProTrpMetGlnAspValLeuLeuProGlnGluTrpAla 300
Qy      1251 GAGATCCACTCCACAGCCTGTGCGCGGGGCCAGCAAA 1289
Db      301 GluIleHisLeuHisSerLeuSerProGlyProSerTyr 313

RESULT 9
US-09-237-543-8
; Sequence 8, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-237-543-8

Alignment Scores:
Pred. No.: 1,4e-114 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 34.16% Indels: 0
Gaps: 0

US-10-705-757-1 (1-2623) x US-09-237-543-8 (1-313)
Qy      351 ATGCTCTTGTCCAAATCAACTCGCTTGCCCACTGGCGCGCGCCCTTCGACGACTTG 410
Db      1 MetLeuLeuSerTyrHisLeuAsnSerLeuAlaHisLeuTyrAlaIaProCysAsnAspLeu 20
Qy      411 CACGCCACAGCTGGCGCGCGCGGCAAGAGAGAGAGCCCTGAGTGCAGTACCAAGTGC 470
Db      21 HisAlaAsnTyrSerLeuAlaProGlyLeuGluLeuProLeuGluSerGlnTyrGlnVal 40
Qy      471 GGCCTCGTACTGGCGAGCGCGGCTTGCTCGCTCACTCAAGCATCCGCTCTCCGAC 530
Db      41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValAlaAsp 60
Qy      531 AACTTGGCGGTGGCCATCAAAACAGTGGAGAGAGAGCCGATTTCCGATGGGAGAGCTG 590
Db      61 AsnLeuProValAlaIleTyrHisValGlnTyrAspArgTyrIleSerAspTrpGlyGlnLeu 80
Qy      591 CCTAATGCACTCGAGTGGCCATGAGGAGTGTCTCTGCTGTAAGAAGAGTGGAGCTCGGGTTTC 650
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Qy      651 TCCGGCTCATTAAGCTCTCGAAGTGTGAGAGGCCGACGATTTGCTGTGATCTCTG 710
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Db      101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120
Qy      711 GAGAGGCCCGACCGGTGGAAGAATCTTTCGACTTCATCAAGGAAGGGAGACCCCTGCA 770
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Qy      771 GAGGAGTGGCCCGGAGCTTCTTTCGAGAGTGTGTGAGGCCGTGCGGCACTGCGCAAC 830
Db      141 GluGluLeuAlaIaArgSerPhePheTrpGlnValLeuGlnValAlaArgHisCysHisAsn 160
Qy      831 TCGGGGGTCTACACCCGCAATCAAGACGAAACATCTTATGACTCAATGCGGCG 890
Db      161 CysGlyValLeuHisIleArgAspIleTyrAspGluAsnIleLeuIleAspLeuAsnArgGly 180
Qy      891 GAGCTCAAGSTCATGACTCGGATCGGGGGGCGCTGCTCAAGACACCGTCTACACGAC 950
Db      181 GluLeuTyrLeuIleAspPheGlySerGlyAlaLeuLeuTyrAspThrValTyrThrAsp 200
Qy      951 TTCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATGCTACATGGC 1010
Db      201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
Qy      1011 AGGTGGCGGGCACTGTGTCCTCGGGGATCTCTGTATATATGTTGTGTGAGATATT 1070
Db      221 ArgSerAlaIaIaValTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
Qy      1071 CCTTGCAGCATGACGAAGATCATCAAGGGGCGAGGTTTCTTCCAGSCAGAGGTTCTCT 1130
Db      241 ProPheGluHisAspGluGluIleValTyrGlyGlnValTyrPheArgGlnArgValSer 260
Qy      1131 TCAGATGTGACGATCTCATTTAATGTGCTTGGCCCTGAGACCATCAATAGAGCCAAACC 1190
Db      261 SerGluCysGlnHisLeuIleArgTyrCysLeuSerLeuAspArgProSerAspArgProSer 280
Qy      1191 TTCGAAGAATCCAGAACCATCATCATGAGATGCAAGATGTTCTCTGCGCCCGCAAGACTGCT 1250
Db      281 PheGluGluIleGlnHisAspHisProTrpMetGlnAspValLeuLeuProGlnAlaThrAla 300
Qy      1251 GAGATCCACTCCACAGCCTGTGCGCGGGGCCAGCAAA 1289
Db      301 GluIleHisLeuHisSerLeuSerProSerProSerTyr 313

RESULT 10
US-09-644-450-8
; Sequence 8, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-644-450-8

Alignment Scores:
Pred. No.: 1,4e-114 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 34.16% Indels: 0
Gaps: 0

US-10-705-757-1 (1-2623) x US-09-644-450-8 (1-313)
Qy      351 ATGCTCTTGTCCAAATCAACTCGCTTGCCCACTGGCGCGCGCCCTTCGACGACTTG 410
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; AUTHORS: Hunter, T.
; TITLE: The protein kinase family
; JOURNAL: Science
; VOLUME: 241
; PAGES: 42-52
; DATE: 1988
US-07-857-224B-41

Alignment Scores:
Pred. No.: 3,93e-89 Length: 257
Score: 1296.50 Matches: 242
Percent Similarity: 97.67% Conservative: 9
Best Local Similarity: 94.16% Mismatches: 3
Query Match: 27.07% Indels: 3
DB: Gaps: 2

US-10-705-757-1 (1-2623) x US-07-857-224B-41 (1-257)

QY 456 TCGCAGTACGAGGTGGGCGCGCTACTGAGGAGCGGCGCTTCGGCTGCTACTCAGGC 515
D 1 SerGlnArgIlnValIGlyProLeuLeuGlySerGlyGlyPheGlySerValTYrSerGly 20
QY 516 ATCCGCGCTCTCCGACAACTTGCCGCGTGCCTCAACAACGCTGAGAGAACCGGATTTC 575
D 21 IleArgValAlaApeApeApeProValAlaIleYehIleValIGluYbaApeArgIleSer 40
QY 576 GACTGGGGGAGAGCTGCTTAATGGCACTGAGTGCCTCCATGGAAGTGTCTGCTGAGAGAG 635
D 41 ApeTPRplYglu-----AamGlyThrArgValProMetGluValIleuLeuYLeY 58
QY 636 GTAGAGCTCGGGGTTTCTCGGGGATTAAGGCTCTGAGTCTGAGTCTGAGGCGCGAGAT 695
D 59 ValSerSerApePheSerGlyValIleArgLeuLeuApeTPRpneGluArgProApeSer 78
QY 696 TTCGCTCTGATCTCTGAGAGAGCGCGGAGCGGAGGATCTTTCGACTTCATCAAGAA 755
D 79 PheValLeuIleLeuGlnArgProGluProValGlnApePheApePheIleThGln 98
QY 756 AGGGAGAGCCCTGCAGAGAGAGCTGGCCCGCAGCTTCTTGGCAGAGTGTGAGAGCCGT 815
D 99 ArgGlyAlaLeuGlnGluApeLeuAlaArgGlyPhePheTPRglnValIleuGlnAlaVal 118
QY 816 CGGACAGTGCACAACTGCGGGGCTACACCGGAGCATCAAGAGCGAAACATCTTATC 875
D 119 ArgHisGlyYehIleApeNcyGlyValLeuHisArgApeIleYbaApeGlnApeIleLeuIle 138
QY 876 GACCTCAATCGCGCGAGCTCAAGCTCATGACTTCGGGTCGGGAGCGCTCAAGAG 935
D 139 ApeLeuSerArgIlyGluIleYbaLeuIleApePheGlySerGlyAlaLeuLeuYbaP 158
QY 936 ACCGTTACACGGAATTGATGGGACCGGAGTGTATAGCCCTTCAGAGTGAATCCGCTAC 995
D 159 ThrValTYrThrApePheApeArgIlyThrArgValTYrSerProProGluTYrIleArgTYr 178
QY 996 CATCGGACATGAGGAGAGTGGGCGGAGCTGCTGGCTCGGGAGATCCGCTGATGAATG 1055
D 179 HisArgTYrHisGlyArgSerAlaAlaValTYrSerLeuGlyIleLeuLeuTYrApeMet 198
QY 1056 GTGTGTGAGATATTCCTTTC---GAGCATGACGAAAGATCATCAGGGCGAGGTTTTC 1112
D 199 ValCYseGlyApeIleProPheApeArgIlnHisApeGlnGluIleIleYbaGlyGlnValPhe 218
QY 1113 TTGAGGAGAGGGTCTTTCAAAATGTCAAGATCTCATTAAGATGTGCTTGGCCCTGAGA 1172
D 219 PheArgGlnThrValSerSerGlyCYseGlnHisLeuIleYbaTYrCYbaSerLeuArg 238
QY 1173 CGATCGATGAGGCGCACTTCGAAGAAATCCAAAGATCCATGATGATGCA 1223
D 239 ProSerApeArgProSerPheGlnGluIleArgHisHisProTPRmetGln 255

RESULT 14
US-09-237-543-5
; Sequence 5, Application US/09237543A
```

```

; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-237-543-5

Alignment Scores:
Pred. No.: 5,21e-78 Length: 455
Score: 1149.50 Matches: 240
Percent Similarity: 66.59% Conservative: 37
Best Local Similarity: 57.69% Mismatches: 66
Query Match: 24.00% Indels: 73
DB: Gaps: 10

US-10-705-757-1 (1-2623) x US-09-237-543-5 (1-455)

QY 43 CGGCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 91
D 58 ProArgGlyGluAlaAlaGlyAlaCYs-GluProLeuGlyGlnLeuProSerThrglyPh 77
QY 92 ----GGGCGCTTCGACAGAGAGCCCAAGAGCGGCTTACCCCGCTTCTAGCCCTGCGCC 147
D 77 earGlnAlaAlaThrglyGlnLeuArgAlaAlaAlaProLeu-----SerAlaAr 94
QY 148 ACCCGCTGGC-----GCGCTCCGCGCC 171
D 94 gProArgGlyAlaArgArgAlaValCYseGlyGlnGluApeArgProProAla 114
QY 172 CAGTCCCGGAGGCGCTCAAGTGTCTCGAGTCTCGGCTTCGCGCAGCAGCA 231
D 114 erValProApeArgIlySerGlu----- 120
QY 232 CAGCCGACGACCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 291
D 121 -----AlaAlaProHisAlaArgProProAla----- 129
QY 292 GTCGCGGCTCTGCGGAGCTCTTGCACGTCCTGCGCGCAGCATTCGAGGTTGA 351
D 130 -----M 130
QY 352 TGGCTTTGTCAAATCAATCGCTTGGCCACCTGCGCGCGCGCC-----TGCAACG 405
D 130 erLeuLeuSerLYsPheGlySerLeuAlaHisIleu---CYseGlyProGlyGlyValApeH 149
QY 406 ACTGCAACGCCACCAAGCTGGCGCGCGGAG---GAGAAAGAGCCCTCGAATCCGAGT 462
D 149 IseLeuProValIlyYsIleLeuGlnProAlaIlybaIlybaPysGlySerPheGluLYbaVal 169
QY 463 ACCAGGTGGGCGCGCTACTGAGGAGGCGGCTTCGGCTCGGCTCAAGGATCGCGG 522
D 169 YrGlnValGlyAlaValIleGlySerGlyGlyPheIlyThrValTYrAlaGlySerArgTY 189
QY 523 TTCGCGACAACTTGGCGGCGCATCAACACGTGAGAGAGACCGGATTTTCGACTGG 582
D 189 IeAlaApeGlyLeuProValAlaValIlyHisIleValIlybaIlybaArgValThrgluTYr 209
QY 583 GAGAGCTGCTTAATGCACTCGAGTCCCATGGAATGTGCTGCTGGAAGAGT----- 638
D 209 IlySerLeu---GlyIlyMetAlaValProLeuGluValIleuLeuArybaGlyValGlyA 228
QY 639 --AGTCTCGGGTTTCTCGGCGCTCATTAAGCTCTGAGTCTGAGAGCGCGACAGTT 696
D 228 IAlaIlyGlyAlaArgGlyValIleArgLeuLeuApeTPRpneGlnArgProApeGlyP 248
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[illegible][illegible]

OY 1177 CAGATAGGCCAACCTTCGAGAAATCCAGAACATCCATGSGATG 1220
|:::|||||:::|
Db 408 exgiuArGProSerleuHepGiniIeAlaAlaH1sProIIPMet 422

Search completed: September 22, 2005, 17:24:27
Job time : 87.9838 sec8

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 16:17:56 ; Search time 85.9602 Seconds
(without alignments)
5871.937 Million cell updates/sec

Title: US-10-705-757-1

Perfect score: 4789
Sequence: 1 gagagagccgagagagc.....aataaaacccttgcttc 2623

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=pir -OPMT=faetan -SUFFIX=n2p.rpr -MIMATCH=0.1 -LOOPT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdt -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pro -NOR=ext -HEAPSIZES=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10705757_@CGN_1_1_256_@runat_22092005_115015_22141 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DEPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

pir_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1670	34.9	313	1 TVHUP1	protein kinase (BC
2	1636	34.2	313	1 S26298	protein kinase (BC
3	1582	33.0	313	1 TVMSP1	protein kinase (BC
4	918	19.2	370	1 S55333	protein kinase p1m
5	620	12.9	363	2 T22255	hypothetical prote
6	486	10.1	409	2 T15435	hypothetical prote
7	402	8.4	1398	2 T13741	hypothetical prote
8	397.5	8.3	481	2 I49072	protein kinase - m
9	385.5	8.0	512	1 JCI446	serine/threonine-s
10	378	7.9	504	2 T10449	probable serine/th
11	376	7.9	1101	2 S66730	hypothetical prote
12	373	7.8	1192	2 T18611	probable serine/th
13	369.5	7.7	512	2 T07788	probable serine/th
14	367	7.7	1358	2 S33653	probable serine/th

15	366.5	7.7	512	2 T52633	serine/threonine-s
16	364.5	7.6	511	1 A56009	serine/threonine-s
17	362.5	7.6	651	2 S52244	p69B3 protein - A
18	361	7.5	798	2 UC7500	gik protein - chic
19	348.5	7.3	887	2 T20941	hypothetical prote
20	348	7.3	469	2 B84644	probable protein k
21	348	7.3	472	2 B90100	SNF-related kinase
22	345	7.2	726	2 T33998	hypothetical prote
23	343.5	7.2	414	2 UN0323	Ca2+/calmodulin-de
24	342.5	7.2	489	2 T04862	probable serine/th
25	342.5	7.2	527	2 A53467	protein kinase SNF
26	342.5	7.2	1558	2 T29253	hypothetical prote
27	342	7.1	639	1 T02784	calcium-dependent
28	341	7.1	502	1 T02306	probable protein k
29	341	7.1	513	1 S60304	serine/threonine-s
30	340.5	7.1	1518	2 S37928	probable purine nu
31	340	7.1	745	2 G01025	serine/threonine p
32	339.5	7.1	504	2 T07415	probable serine/th
33	337.5	7.0	520	2 G86414	probable protein k
34	337	7.0	713	2 S27866	probable serine/th
35	336.5	7.0	445	2 T50802	serine/threonine p
36	336.5	7.0	891	2 A38903	protein kinase I -
37	336.5	7.0	891	2 T40503	calcium-dependent
38	332.5	6.9	553	1 T02139	calcium-dependent
39	331.5	6.9	513	1 S60303	serine/threonine-s
40	331.5	6.9	529	1 S71774	calcium-dependent
41	331.5	6.9	540	1 T01989	probable calcium-d
42	331.5	6.9	582	2 B84721	probable serine/th
43	331.5	6.9	774	2 I48609	probable protein k
44	331	6.9	435	2 E84707	serine/threonine-s
45	330.5	6.9	339	2 S56719	

ALIGNMENTS

RESULT 1

TVHUP1 protein kinase (BC 2.7.1.37) p1m-1 - human

N/Alternate names: kinase-related transforming protein p1m-1; p1m-1 proto-oncogene prot C/Species: Homo sapiens (man)

C/Date: 31-Mar-1989 #sequence revision 07-Oct-1994 #ext_change 09-Jul-2004 A/Accession: J00327; A46554; A27476; I58412

R/Reeves, R.; Spies, G.A.; Klefer, M.; Barr, P.J.; Power, M.

Gene 90, 303-307, 1990 A/Title: Primary structure of the putative human oncogene, p1m-1.

A/Reference number: J00327; MUID:90382681; PMID:2205533

A/Accession: J00327

A/Molecule type: DNA

A/Residues: 1-313 <RES>

A/Cross-references: UNIPROT:P11309; GB:M27903; NID:G189958; PIDN:AAA60090.1; PID:G38702.

R/Weeker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M.

J. Cell. Biochem. 35, 105-112, 1987

A/Title: Cloning and characterization of the human p1m-1 gene: a putative oncogene rela

A/Reference number: A46554; MUID:88115604; PMID:3429489

A/Accession: A46554

A/Molecule type: mRNA

A/Residues: 1-313 <RES>

A/Cross-references: GB:M24779; NID:G1066790; PIDN:AAA81553.1; PID:G1066791

R/Zakut-Houri, R.; Hazum, S.; Givol, D.; Teitelman, A.

Gene 54, 105-111, 1987

A/Title: The cDNA sequence and gene analysis of the human p1m oncogene.

A/Reference number: A27476; MUID:87277423; PMID:3475233

A/Accession: A27476

A/Molecule type: mRNA

A/Residues: 1-14, 'RA', 17-313 <ZAK>

A/Cross-references: GB:M16750; NID:G189956; PIDN:AAA60089.1; PID:G189957

R/Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.

Oncogene Res. 1, 103-112, 1987

A/Title: Comparison of the human and mouse p1m-1 cDNAs: Nucleotide sequence and immunolo

A/Reference number: I58412; MUID:88217305; PMID:3329709

A/Accession: I58412

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

QY 651 TCGGCGCATTTAGGCTCTGGAAGTGGTGGAGAGCCGCAAGATTTCCTGATCTG 710
 Db 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
 QY 711 GAGAGCCCGAGCCGCTGCAAGATCTCTTCAGATTCTACGGAAGAGGAGCCCTGCA 770
 Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 771 GAGAGCTGGCCCGCAGCTTCTTGGAGAGGTGCTGAGAGCCGCTGCGACATGCGCAAC 830
 Db 141 GluGluLeuLeuAlaArgSerPhePheTrpGlnValIleLeuGluAlaValArgHisCysHisAsn 160
 QY 831 TGGGGGGTGGTACACCCCGACATCAAGAGCAAAACAATCTTATCGACCTCAATCGCGG 890
 Db 161 CysGlyValLeuHisAsnArgAspIleLeuAspGluAsnIleLeuIleAspLeuAsnArgGly 180
 QY 891 GAGCTCAAGCTCATCGACTTCGAGGTGCGGGGCGCTGCAAGAGCAACCGTCTACACGAG 950
 Db 181 GluLeuArgLeuLeuIleAspPheGlySerGlyAlaLeuLeuArgAspTrpValTyrThrAsp 200
 QY 951 TTGAGTGGAGCCCGAGTGTATAGCTTCCAGAGTGAATCCGCTACATGCTGACATGAGC 1010
 Db 201 PheAspArgIleThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisArgGly 220
 QY 1011 AGGTGGCGGCGCAGTCTGCTCCCTGGGAGATCTGCTGTATGATATGCTGTGTGAGATATT 1070
 Db 221 ArgSerIleAlaValIleTrpSerLeuGlyIleLeuLeuArgAspMetValCysGlyAspIle 240
 QY 1071 CCTTTCAGAGTACAGAAAGATCATCAAGAGGAGGAGGAGTTTCTTCAGAGAGAGGAGTCT 1130
 Db 241 ProPheGluIleHisAspArgIleGluIleValIleValGlyGlnAlaTyrPheArgGlnArgValSer 260
 QY 1131 TCAGATGTCAAGCATCTCATTTAGATGCTGTGGCCCTGAGACCATCATGATAGGCCAAC 1190
 Db 261 SerGluCysGlnHisIleAspIleArgTyrCysLeuSerLeuArgProSerAspArgProSer 280
 QY 1191 TTGGAAGAATCCAGAACCATTCATGATGATGATGATGATGATGATGATGATGATGATG 1250
 Db 281 PheGluIleValIleGlnAsnHisAspTrpMetGlnAspValIleLeuProGlnAlaThrAla 300
 QY 1251 GAGATCCACCTCCACAGCTGTGCGCGGAGCCGACGAA 1289
 Db 301 GluIleHisIleHisSerLeuSerProSerProSerLys 313

RESULT 3

TWMSPI

protein kinase (EC 2.7.1.37) p1m-1 - mouse

N/Alternate names: kinase-related transforming protein p1m-1; p1m-1 proto-oncogene prote

C/Species: Mus musculus (house mouse)

C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004

C/Accession: A24169

R/Selten, G.; Cuyper, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen, J.;

Cell 46, 603-611, 1986

A/Title: The primary structure of the putative oncogene p1m-1 shows extensive homology w

A/Reference number: A24169; MUID:86272105; PMID:3015420

A/Accession: A24169

A/Molecule type: DNA

A/Reads: 1-313 <SEL>

A/Cross-references: UNIPROT:P06803; GB:M13945; GB:M13946; NID:g20052; PIDN:AAA39930.1;

C/Comment: p1m-1 autophosphorylates at unknown sites.

C/Genetics:

A/Gene: p1m-1

A/Introns: 28/1; 63/3; 80/3; 203/1; 262/1

C/Function:

A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

C/Superfamily: kinase-related transforming protein; protein kinase homology

C/Keyword: ATP; autophosphorylation; phosphotransferase; proto-oncogene; serine/threonin

P/36-220/Domain: protein kinase homology <KIN>

P/44-52/Region: protein kinase ATP-binding motif

P/67/Active site: Lys #status predicted

Alignment Scores:

	Pred. No.:	2,866-60	Length:	313
Score:	1582.00	Matches:	294	
Percent Similarity:	97.12%	Conservative:	10	
Best Local Similarity:	93.93%	Mismatches:	9	
Query Match:	33.03%	Indels:	0	
DB:	1	Gaps:	0	

US-10-705-757-1 (1-2623) x TWMSPI (1-313)

QY 351 ATGCTCTTGTCCAAATCACTGCTTGGCCACCTGCGCGCGCCCTGCAAGACTG 410
 Db 1 MetLeuLeuSerLysIleAsnSerLeuAlaHisIleLeuArgIleArgProCysAsnAspLeu 20
 QY 411 CAGGCCACCAAGCTGGCGCGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
 Db 21 HisAlaThrIleArgLeuAlaProGluIleGluIleGluIleGluIleGluIleGluIleGluIle 40
 QY 471 GAGCCGCTACTGGGCGAGCGCGCGCTTCGCGCTGCTTACTCAGGACATCCGCTCCGAC 530
 Db 41 GlyProLeuLeuGlySerGlyIlePheGlySerValTyrSerGlyIleArgValAlaAsp 60
 QY 531 AACTGCCGCTGCGCATCAACACGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
 Db 61 AsnLeuProValAlaIleLeuHisValGluIleAspArgIleSerAspTrpGluLeu 80
 QY 591 CCTAATGGCACTGAGTCCCATGAGAGAGTCTCTGTAAGAGAGTGAAGTGGCTTTC 650
 Db 81 ProAsnGlyIleThrArgValProMetGluValIleLeuLeuArgValIleSerSerAspPhe 100
 QY 651 TCGGCGCATTTAGGCTCTGCAAGTGGTTCGAGAGGCGCGCAAGTTTCGCTGATCTG 710
 Db 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
 QY 711 GAGAGCCCGAGCCGCTGCAAGATCTTTCATTCATCAACGAAAGGAGGAGCCCTGCA 770
 Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 771 GAGAGACTGGCCCGCAGCTTCTTCTGAGAGTCTGAGAGGCGCGCTGCGACATGCGCAAC 830
 Db 141 GluAspLeuAlaArgIlePhePheTrpGlnValIleGlnAlaValArgHisCysHisAsn 160
 QY 831 TGGGGGGTGGTACACCCCGACATCAAGAGCAAAACATCTTATCGACCTCAATCGCGG 890
 Db 161 CysGlyValLeuHisAsnArgAspIleLeuAspGluAsnIleLeuIleAspLeuAsnArgGly 180
 QY 891 GAGCTCAAGCTCATCGACTTCGAGGTGCGGGGCGCTGCAAGAGCAACCGTCTACACGAG 950
 Db 181 GluIleLeuLeuLeuIleAspPheGlySerGlyAlaLeuLeuArgAspTrpValTyrThrAsp 200
 QY 951 TTGATGGAGCCCGAGTGTATAGCTTCCAGAGTGAATCCGCTACATGCTGACATGAGC 1010
 Db 201 PheAspArgIleThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisArgGly 220
 QY 1011 AGGTGGCGGCGCAGTCTGCTCCCTGGGAGATCTGCTGTATGATGATGATGATGATGATG 1070
 Db 221 ArgSerIleAlaValIleTrpSerLeuGlyIleLeuLeuArgAspMetValCysGlyAspIle 240
 QY 1071 CCTTTCAGAGTACAGAAAGATCATCAAGAGGAGGAGGAGTTTCTTCAGAGAGAGGAGTCT 1130
 Db 241 ProPheGluIleHisAspArgIleGluIleValIleValGlyGlnAlaPheArgGlnArgValSer 260
 QY 1131 TCAGATGTCAAGCATCTCATTTAGATGCTGTGGCCCTGAGACCATCATGATAGGCCAAC 1190
 Db 261 SerGluCysGlnHisIleAspIleArgTyrCysLeuSerLeuArgProSerAspArgProSer 280
 QY 1191 TTGGAAGAATCCAGAACCATTCATGATGATGATGATGATGATGATGATGATGATGATG 1250
 Db 281 PheGluIleValIleGlnAsnHisAspTrpMetGlnAspValIleLeuProGlnAlaThrAlaSer 300
 QY 1251 GAGATCCACCTCCACAGCTGTGCGCGGAGCCGACGAA 1289
 Db 301 GluIleHisIleHisSerLeuSerProGlySerSerLys 313

RESULT 4

S55333

protein kinase pim-2 (EC 2.7.1.-) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 10-Oct-1995 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004

C/Accession: S55333; A43093

R/van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; van der Gulden, H.; Allen

EMBO J. 14, 2536-2544, 1995

A/Title: Proviral tagging in E-mu-myc transgenic mice lacking the Pim-1 proto-oncogene 1

A/Reference number: S55333; MUID:95300786; PMID:7781606

A/Accession: S55333

A/Molecule type: mRNA

A/Residues: 1-370 <VAN>

A/Cross-references: UNIPROT:Q62070; GB:L41495; NID:g765065; PIDN:AAA98922.1; PID:g765066

A/Note: 40K form

A/Accession: A43093

A/Molecule type: mRNA

A/Residues: 'M', 27-370 <VA>

A/Cross-references: GB:L41495; NID:g765065; PIDN:AAA98924.1; PID:g765068

A/Note: 37K form

A/Accession: B43093

A/Molecule type: mRNA

A/Residues: 'W', 61-370 <VA>

A/Cross-references: GB:L41495; NID:g765065; PIDN:AAA98924.1; PID:g765068

C/Comment: Pim-2 autophosphorylates at unknown sites.

C/Genetics:

A/Gene: Pim-2

A/Map position: X

A/Start codon: CTG

A/Note: locus between A-raf and Act-7, near Kv4.1

C/Function:

A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

C/Superfamily: kinase-related transforming protein kinase homology

C/Keywords: alternative initiator; ATP; autophosphorylation; phosphoprotein; phosphotra

F/89-345/Boman: protein kinase homology <KIN>

F/97-105/Region: protein kinase ATP-binding motif

F/120/Active site: Lys #status predicted

Alignment Scores:

Pred. No.:	3,896-32	Length:	370
Score:	918.00	Matches:	195
Percent Similarity:	62.44%	Conservative:	51
Best Local Similarity:	49.49%	Mismatches:	104
Query Match:	19.17%	Indels:	44
DB:	1	Gaps:	9

US-10-705-757-1 (1-2623) x S55333 (1-370)

```

QY 153 GGTGGGCGGCTCCCGCGAGTCCCGGCA-----GCGCTCAGTTGTCCTCCGACTCG 206
DB 15 AlSerGlyProProAspSerLeuProSerThrLeuAlaProPro--SerProGlySer 33
QY 207 CCCTCGGCTTCGCGAGCGACGACGCGCGACGCGACGCGACGACGACGACGACGCC 266
DB 34 ProAlaAlaLeuProAlaSerThr----- 42
QY 267 CAGGATAGCTTGGGCGACGACCGCGCTCCGCTCTGGCGAGCTCC-----TCTGGC 320
DB 43 -----ProGlyLeuSerGlyPheSerGly 51
QY 321 ACCTCCGCGCGACATTCGAGGTGAGTCTTTCGCAAAATCACTGCTTGC 380
DB 52 LeuAsnIleArgSerThrSerSer-----MetLeuThrIys----- 63
QY 381 CACCTGGCGCGCGCGCTTCGACGACGACGCGACGCGACGCGCGCGCGCGCAAGAG 440
DB 64 ProLeuGlnIleHisProSerProProAlaThrProThrGlnProProGlyIleAsp 83
QY 441 AAGAGGCCCTGAGTGCAGTACGAGTGGGCGCGCTTACTGGGCGACGCGCGCTTCGCG 500
DB 84 ArgAlaAlaPheGlnAlaGlnIleArgLeuGlyProLeuLeuGlyIleGlyIlePheGly 103

```

QY 501 TCGGTCTACTCAGGATCCGCTCTCCGCAACTTGCAGTCCGAGTCCATCAACAGTGGAG 560

DB 104 ThrValPheAlaGlyHisArgValThrAspArgGlnValAlaIleLeuValIleSer 123

QY 561 AAGACCGGATTTCCGACTGGGAGAGCTGCTTAATGGCATTCGAGTCCATGGAAGTG 620

DB 124 ArgAsnArgValLeuGlyIleThrSerThrAlaSerAspSerValThrCysProLeuGlnVal 143

QY 621 GTTCGCTGCAAGAAGTG-----AGCTCGGTTTCTCCGGGTATTAAGTCCCTGGAC 674

DB 144 AlaLeuLeuTrpIleValGlyGlnValGlnIleAspProGlyValIleArgLeuLeuAsp 163

QY 675 TGGTTGAGAGGCGCGACGTTTCGCTCGATCTCGAGAGGCGCGGCGGTGCAAGAT 734

DB 164 TrpPheGlnThrProGlnGlyPheMetLeuValLeuGlnIleArgProMetProAlaGlnAsp 183

QY 735 CTCTTGACTTCATCACGGAAGGAGCGCTTCGCAAGAGAGCTGGCCCGCAGCTTCTTC 794

DB 184 LeuPheAspTrpIleThrGlnIleGlyProLeuGlyIleSerCysSerArgSerPhePhe 203

QY 795 TGGCAGGTGCTGAGAGCGCGTGGCGACTGCGCAACTGCGGGGTGCTACACCGGACATC 854

DB 204 ThrGlnValValAlaAlaValGlnHisCysHisAlaArgGlyValAlaHisArgAspIle 223

QY 855 AAGACGAAACATCTTATCGACCTTCATTCGCGCGAGCTCAAGCTCATTCGACTTCGGG 914

DB 224 LysAspGlnAlaIleLeuIleAspLeuGlySerArgGlySerIleLeuLeuIleAspPheGly 243

QY 915 TCGGGGCGCTGCTCAAGGACCGCTTCACAGCACTTCGAGTGGGACCGGAGTGTATAC 974

DB 244 SerGlyAlaLeuLeuHisAspIleProIleProIleThrAspPheAspGlyThrArgValIleSer 263

QY 975 CCTTCAGGTGATTCGCTACCATCGCTTACATGAGAGTCCGCGGCGAGTCTGCTCCG 1034

DB 264 ProProGlnIleTrpIleSerArgHisGlnIleHisAlaLeuProAlaThrValIlePheSerLeu 283

QY 1035 GGGATCTGCTGATATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1094

DB 284 GlyValLeuLeuIleValAspMetValCysGlyAspIleProPheGlnIleArgAspGlnIle 303

QY 1095 ATCAGGGGCGAGTTTCTTCAGGCGAGGAGGCTCTTCAGATATGCATCTCATTTAA 1154

DB 304 LeuGlnAlaGlnLeuHisPheProAlaHisValIleSerProAspCysGlyAlaLeuIleArg 323

QY 1155 TGGTGTGGCGCTGACATCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 1214

DB 324 ArgCysLeuAlaProIleProIleProIleProIleProIleProIleProIleProIlePro 343

QY 1215 TGGATGCAAGATGTTCTCTGCGCGCGAGAACTGTCGATGATGATGATGATGATGATGATG 1274

DB 344 TrpMetGlnSer-----ProAlaGlnIleValProIleAsnSerSerIleGlySer 360

QY 1275 CCGGGGCCGCAAAATAGCAGCTTTCGCGAGGCTCTCC 1316

DB 361 ProThrProLeuPro-----TrpSerLeuLeuPro 370

RESULT 5

T22255

hypothetical protein F45H7.4 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T22255

R/Pericy, C.

submitted to the EMBL Data Library, June 1994

A/Reference number: Z19538

A/Accession: T22255

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-363 <WIL>

A/Cross-references: UNIPROT:Q20443; EMBL:Z34800; PIDN:CAA84323.1; GSPDB:GN00021; CBSP:F

A/Experimental source: clone F45H7

C/Genetics:

A/Gene: CBSP.F45H7.4

Db 175 thr|gylvalval|yleuval|a|sphe|gyl|a|thr|a|a|tyr|a|a|a|u|a|a|u|a|a|a|thr|y|s 194

Gy 945 ACGAGCTTCGATGGAGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTAC 100

Db 195 LysGIuPhe|ng|In|y|Thr|Arg|Ser|y|y|Cys|Pro|Pro|Glu|u|Tr|Phe|Arg|Asp|In|eu|y|z 214

Gy 1005 CATGGCAGGTCGGCGGACATCTGTGCTCCGCGGATCCTCTGTATATATGAGTGTGGA 106

Db 215 Leu|Pro|Leu|Glu|u|a|Thr|Ser|Trp|Ser|Leu|u|Gly|Val|Leu|Leu|Phe|I|le|u|eu|Thr|Gly 234

Gy 1065 GATATTCCTTCCTGGAGCATACCAAGATATCATGAGGGCCAGGTTTCTTCAGGCAAGAG 112

Db 235 LysLeu|Pro|Phe|Arg|Asp|In|u|I|e|G|In|I|e|Cys|Leu|Gly|Asn|Val|y|s|Phe|Pro|Asp 254

Gy 1125 GTCTCTTCGATGTCCAGCATCTTCATTAAGTGGCTTGACCCCTGAGACCATCAGATAG 118

Db 255 Leu|Ser|y|g|l|u|a|l|Cys|e|In|eu|Val|y|s|er|Cys|Leu|Thr|Thr|Ser|Thr|Ser|a|a|g 274

Gy 1185 CCAACCTTCGAAGAAATCCAGAACCATTCATGATGCA 1223

Db 275 Ala|Ser|Leu|a|g|In|I|e|a|a|a|a|a|a|s|P|ro|Trp|Met|Glu 287

RESULT 7

hypothetical protein 22E5.8 - fruit fly (*Drosophila melanogaster*)
C|Species: *Drosophila melanogaster*
C|Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C|Accession: F13741
R|Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
A|Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.
A|Reference number: Z17668
A|Accession: F13741
A|Status: preliminary; translated from GR/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 1-1398 <MOR>
A|Cross-references: UNIPROT:O77268; EMBL:AL031765; NID:e1371523; PID:e1329905; PIDN:CAA
C|Genetic8:
A|Cross-references: FLYBase:FBgn0000667
A|Introns: 205/3, 227/1, 322/3, 688/3, 782/3, 814/2, 1363/3
A|Note: EG:22E5.8

Alignment Scores:

Pred. No.:	2,266-10	length:	1398
Score:	402.00	Matches:	123
Percent Similarity:	43.82%	Conservative:	72
Best Local Similarity:	27.64%	Mismatches:	154
Query Match:	8.39%	Indels:	96
DB:	2	Gaps:	17

US-10-705-757-1 (1-2623) x T13741 (1-1398)

```

QY 27 AGCGGCGGCGGCGGAGCCGGGACAGCAGCAGCAGCAGCAGCAACCACTGAGCTCT 86
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 7 AIAAIAAIAAGIAGIuAnslYserGIuAlALysSerGIuGIuSerGIu-----Pro 24
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 87 GCCCGCGCGCTGTGCAGCAGCC---CAAGAG----- 116
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 25 GIuAerGIuInLyLeYserGIuProGIuInHIGIuAAGAnGIuLeYserGIuLeuAerLy 44
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 117 CGGCTACACCCCGCGCTTCACAGCGCTGCCGACCCCGCTGGCGCG----- 161
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 45 ProGIuAenLeuProGIuAnslYserGIuInHIGIuAlALysGIuAlAGIuGIuALaCySer 64
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 162 ---CCCTCCC-----GCCGCACTGCCG 179
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 65 HIsProProLeuAerAlaLeuArGserSerValLeuLeuAerAlaGIuAlAlaIAserPro 84
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 180 GGAGGGCCCTCAATTGCTCTCCCACTGGCCCTGGGCTTGCGCGAGCGCAGCAGCCGCA 239
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 85 SerIleAerAlaIleValaIaCyuLyAerAlaLeuLeuAlaGIuInLyAerPheAlaSer 104
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 240 CGCAGCGCGCAGCAGCAGCAGCAGCCCGCAGGCACTTTCGCGACAGCCCGGCTCCGC 299

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Db	105	-----		107
Qy	300	TCCTGGGAGACTCTCTTGGACAGCTCCCTGGGCGACATTTCTGAGGTTGGATGCTCTTG		359
Db	108	SeTThrProGlyProSerProThSerSerAlaValAlaGlyGly-----		123
Qy	360	TCGAAATCAACTGGCTTGGCCGACCTGGGCGGCGGCGCTGGACAGACCTGGACGCGCAC		419
Db	123	-----		123
Qy	420	AAGCTGGGCGCGGACAGAG-----		464
Db	124	-----		141
Qy	465	CAGGTGGGCGCGGCTTGGGCGAGCGGCGGCTTGGGCTGGT---		521
Db	142	AspIleGluArgThrIleGlyLysValAsnProAlaValValLysLeuAlaArgHisArg		161
Qy	522	GTCTCCGACAACTTGGCCGGGTGCGCTTCAAAACSTGGAGAAAGACCGGATTTCCGACTGG		581
Db	162	IleThrLysValen--GluValAlaIleLysIleIleAspLysSerGlnLeu-----		177
Qy	582	GGAAGAGCTGCTTAATGGCACTGGAGTGGCCCATGAGAGTGGTCTGCTGAAGAGCTGAC		641
Db	178	--AspGlnThrAsnLysLeuGlnLysValLysArgGlnValGlnLysMetLysArgLysLys		196
Qy	642	TCGGGTTCTCCGGGCTATTAGGCTTGGGCTGGGACTGTTCCAGAGGCGCGACGTTTCCGTC		701
Db	197	-----		214
Qy	702	CTGATCTGGAGAGGCGCGGACCGGCTGGACAGATCTTTCGACTTATCAGGAAAGGGA		761
Db	215	IleValSerGlnArgLysArgGln--GlyGlnIlePheAspTyrIleLysLysArgLys		233
Qy	762	GCCCTGCAAGAGAGAGCTGGCCCGGACGTTCTTGGGAGGTCGTCGAGGCGGCTGGGCGAC		821
Db	234	ArgMetSerGlnSerAlaAlaArgPheLysPheTrpGlnIleIleSerAlaValGluArg		253
Qy	822	TGCCCAACTGGGCGGCTGCTACACCGGACATCAACAGAGAAACATCTTATGCACTC		881
Db	254	CysHisLysLysGlyIleValHisArgPheLysLysValGlnLysLeuLysLeuLysLeu		273
Qy	882	AATCGCGGCGAGCTAAGCTCATGACTTTCGGG--TCGGGCGGCGCTGCTCAAGGACCC		938
Db	274	AsnMet--AsnIleLysIleLysArgPheGlyPheSerAsnHisPheLysArgGln		292
Qy	939	GTTCTACAGCACTTGGAGTGGGCGCGGAGTGTATGACCCCTCCGAGGTGATCCGCTACAT		998
Db	293	LeuLeuAlaThrTrpCysLysSerProProTyrAlaAlaProGluValPheGluGlyLys		312
Qy	999	CGTACACATGGCAGGTCGCGGCGAGCTGGTCCCTGGGAGATCCTGCTATGATATGTCG		1055
Db	313	GlnTyrThrGlyProGlnIleAspIleTrpSerLeuGlnValValLeuLysValLeuVal		332
Qy	1059	TGTGGAGATATTCCTTTCGAGATAC-----		1100
Db	333	CysGlyAlaLeuProPheAspGlySerThrLeuGlnSerLeuLysArgAspArgValLeuSer		352
Qy	1101	GCGCCAGTTTCTTCAGGCGAGAGGCTCTTTCAGAAATGCAAGATCTCATTAAGTGGTC		116
Db	353	GlyArgPheArgGlyIleProPhePheMetSerSerGlyCysGlnHisLeuIleArgGlyMet		372
Qy	1161	TTGGCCCTGAGACCATCAAGATAGGCGAACCTTTCGAAAGAAATCCAGAACCATCATGAGATG		122
Db	373	LeuValIleGluProThrArgArgGlyThrHisAspGlnIleLysArgHisArgTrpMet		392
Qy	1221	CAAGATGTTCTCTG 1235		
Db	393	CysProGlnLeuLeu 397		

protein kinase - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C.Accession: I49072
R.Rutz, J.C.; Conlon, F.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A.Title: Identification of novel protein kinases expressed in the myocardium of the deve
A.Reference number: I49071; MUID:95200798; PMID:7893599
A.Accession: I49072
A.Status: preliminary; translated from GB/EMBL/DBD
A.Molecule type: mRNA
A.Residues: 1-481 <RES>
A.Cross-references: EMBL:U1494; NID:G595420; PIDD:AAA67926.1; PID:G595421
C.Superfamily: protein kinase homology
C.Keywords: ATP
P:71-324/Domain: protein kinase homology <KIN>
F:79-87/Region: protein kinase ATP-binding motif

Alignment Scores:

Pred. No.:	4,29e-10	Length:	481
Score:	397.50	Matches:	79
Percent Similarity:	42.17%	Conservative:	79
Best Local Similarity:	26.89%	Mismatches:	166
Query Match:	8.30%	Indels:	113
DB:	2	Gaps:	21

US-10-705-757-1 (1-2623) X I49072 (1-481)

OY GCTGGAGCGGCTCCGCCGCAGTCCGGAGAAGGCGCATTGGTCGTCCACTGCCCTCG 212
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd AATARGAATAAAAlalaaaleuaalaaaalaglythrallaglythrglyValglu 24
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 213 GCCTTGCGACGGCACCAAGCCGACCACCGAGACAAGAACAGCACAGCCCAGSca 272
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd LeuuhaalaagluthrghlaVaLaLaseArVgAl ----- 35
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 273 TAGCTTGGACAGACCCCCGCGCTCCGCGCTCGCGSAGCTccttgcgaactccctcgcc 332
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 36 ----- glySerArgArgALaAgLuVALArg 44
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 333 CGAcAttCTGAAGTTGaTgAtGCTCTgtCCAATATCATCTGCATGCCACCTGCGAGCc 392
::: |::| :::::: |::| :::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 45 ProGluala-----MetvalIle-----MetSerGIuPharAla 56
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 393 GCGCGCTGCAGACGActGCACCGCACAGCTGCGCGCCGCGAMAGAMAAGAccCTG 452
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 57 ValProser-----glyThrGLYARgsErInLyProuLeu 68
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 453 GAG---TCGAGATACCaGeTggScCGGCTTAChTGGCACGGCGGTTGGCTCGCTC-- 506
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 69 ArgValGIyPherYArPaVLGuArThrlEugLYlYGlyAsnPhaalavaVallys 88
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 507 TACTCAGGCATCCGCGCTCCCGACAATTGCCGSGTGCATCAAACAGTAGMAAGAC 566
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 89 LeuarGslYIArGalrhrr---lysrHrnValAIAlIElylleILeApLyThr 107
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 567 CCGATTTCCGACTGGGAGAGCTGCTTAATGCATCGAGTrGCCATGAAAGTGrCTG 626
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 108 ArGLEu-----APseSeRsaenLEUGluYLIEtyrArgLUvaIGlnLeu 123
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 627 CTGAAGAAGTGAGCTCGGGTTTTCTCGCGCGTCAATTagCTGCTGGAAGCTGGTGCAGAGG 686
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 124 MetGylaeuleuan----HisPrOanIIellIElybYeurygrINvaimetGIUthr 141
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 687 CCCGACAGTTTCGTCTGATCTCGAGAGGCCGAGCCGGTGCAGATCTTGCACTTC 746
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 142 LysAprMetLeutyriLeeValThnrGIUPheALIayAsn---GLyGIUmEtPhEAstyr 160
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 747 ATCAcGSAAGGGGAGCGCTGCAGAGAGAGCTGSCGCCAGCTTCTTCTGCSAGSTCG 806
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 161 LeutHiserAnoGIyHIleuseSERGIUAENGluLAhgLIuLYbPhETPgIlmIElu 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 807 GAAGCCGTGGGCACTGCCACAATCGGGGTGTCAACCGGACATTCAGAGAAAAC 866
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 SerIaValaIGluTrCysHisAsnHisHisIleValHisArgAspLeuLysThrGluAsn 200
QY ATCTTTATGCACTCAATCGCGGAGCTCAAGCTCACTTCAGCTTCGGGTGGGGCGCTG 926
Db 201 LeuLeuLeuAspSerAsnMet--AspIleValLeuAlaAspPheGlyPheGlyAsnPhe 219
QY CTCAG--GACACCGCTACACGAGACTTCGATGGACCCGAGGTATAGCCCTCCAG 983
Db 220 TyrIysProGlyGluProLeuSerThrCysValGlySerProProTyrAlaAlaProGlu 239
QY TGGATCCGCTACATCGCTACATGAGGACGCGGAGCTGGCTGCTCCGGGATCGTG 1043
Db 240 ValPheGluGlyLysGluTyrGluGlyProGluLeuAspValIlePheSerLeuGlyVal 259
QY CTGTATGATATATGTTGTGAGATATTTCTTTCAGCATGAC-- 1085
Db 260 LeuTyrValLeuValCysGlySerLeuProPheAspGlyProAsnLeuProThrLeuArg 279
QY GAAGAGATCATCAGGGGCGAGCTTTCTTACGACGAGGCTCTTCAAGATGCACAT 1145
Db 280 GlnArgValLeuGluGlyArgPheArgIleProPhePheMetSerGlnAspCysGluThr 299
QY CTCATTGATGTCGTCCTGAGCCCTGAGACCATCATATGAGCCCACTTCGAAAGATCAG 1205
Db 300 LeuIleArgMetLeuValValAspProAlaLysArgIleThrIleAlaGlnIleArg 319
QY AACCATTCATGAGTCAAA--GATGTTCTCCGCGCCAGAACATCGCTGAGATCCAC 1259
Db 320 GlnHisArgTrpMetGlnAlaAspProThrLeuLeuGlnGlnAspProAlaPheAsp 339
QY CTCACAGCGCTGCGCGGG-- 1280
Db 340 MetGlnGlyTyrThrSerAsnLeuGlyAspTyrAsnGluGlnValLeuGlyIleMetGln 359
QY 1281 -----CCACCAATAGACGCT 1288
Db 360 AlaLeuAlaIleAspArgGlnArgThrIleGluSerLeuGlnAsnSerTyrAsnHis 379
QY TTTCGGAGCGTCCTCCCTCTTGTCAAGATGCGGAGGAGGGAGCTTCGTCTCA 1358
Db 380 PheAlaIleIleTyrTyrLeuLeuGlnArgLeuLysGlnSerAlaGlnPro 399
QY GCTTCCGAGTACAGTACACGCTCTGCGAAGCAGACAGTCTGATACAGAACAC 1418
Db 400 SerSerArg--ProThrProAlaProThrArgLysProGln-----LeuArgSerSer 416
QY 1419 ATTTACATCTATTCACAGATCCAGGCCCTGAGAGCTGCTCTCCCAACAGTGGGAAG 1478
Db 417 AspLeuSerSerLeuGlnValPro-----GlnGlu 426
QY 1479 TGACTCTCCAGGGTCT--AGGCTCAACTCTCCCATAGATACCTCTTCTTCAT 1535
Db 427 IleLeuProCysAspProPheArgProSerLeuLeu----- 438
QY 1536 AGGTGTCCA-----GATTGCTGAGCTCTGAATA 1565
Db 439 ---CysProGlnProGlnAlaLeuAlaGlnSerValLeuGlnAlaGlnIle 454

RESULT 9
JC1446
serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana
N.Alternate names: protein kinase SNF1 homolog
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 30-Sep-1993 #sequence,revision 30-Sep-1993 #text,change 09-Jul-2004
C.Accession: JC1446; S58266; S66334
R.Liequen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
Gene 120, 249-254, 1992
A.Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein
A.Reference number: JC1446; MUID:93013041; PMID:1339373
A.Accession: JC1446
A.Molecule type: DNA
A.Residues: 1-512 <LRG>

A:Cross-references: UNIPROT:Q38997, GB:M93023, NID:gl66599; PIDN:AAA32736.1; PID:gl66600
R:Thummler, F.; Kirchner, M.; Teuber, R.; Ditttrich, P.
Submitted to the EMBL Data Library, May 1995
A:Description: Differential accumulation of the transcripts of 22 novel protein kinase g
A:Reference number: S58256
A:Accession: S58256
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 144-198 <THU>
A:Cross-references: EMBL:X86966, NID:g928909; PIDN:CA60529.1; PID:g928910
Plant Mol. Biol. 29, 551-565, 1995
R:Thummler, F.; Kirchner, M.; Teuber, R.; Ditttrich, P.
A:Title: Differential accumulation of the transcripts of 22 novel protein kinase genes i
A:Reference number: S66314; MUID:96123233; PMID:8534852
A:Accession: S66314
A:Molecule type: DNA
A:Residues: 144-198 <TH2>
A:Cross-references: EMBL:X86966, NID:g928909; PIDN:CA60529.1, PID:g928910
C:Comment: This enzyme plays an important role in a signal transduction cascade regulat
C:Gene(s):
A:Gene: AK1n10; AK21
A:Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F:1-17-271/Domain: protein kinase homology <KIN>
F:25-33/Region: protein kinase ATP-binding motif
F:48,67,142,144/Active site: Lys, Glu, Asp, Lys <status predicted
F:147,151/Binding site: magnesium (Asn, Asp) <status predicted

Alignment Scores:

Pred. No.:	1,37e-09	Length:	512
Score:	385.50	Matches:	138
Percent Similarity:	46.15%	Conservative:	78
Best Local Similarity:	29.49%	Mismatches:	182
Query Match:	8.05%	Indels:	70
DB:	1	Gaps:	19

US-10-705-757-1 (1-2623) x JC1446 (1-512)

```

Oy 425 GGGCCCCGGCAAGAGAAAGAGCCCTTGAGTCCGACAGTACCAAGGTGGGCCCCGATCTAGG 484
Db 7 GlySerAlaArgSerGly-ValGluSerIleLeuProAsnIlyrIysLeuGluGlyArgThrLeuGI 26
Oy 485 CAGCGGCGCGCTTCGGCTCGCTCTACTACAGGATCCGCGCTTCGCAACAATTGCGGGTGGC 544
Db 26 yIleGIySerThrheGIyArGValyIleAlaGluHisAlaLeuThrGIyHisIyValAl 46
Oy 545 CATCAACAACGTGAGAGAGAGACCGGATTTCCGACTGGGAGAGAGCTGCTTAATGGCACTCG 604
Db 46 aIleIySAlleuAsnArGArgLySAlleIyAsn-----MetGIuMetGIuGIuLy 63
Oy 605 AGTGCCCATGGAAGTGTCTCGCTGAGAGAGAGGTAGACTCGGGATTTCTCCGGCGATCATTAG 664
Db 63 eValAlArGArgGluIleIySAlleIyLeuArGLeuPheMet-----HisProHisIleIleAr 81
Oy 665 GCTCTCGAGCTGGTGTGAGAGAGGCCGACAGATTGCTGCTGTATCTGAGAGAGGCCCGAGCC 724
Db 81 GluPtyrGIuValIleGIuThrProThrAspIleTyrLeuValMetGIuTyrValAlaAsn 101
Oy 725 GGTGCAAGATCTCTTCGACTTCATCAGCGAAAGGGAGACCTCGCAAGAGAGAGTGGCCCG 784
Db 101 r--GlyIuLeuPheAspTyrlleValGIuIySAlleIyArGLeuGluGluAspGIuAlaAr 120
Oy 785 CAGCTCTCTTCGGCAGGTGTGAGAGCGCGTGGCGACACTGCACCACTCGGGGTGTCTACA 844
Db 120 GAsnThrheGluGluGluIleIleSerGIyValGIuTyrCyHisAlaArgAsnMetValAlaHis 140
Oy 845 CCGGACATCAAGAGCGAAACAATCTTATGCACTCAATGCGGCGAGCTCAAGCTCAT 904
Db 140 sArGAspLeuIySProGIuAsnIleuLeuAsnSp---SerIyS CyAsnValIySAlleAl 159
Oy 140 sArGAspLeuIySProGIuAsnIleuLeuAsnSp---SerIyS CyAsnValIySAlleAl 159

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QY	CGAATTGGGGGCGGGGGCGGCGGTCAAGACACCGTGTATACACGAGACTTCGAT---	GGGAC	964
Db	159	aaspphegllleuysersanillemeccagaabgdlgnhsphleuylthrserycagllse	179
QY	962	CCGAGTGTATAGCCCTCCAGAGTGGATCCCGCTACATCGCTACCATGGACAGTCCGGCGC	1021
Db	179	rproanttyrlalalaprogluvalilleserdylyleuylrhlaladyprogluvala	199
QY	1022	AGTCTGGTCCCTGGGGATCCTGCTGTATGTATATGCTGTGTGGAGATATTCCTTTCCAGCA	1081
Db	199	pvaltrpsercyagllvalilleuylrhlaleuylcysgllthrxleuprophear--	218
QY	1082	TGACGAAGAGATC-----ATCAGGGGCGACGGTTTTCC--TTACAGCA	1120
Db	219	-aspglusanilleproanleuhyelyvyllelyagllglllylleuylrhlreuprose	238
QY	1121	GAGGCTCTCTTCAGAAATGTACAGATCTCATTTAGATGTGTGTGGCCCTCGAGACATCGA	1180
Db	238	rhlleuyserrprodlgnlalnrgahpelleproahgmetleuvalvalaspprometly	258
QY	1181	TAGGCCAACCTTCGAGAAATCCAGAAACATCCATCCATGGATGCAAGANTTCTCTGCCCCA	1240
Db	258	sargvalthrilleprogluileahglnlshsprotprphgelin--alanhsleuprox	277
QY	1241	GGAATCGTCAGATTCACACTCCACACCTGTGCGGGGCGCCGACCAATAGACGCTTT	1300
Db	277	gtryleuadlaal--proproproaherrthvalglnlmaluylvylle-ahrglu--	295
QY	1301	CTGGCAGGTCCTCCCTCTCTGTTCACATATCCCGAGGAGAGGGAGACTTCTGTCTCCAGC	1360
Db	296	----gluileuadlnlvalilleahmetgilyphasbrghashilleuilegluse	314
QY	1361	TTCCCGAGTACCAAGTACACAGTCTCGCCAAAGACAGACAGCTGGTATACAGAAACAAT	1420
Db	314	rleuahrg-----ashnrgthrglnaanaahrglythrvalthrtyrtyrleuilele	331
QY	1421	TTACAACTCATTCACAGATCCAGGCCCTCGAGGCTGCCCTCCAAACAGTGG--	1472
Db	331	uasppashnrgpheary-----alasersegllytryleuyl	343
QY	1473	-----GAAAGTGAATCTTCACAGGGGTCTAGGCTCAACTCTCCCATGATACT	1522
Db	343	yalgluapheglnlgnlthmetglnlythrproahgmetlshproalaeglusevala	363
QY	1523	CTCTTCT---TTCATAGTGTCCAGCATTCCTGAGACTGMAATATCCGGGGGTGGG	1579
Db	363	aserrprovalserlshnrgleuproglyleuemetglnlygln-----gl	378
QY	1580	GGTGGGGGTGGGCGAAACCTCGCCCAATGGAACCTTTCTTCATATAGATTTCTGTGAAT	1639
Db	378	yvalgilyleuahrgserglntryprovalgln-----	388
QY	1640	GCCGGAAATGGGTCAAGTAAAGGGGGAACAGATTGGATGGGATAGCATATTTA	1699
Db	389	-arglyustrpala-----leagillyleuagln-serahglahls-----	400
QY	1700	AGTCCCTGTCACTCTTCCGACTTTTCTGAAGCTT-----CTGTGGGAGCTCCGCG	1753
Db	401	-----proahglnlilemethrhgluvalleuylvalaleuaglnahpseudhny	417
QY	1754	TGTGCTGGAGAA	1767
Db	417	alcystrpilyelys	421

RESULT 10

probable serine/threonine-specific protein kinase (EC 2.7.1.1) - cucumber
 MAltternate names: SMT1-related protein kinase
 CSpecies: Cucumis sativus (cucumber)
 CDate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 CAccession: J10449
 R.Gumpel, N.J.
 submitted to the EMBL Data Library, December 1996

A/Reference number: 217020
 A/Accession: T10449
 A/Status: preliminary; translated from GB/EMBL/DBD
 A/Molecule type: mRNA
 A/Residues: 1-504 <GM>
 A/Cross-references: UNIPROT:P91113; EMBL:Y10036
 A/Experimental source: cv. Masterpiece; cotyledon
 C/Function:
 A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 C/Superfamily: AMP-activated protein kinase; protein kinase homology
 C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F/6-260/Domain: protein kinase homology <KIN>

Alignment Scores:

Pred. No.:	2.86e-09	Length:	504
Score:	378.00	Matches:	122
Percent Similarity:	47.71%	Conservative:	76
Best Local Similarity:	29.40%	Mismatches:	160
Query Match:	7.89%	Indels:	57
DB:	2	Gaps:	17

US-10-705-757-1 (1-2623) x T10449 (1-504)

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QY 462 TACCAAGTGGAGCCCGCTACTGGAGCGCGCTTCGGCTCGGTACTCAGGCAATCCGC 521
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 8 Tyrlvalencllythrleuglylleglyserpheglyvallyllealaglunle 27

QY 522 GTCTCCGACAACTTGGCGGTGGCCATCAACACGTGAGAGAGACCGGATTTCCAGTGG 581
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 28 Alaleuthrclythleuvalalellelylleleuamharglyllelysban--- 46

QY 582 GGAAGACTGCTTAATGCACTCGATGCCATGAAATGCTCTGCTGAAAGAGAGC 641
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 47 -----Leuamphetclugllyvalargarghullelylleuaglyleuphemet 64

QY 642 TCGGGTTTCTCCGCGCTTCGAGCTTCGAGCGCTTCGAGCGCCGACGTTTCGTC 701
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 -----Hisprohietlelleargleuylrcilualillelunhprosearphletyr 82

QY 702 CTGATCTTGAGAGAGCCCGACCGCGGTGACAGATCTTTCGACTTCATCAGAAAGGGA 761
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 valvalmetclunlyrvallyser---glyluleuphemerylilevaliglygly 101

QY 762 GCCCTCAAGAGAGAGCTCGCCCGCACTTTCTGCGAGTGTCTGAGCGCGTGGGAC 821
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 102 Argleuglnclyluparglualaargamphetheglncilleleserlyvalglutyr 121

QY 822 TGCCACAATCGCGGGGTGTACACCGGACATCAAGAGAGAAACATCTTATCGACCTC 881
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 Cyshleargammetvalvalhshargapneulypbroglylunleuamph--- 140

QY 882 AATCGCGGAGCTCAAGCTCATCGATTCGGGTTCGGGGCGCTGCTCAGACACCGCTC 941
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 141 Serlycyabanvallylserllealeapbheglyleuseramillemetargarglylis 160

QY 942 TACACGCACTTCAT---GGGACCCGAGTATAGCCCTTCAAGTGGATCCGCTACAT 998
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 161 pheleulyrthsercybeglyserproamlyrallalabroglylualilleserglylys 180

QY 999 CGTACCATCGAGAGTTCGGCGGAGTCTGCTCCGCGGAGTCTGCTGATATGATAGAG 1058
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 leuylrhalaglyprogluvalabpvaltrpsercyeglyvalilleuylrallaleuleu 200

QY 1059 TGTGAGATATTCCTTTCGAGATGACGAGAGATC-----ATCAGG 1100
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 201 Cyeglylthleuprophleap---Aspgluamilleproamleuphelyslyllelys 219

QY 1101 GGCACAGTTTC---TTCAAGGAGAGGCTCTTTCAGATGTACGATCTCATTAATGG 1157
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 220 Glyglyllylelyrthleuprosearhaleuserserglylalaarglylunleuprosear 239

QY 1158 TGGTTGGCCCTGAGACATCAGATGAGCCAACTTCGAGAAATTCAGAAACATCATGAG 1217
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 240 Metleuvalalasprometlylserglyllethrilleproglullearglunhispotypr 259

QY 1218 ATGCMAAGATGTTCTCGCCCAAGAACTGCTGAATCCACTCCACAGCTGTGCGCG 1277
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 260 pheglh---Alahislepuproarglyrleuallaval-Propropoasprthmetcglng 278

QY 1278 GGGCCGAGAAATAGACGCTTCTGCGAGCTCCCGCTCCCTGTTGTCAGATCCCGAGG 1337
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 278 Imhalylyllylle-Aspglu-----Aspilleleuglnclyluallyllymetglyphe 295

QY 1338 GAGGGAGAGCTTGTCTGCTCAGCTCCGAGTACAGTACAGCTGTCCGCAAGAGAG 1397
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 296 Aspargargamglneulvalgluserleahg-----Asmhrglleghamgluala 312

QY 1398 AGTCTTGATACAGAAACAACTTACAACTCATTCAGATCCGAGCCCTGAGAGCTG 1457
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 313 Thrvalalatytyrleuleuleuamhargphargval----- 326

QY 1458 CCTCCCAAGATGGG-----GAGAGTGACTCCAGGGT----- 1493
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 327 -----Sersestlytyrleuglyalaglupheglnclylunhmetclunhrglypheasn 344

QY 1494 -----CTTAGGCTCAACTCTCCCATAGATCTCTTCTTCATAGTGTCCA 1544
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 345 Argmethisprosearprothraenpro-----Alavalglysharglyleupro 361

QY 1545 GCATTGCTGACTTCGAA-----ATATCCGGGGGTGG 1577
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 362 Glytyrmetleaspryrclylnclylmetglyleuarglalnphprovalgluarglystpr 381

QY 1578 GGGGTGGGGGTG---GGCAGAACCTCGCCATGGAATC 1613
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 382 Alaleuglyleuglnclylserarglalnphproarglylunle 394

```

RESULT 11

S66730
 hypothetical protein Y0L045W - yeast (Saccharomyces cerevisiae)
 N/Alternate names: hypothetical protein O2034

C/Species: Saccharomyces cerevisiae
 C/Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 16-Aug-2004

C/Accession: S66730
 R/Annotator: W. J. Bensch, V. J. Reckmann, S. J. Schwager, C. J. Teodoru, C. J. Voss, H. J. Wiemann, S

submitted to the Protein Sequence Database, July 1996

A/Reference number: S66723
 A/Accession: S66730
 A/Molecule type: DNA

A/Residues: 1-1101 <ANS>
 A/Cross-references: UNIPROT:Q08217; EMBL:Z74788; NID:G1419846; PIDN:CAA99051.1; PID:e251

A/Experimental source: strain S288C
 C/Genetics:

A/Cross-references: SGD:S0005405
 A/Map position: 15L
 C/Superfamily: protein kinase homology

C/Keywords: ATP
 F/839-1099/Domain: protein kinase homology <KIN>
 F/847-855/Region: protein kinase ATP-binding motif

Alignment Scores:
 Pred. No.: 2.99e-09 Length: 1101
 Score: 376.00 Matches: 87
 Percent Similarity: 54.68% Conservative: 59
 Best Local Similarity: 32.58% Mismatches: 105
 Query Match: 7.85% Indels: 16
 DB: 2 Gaps: 6

US-10-705-757-1 (1-2623) x S66730 (1-1101)

```

QY 456 TGGCAGTACAGAGTGGCCGCTACTGGGACGCGGCTTGCTGCTACTCAGGC 515
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 839 Serasprpetherthilleuenclylmetcglylnclylualatrglylvalamleucys 858

QY 516 ATCCGGGTCTCGACAACTTGGCGGAGCATCAACACGTGAGAGAGAGGATTT--- 572
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 859 ILehtSaenaAggUlnHtYrIleValValIleuYbMetIlePheUySgUlnAggIleUeu 878

Qy 573 ---TCCGACTGGGAGAGAGCTGCTTAATGAGCACTGAGTGGCCCATGAGAGTGGCTGCTG 629

Db 879 ValAepHrTPrValArgAspArgUyLeuUdYlYhrIleProSerGlnUleGlnIleMet 898

Qy 630 AAGGAAGGTGAGC---TCGGGTTTCTCCGGGCTCATTAAGCTCTTCGACTGGTTCCGAGAG 666

Db 899 ALAthrLeuAenUyASnSerGlnGlnAenUySLeuUySLeuAepPhePheGlnAap 918

Qy 687 CCCGACAGTTTCGTCCTGATCCTGAGAGAGCCGACGCGGTGCA----- 731

Db 919 AepAepUyTPrYrYrIle-----GlnHrProValHnSgUyGlnUlnHrGlySer 934

Qy 732 ---GATCTCTTCGACTTCATCAGCGAAAAGGAGAGCCCTGCAAGAGAGACTGGCCCGAGC 788

Db 935 IleAepUeuPheAepValIleGlnUyPheUyValAepMetValGlnHnSgUlnAlaUyLeu 954

Qy 789 TTCCTTCGCGAGGTGCTGAGAGCCGTCGCGAGCTGCCAACACTCCGGGTTGCTACACCC 848

Db 955 ValPheUySgUlnValAlaSerIleUyHnAenUyASnSerGlnUyIleValHnAarg 974

Qy 849 GACATCAAGACGAAACATCCTTAATGCACTCAATGCGCGGCGAGCTCAAGCTCATGAC 908

Db 975 AepIleUyAepUlnAenValIleValAep---SerHnSgUyPheValUyLeuIleAep 993

Qy 909 TTCGGGTCGGGAGCGCTGCTCAAGAGACACCGTCTACACGACTTCGATGGAGCCCGAGTG 968

Db 994 PheGlySerAlaAlaUyIleUyIleUySerGlyProPheAepValPheValGlnUlnMetAap 1013

Qy 969 TPrAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGCAAGTGGCGGAGCTGCG 1028

Db 1014 TyrAlaAlaPProGlnUlnValLeuUyGlySerSerUyTPrUySgUySProGlnAepIleTPr 1033

Qy 1029 TCCCGGGGAGCTCGCTGATGATAGTGGTGTGAGATATTCCTTTCGACAGACGAA 1088

Db 1034 AlaLeuUyAlaUlnLeuUyTThrIleUyIleUySgUlnAepUyTPrYrAenIleAep 1053

Qy 1089 GAGATCATCAGAGGCGCAGGTTTCTTC-----AGCGAGAGGCTCTTCAGATGTCAg 1142

Db 1054 GlnUleUeuUyGlnUyGlnUeuAargPheAepUySerGlnHnSValSerGlnUyGlyle 1073

Qy 1143 CATCTCATTAAGTGGTCTTGCGCCCTGAGACCATCATAGTAGGCCAACCTTGAAAGAAATC 1202

Db 1074 SerUeuUyIleUyASnGlyIleUeuThraGlnUlnValAepUyAargProThrIleAepGlnUle 1093

Qy 1203 CAGAACCATCCATGATGATGCA 1223

Db 1094 TyrGlnAepUySTPrUeuUy 1100

RESULT 12

T18611

probable serine/threonine-specific protein kinase (EC 2.7.1.-), long splice form - Caenorh

N:containing: probable serine/threonine kinase, short splice form

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T18611; T18610; T23144; T23143

R:McMurray, A.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z18997

A:Accession: T18611

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1192 <W11>

A:Cross-references: UNIPROT:Q9TWT45; EMBL:Z81027; PIDN:CA854179.1; GSPDB:GN00023; CESP:H3

A:Experimental source: clone AH10

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-487,536-1192 <W12>

A:Cross-references: EMBL:Z81027; PIDN:CA854178.1; GSPDB:GN00023; CESP:H39E23.1b

A:Experimental source: clone AH10

R:McMurray, A.

[illegible]

```

Db      208  -----ProSerSerLeuGlnLysLeuPheArgIleValLysIleMetLysGlnLeu 224
QY      639  AGCTGGGGTTTCTCCGGCGTCATTAAGCTCTGGAGCTGGTTCAGAGCCCGACAGTTTC
Db      225  Asp-----HisProAsnIleValLysLeuTyrGlnValMetGlnThrGlnThrLeu 242
QY      699  GTCCATCTGGAGAGCCCGACCGGTGCAGATCTCTGATCTTCATTCACAGAAAG 758
Db      243  TyrLeuValLeuGlnTyrAlaSerGly---GlyGlnValPheArgTyrLeuValAlaHis 261
QY      759  GAGCCCTGCAGAGAGAGCTGGCCCGACGCTTCTGGAGAGCTGGAGCCGCTGG 818
Db      262  GlyArgMetLysGlnLysGlnLysAlaArgLysLeuPheArgGlnIleValSerAlaValGln 281
QY      819  CACTGCCCAACATCGCGGGGTCTACACCGGACATCAAGACGAAACATCTTATGAC 878
Db      282  TyrLeuHisSerLysAsnIleIleHisArgAspLeuLysAlaGlnAsnLeuLeuAsp 301
QY      879  CTGAATGGGGCGGAGCTCAAGCTCATGACTGGG---TCGGGGGGCGCTTCAGAGAC 935
Db      302  GlnAspMet---AsnIleLysIleAlaAspPheGlyPheSerAsnThrPheSerLeuGly 320
QY      936  ACCGTTACACAGGACTTCGATGGGACCCGAGTGAATGAGCCCTTCAGAGTGCCTAC 995
Db      321  AsnLysLeuAspThrPheArgGlySerProProTyrAlaAlaProGlnLeuPheSerGly 340
QY      996  CATCGCTACATGAGGAGGTGGCGGCGAGTGTGCTCCCTGGAGATCTGCTATGATG 1055
Db      341  LysLysGlyArgGlyProGlnValAspValIlePheSerLeuGlyValIleLeuTyrThrLeu 360
QY      1056  GTCTGTGAGATATTCCTTTC-----GAGCATGACGAAAGATCATC 1097
Db      361  ValSerLysSerLeuProPheAspGlyGlnAsnLeuLysGlnLysArgGlnValLeu 380
QY      1098  AGGCGACGAGGTTTCTTTCAGGACAGAGGCTCTTTCAGAAATGTCAGCATCATTAAGTG 1157
Db      381  ArgGlyLysGlyArgGlyLeuProPheTyrMetSerThrAspCysGlnAsnLeuLysLys 400
QY      1158  TGGTTGGCCCTGAGACCATCATAGGCCCACTTCGAGAAATCCAGAACCATTCATG 1217
Db      401  PheLeuValIleAsnProGlnArgSerSerLeuAspAsnIleMetLysAspArgTyr 420
QY      1218  ATG-----CAAGATGTTCTCTGCCCC 1238
Db      421  MetAsnValGlyTyrGlnAspAspGlnLeuLysPro 432

RESULT 13
T07788
probable serine/threonine-specific protein kinase (EC 2.7.1.1-) SNF1 - potaco
NAlternate names: Scd5SNF1 protein
CSpecies: Solanum tuberosum (potato)
CDate: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
CAccession: T07788
R:Lakatos, L.; Banfalvi, Z.
submitted to the EMBL Data Library, January 1997
AReference number: Z16133
AAccession: T07788
AStatus: preliminary; translated from GB/EMBL/DBJ
AMolecule type: mRNA
AResidues: 1-512 <LAK>
ACross-references: UNIPROT:O04122; EMBL:U03797; NID:G1935915; PIDN:AAB52224.1; PID:G193
AGene: SNF1
CFunction:
ADescription: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
CSuperfamily: AMP-activated protein kinase; protein kinase homology
CKeywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:17-271/Domin: protein kinase homology <KIN>

Alignment Scores:
Pred. No.: 6.53e-09 Length: 512
Score: 369.50 Matches: 124

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Percent Similarity: 44.62% Conservative: 79
Best Local Similarity: 27.25% Mismatches: 180
Query Match: 7.72% Indels: 72
DB: 2 Gaps: 18

US-10-705-757-1 (1-2623) x T07788 (1-512)

QY      462  TACCAGGTGGGCGGCTTACCTGGAGCGGCGGCTTGGCTCGGTACTACAGCATCCG 521
Db      19  TyrLysLeuGlnLysThrLeuGlnGlyIleGlySerPheGlyLysValLysIleAlaGlnHis 38
QY      522  GTCTCCGACAACTTGGCCGGGTCATTAAGCTTCAGATGAGAGAGAGAGAGAGAGAG 581
Db      39  ThrLeuIleGlyHisLysValAlaValLysIleLeuAsnArgLysIleAlaGln--- 57
QY      582  GAGAGCTGCTTAATGAGCACTCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 641
Db      58  -----MetAspMetGlnGlnLysValSerArgGlnIleLysIleLeuArgLeuPheMet 75
QY      642  TCGGTTTCTCCGGCGCTCATTTAGGCTCTGAGCTGTGAGAGGCCCGACAGTTTCGCT 701
Db      76  HisGlyHis-----IleSerArgLeuTyrGlnValIleGlnThrProSerAspIleTyr 93
QY      702  CTGATCTGGAGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 761
Db      94  ValValMetGlnTyrValLysSer---GlyGlnLeuPheAspTyrIleValGlnLysGly 112
QY      762  GCCCTGCAGAGAGAGAGCTGGCCCGGACGCTTCTTGGCAGAGTGCAGAGCCGCGGAC 821
Db      113  ArgLeuGlnGlnAspGlnLysAlaArgAsnPhePheGlnGlnIleIleSerGlyValGlnTyr 132
QY      822  TGGCAACATGCGGGGTCTACACCGGACATCAAGACGAAACATCTTATGACCTC 881
Db      133  CysHisIleAsnMetValValHisArgAspLeuLysProGlnAsnLeuLeuAsp--- 151
QY      882  AATCGGGGAGGATCAAGCTCATGAGCTTCGAGTGCAGAGTGCAGAGTGCAGAGTGC 941
Db      152  SerLysTrpAsnAlaLysIleIleAlaAspPheGlyLeuSerAsnIleMetCysArgGlyHis 171
QY      942  TACACGCACTTCGAT---GGACCCGAGTGTATAGCCCTTCAGAGTGAATCCGCTACAT 998
Db      172  PheLeuLysThrSerCysGlySerProAsnTyrAlaAlaProGlnValIleSerGlyLys 191
QY      999  CGCTACATGAGCAGAGTGGCGGCGAGTGTGCTCCCTGGAGATCTGCTGATGATGATG 1058
Db      192  LeuTyrAlaGlyProGlnValAspValIlePheSerCysGlyValIleLeuTyrAlaLeuLeu 211
QY      1059  TGGGAGATATTCCTTTCGAGCATGAC-----GAAGATCATCAGAG 1100
Db      212  CysGlyThrLeuProPheAspAspGlnAsnIleProAsnLeuPheLysIleLysGly 231
QY      1101  GGCAGAGTTTCTTTCAGGACGAGGCTCTTTCAGATGTCAGACATCTCATTAAGTGTGC 1160
Db      232  GlyTyrIleThrLeuProSerHisLysSerAlaGlyAlaArgAspLeuIleProAspMet 251
QY      1161  TTGGCCCTGAGACCATCATGAGCCCACTTCGAGAAATCCAGAAACCATTCATGATG 1220
Db      252  LeuIleValAspProMetLysArgMetThrIleProGlnIleArgGlnHisProTyrPhe 271
QY      1221  CAAGATGTTCTCTGCGCCGACGAGAACTGAGATTCACCTCCACAGCTGTGCGCGGG 1280
Db      272  Gln-----AlaHisLeuProArgTyrLeuAlaValProPro 283
QY      1281  CCCAGCAATAGACAGCTTTCTGGAGAGTCTCCCTCTTGTACAGATGCCGAGGAGAG 1340
Db      284  ProAspThrMetGln-----Gln 289
QY      1341  GGAAGCTTCTTCTTCAGCTTCCGAGTACAGTGAACAGTCTGCGCAAGACAGACAGT 1400
Db      290  AlaLysLysIleAspGlnGlnIleLeuGlnGlnValValMetGlyPheAsp----- 307
QY      1401  GCTTATACAGAGAACAACTTACAACTTCAGATCCAGATCCAGAGGCCCTGAGAGCTGCT 1460

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Db 308 -----ArgAsnAsnLeuThrGlnSerLeu-ArgAsnArgValGln----- 320
QY 1461 CCCAAGAGGGGAAAGAGGACCTCCAGGGGCTCCAGGCCCTCAACTCCTCCATGATA 1520
Db 321 -----AaangLuglyThrValProTyrrTyrrLeuLeuAspAsnArgHisArgVal 337
QY 1521 CTTCTTTCTTCATGAGTGTCCAGCATTCGTGCACTGCAATATATCCGGGGGTGGGG 1580
Db 337 lserThrGlyTyrrLeuGlnValArgGlnPheProLleGlnArgLysTrp--Al 391
QY 1581 GTGGGGGTGGGCAAA-----CCCTGCCAATGAGCACTTTTC--TT 1619
Db 353 yTyrrAsnArgLleAsnSerAsnGlnProLeuLeuProCys---TrpGlnArgPheProL 372
QY 1620 CATTCAGAGTTCGTGCAATGCCGGCATGGGTAGGGGGGAAACAGTTGGGATG 1679
Db 372 ylleMetAspTyrrGlnGlnHisValArgGlnPheProLleGlnArgLysTrp--Al 391
QY 1680 GATAGAGCTA-----GCACATTTTAAATCCCTGTGCACTCTTCCGACCTTTCTGA 1730
Db 391 aleuGlyLeuGlnSerArgHis-----ProArgGlnlleMetThrG 406
QY 1731 GTGCCTT-----CTGTGGGACTCCGGCTGTCTGGAGAAA 1767
Db 406 uValleuLysAlaLeuGlnGlnLeuAsnValCysTrpLys 420
RESULT 14
S33653
probable serine/threonine protein kinase (BC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N/Alternate names: protein YAL002; protein YAL017w; secretory protein S8P138
C/Species: Saccharomyces cerevisiae
C/Date: 30-Sep-1993 #sequence revision 02-Aug-1994 #text_change 16-Aug-2004
R/Accession: S33653; S36717; S36732; JH0486
R/Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton, A.; Kabac
Yeast 9, 543-549, 1993
A/Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae enc
A/Reference number: S33653; WUID:93311122; PMID:8322517
A/Accession: S33653
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-1358 <CL>
A/Cross-references: UNIPROT:P31374; EMBL:L05146
R/Ouellette, B.F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; D
submitted to the EMBL Data Library, January 1993
A/Description: Sequencing of Chromosome I from Saccharomyces cerevisiae: analysis of a 3
A/Reference number: S36711
A/Accession: S36717
A/Molecule type: DNA
A/Residues: 1-864,867-1358 <OE>
R/Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Bussey, H.
Yeast 8, 133-145, 1992
A/Title: Identification of a Saccharomyces cerevisiae homolog of the SNF2 transcriptions
A/Reference number: S22266; WUID:92221690; PMID:1561836
A/Accession: S36732
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-862 <CL>
A/Cross-references: EMBL:S93805
R/Sidhu, R.S.; Mathew, S.; Bollen, A.P.
Gene 107, 111-118, 1991
A/Title: Selection of secretory protein-encoding genes by fusion with PHOS in Saccharomy
A/Reference number: JH0483; WUID:92077420; PMID:1743509
A/Accession: JH0486
A/Molecule type: DNA
A/Residues: 1-72, 'E', 74-154 <SD>
C/Genetics:
A/Genes: SGD:FUN31; SSPL38
A/Cross-references: SGD:S0000015; MIPS:YAL017w
C/Map position: 1L
C/Superfamily: protein kinase homology
C/Keywords: ATP; glycoprotein; phosphotransferase; serine/threonine-specific protein kin
F/1096-1356/Domain: protein kinase homology <KIN>

F/1104-1112/Region: protein kinase ATP-binding motif
F/8,128/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/1232/Active site: Asp #status predicted
Alignment Scores:
Pred. No.: 6,91e-09 Length: 1358
Score: 367.00 Matches: 87
Percent Similarity: 54.26% Conservative: 53
Best Local Similarity: 33.72% Mismatches: 102
Query Match: 7.66% Indels: 16
Gaps: 6
US-10-705-757-1 (1-2623) x S33653 (1-1358)
QY 480 CTGGCAGCGGGGCTGGCTCGCTCGATCTGAGGATCCGGCTCCGACAACTTGGCCG 539
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QY 540 GTGGCCATCAACACAGTGGAGAGACCGGATT-----TCGACTGGGAGAGCTGCT 593
Db 1124 ValVallleTyrrMetllePheLysGlnArglleValValAspThrTrpValArgAspArg 1143
QY 594 AATGGCACTCGAGTCCCATGGAATGGTCTGCTGGAAGAGGTAGC---TCGGTTTC 650
Db 1144 LysLeuGlyThrLleProSerGlnlleGlnlleMetAlaThrLeuAsnLysLysProHis 1163
QY 651 TCCGGCGTCATAGGCTCCTGATCGTGTGAGAGCCGACAGTTTCCTGATCTTG 710
Db 1164 GluAsnilleLeuAsnLysLysLysPhePheGlnAspAspAspTyrrTyrrlle----- 1181
QY 711 GAGAGCCCGAGCCGGTCA-----GATCTTCGACTTCATCAG 752
Db 1182 -----GluThrProValHisGlylleGlylleThrGlyCyslleAspLeuPheAspLeuLleGlu 1199
QY 753 GAAAGGAGCCCTCGACAGAGAGAGCTGGCCGACCTTCTTGCGAGTGTGAGAGGCC 812
Db 1200 PheLysThrAsnMetThrGlnPheGlnValAlaLysLysLysLysGlnValAlaGly 1219
QY 813 GTGGGCACTGCGCAACACTGCGGGGTGTACACCGCATCATGAGACGAAACATCTT 872
Db 1220 lleLysHisLeuHisAspGlnGlylleValHisAspAspilleLysAspGlnAsnVallle 1239
QY 873 ATCGACTTCATATCGGGGAGCTCAAGCTCATGCACTTGGGCTGGGGCGCTGCTCAAG 932
Db 1240 ValAsp---SerLysGlyPheValLysllelleAspPheGlySerAlaLysValLys 1258
QY 933 GACACCGTTCACGCACTTCGATGAGCCGAGGTATAGCCCTCGAGGTGATCCGC 992
Db 1259 SerGlyProPheAspValPheValGlyThrLleAspTyrrAlaAlaProGlnValleuGly 1278
QY 993 TACCATCGCTACCATGAGAGTGGCGGAGTGTGCTGCTGGGATCTGCTGATGAT 1052
Db 1279 GlyAsnProTyrrGlnGlyGlnProGlnAspilleTrpAlaGlylleLeuLeuTyrrTr 1298
QY 1053 ATGTGTGTGAGATATTCCTTTCCAGCATGACGAAAGATCATCAGGGGCCAGTTTC 1112
Db 1299 ValValPheLysGlnAsnProPheTyrrAsnilleAspGlnlleLeuGlnLysLysLys 1318
QY 1113 TTCAGG-----CAGAGGCTCTTCAGATGACATGACCATCTTATGATGATGGCC 1166
Db 1319 PheAsnAsnAlaGlnGlnValSerGlnLysPheGlylleGlnLysLysSerlleLeuAsn 1338
QY 1167 CTGAGACATCATGATGAGCCCACTTCGAAAGATTCAGAACATTCATCATGATG 1220
Db 1339 ArgCysValProLysArgProThrilleAspAspilleAsnAsnAspLysTrpLeu 1356
RESULT 15
T52633
serine/threonine-specific protein kinase (BC 2.7.1.-) AKIN11 [validated] - Arabidopsis
N/Alternate names: SNF1 protein kinase omolog AKIN11
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C/Accession: T52633

R/Bhalerao, R.P.; Saichert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machida
Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999
A/Title: Regulatory interaction of PRL1 WD protein with Arabidopsis SNF1-like protein K1
A/Reference number: Z25116; MUID:99238529; PMID:10220464
A/Accession: T52633

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA

A/Residues: 1-512 <BHA>

A/Cross-reference: UNIPROT:P92958; EMBL:X99279; PTDN:CAA67671.1

A/Experimental source: cultivar Columbia

C/Genetic:

A/Gene: AKIN11

C/Function:

A/Description: EC 2.7.1.-; serine/threonine-specific protein kinase AKIN11 [validated, K

completeness SNF1 mutations in yeast

C/Superfamily: AMP-activated protein kinase; protein kinase homology

C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Alignment Scores:

Pred. No.:	8,758-09	Length:	512
Score:	366.50	Matches:	130
Percent Similarity:	44.02%	Conservative:	76
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Query Match:	7.65%	Indels:	84
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US-10-705-757-1 (1-2623) x T52633 (1-512)

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QY 444 GACCCCTGAGTGCAGACAGTGGGCGGCTACTGGACGGCGGCTTCGGCTG 503
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DB 14 GUSerleuProAntyTyrIleuGlyIleuThrIleuGlyIleuSerPheGlyIle 33
QY 504 GTTACTACGACATCCGCTTCGACAACTTCGCGGTGGCCATCAACAGTGAAG 563
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DB 34 ValIleIleIleValIleValIleThrGlyIleValIleValIleIleValIle 53
QY 564 GACCGGATTCGACCTGGGAGAGCTCCATATGGACCTGACATGCCATGGAAGTGC 623
    |||:::|||||
DB 54 ArgIleIleIleValIleValIleValIleValIleValIleValIleValIle 70
QY 624 CTGCTGAAGAGGTGAGCTCGGTTCTCCGCGCTTAGAGCTTCCTGACGTGCAAG 683
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DB 71 IleIleuArgIleuPheMet-----HisProHisIleIleArgIleuGlyIle 88
QY 684 AGGCGGACAGTTTCGCTGATCTGAGAGGCGGCGGCTGCAAGATCTTTCGAC 743
    |||:::|||||
DB 89 ThrThrSerAspIleTyrValIleMetGlyTyrValIleSer---GlyGluLeuPhe 107
QY 744 TTGATCAGGAGGAGGAGCGCTGCAAGAGAGCTGCGCGAGCTTCTTGGCAGTGC 803
    |||:::|||||
DB 108 TyrIleValGlyIleuValGlyIleuGlnGlnIleuAspGlnIleuPheGlnIle 127
QY 804 CTGAGGCGCTGCGGCACTGCCACAACTGCGGGGTGCTACACGCGCATCAAGAG 863
    |||:::|||||
DB 128 IleSerGlyValGlyIleuTyrGlyIleuArgIleuMetValIleIleArgIleu 147
QY 864 AACATCTTATGCACTGCAATCCGCGGAGCTCAAGCTCATGCTTCGGGTGCGGCG 923
    |||:::|||||
DB 148 AsnIleuLeuPheSer---SerArgCysAsnIleIleValIleAspPheGlyLeu 166
QY 924 CTGCTCAAGAGCACCGCTACAGGACTTGAT---GGACCGGAGTGTACGCTCCA 980
    |||:::|||||
DB 167 ValMetArgAspGlyIlePheLeuIleuThrSerCysGlySerProAsnTyrIle 186
QY 981 GAGTGAATCCGCTACATCCGCTACATGAGAGTGGCGGAGCTGCTGCTGGAGATC 1040
    |||:::|||||
DB 187 GluValIleSerGlyIleuTyrIleuValIleProGluValIleIlePheSerCys 206
QY 1041 CTGCTGATGATGATGCTGTGTGAGATATTCCTTTCGACATGACGAAGATC----- 1094
    |||:::|||||
DB 207 IleIleuTyrIleuLeuCysGlyIleuThrLeuProPheSer---AspGluAsnIle 225
    |||:::|||||
QY 1095 -----ATCAGGGGCGCAGGTTTC---TTCAGGCAAGGAGTCTTCGAGATG 1139

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DB 226 LeuPheIleValIleIleuSerGlyIleTyrThrIleuProSerHisIleuSerGlu 245
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QY 1140 CAGCATCTCATTAAGATGCTGCTGGCCCTGAGACCATCAATGAGCCACTTTCGAA 1199
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DB 246 ArgAspIleuIleProArgMetIleuIleValAspProValIleuArgIleThrIle 265
QY 1200 ATCCAGAACCTCATGATGACAGAT-----GTTCTCCGCCCCAG 1241
    |||:::|||||
DB 266 IleArgGlnHisArgThrPheGlnThrHisIleuProArgTyrIleuIleValSer 285
    |||:::|||||
QY 1242 GAACCTGCT-----GAGATCACTCCACAGCGTGGCGG 1277
    |||:::|||||
DB 286 AspThrValGlyIleuIleValIleuGlnIleuValIleGlnIleuValIleMet 305
    |||:::|||||
QY 1278 GGGCCGAGAAATGAGAGCTTTCGAGAGTCCGCTCCCTTCTGCAATGCCGAGG 1337
    |||:::|||||
DB 306 GlyPheAspArg-----AsnGlnValIleuGluSerIleu----- 316
QY 1338 GAGGGAGAGCTTCTGCTCCAGCTCCGAGTACAGTACAGCTTCGCGCAAGAG 1397
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DB 317 -----ArgAsnArgThrGlnAsnAspAla 324
QY 1398 AGTCTGATACAGAAACATTTACATGATTCAGATCCAGATCCAGGCGGAGAGCTG 1457
    |||:::|||||
DB 325 ThrValThrTyrTyrIleuLeuIleuAspAsnArgPheArgValProSerGlyTyr 343
    |||:::|||||
QY 1458 CTTCCCAACAGTGGGAGAGTGAATCTCCAGGGTCTTAAGCTCACTCCGCTAG 1517
    |||:::|||||
DB 344 ---GluSerGluPheGlnIleuThrThrAspSerGlySerAsnProMetArgThrPro 362
QY 1518 ATATCTCTTCT-----TTCATAGAGTGTCCAGATTCGTGACCTGAAATATCCG 1571
    |||:::|||||
DB 363 AlaGlyAlaSerProValGlyHisIleuIleuProAlaHisIleuValAspHis----- 378
QY 1572 GGGTGGGGTGGGGGAGGAGAGCCATGCAATGCAATCTTTTATATGAGTTC 1631
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DB 379 ---TyrGlyLeuGlyAlaArgSerGlnValProValAsp----- 390
QY 1632 TGCTGAATCCGAGATGAGTCAAGTGAAGGAGGAGAAACAGTTGGAGATGAGTAC 1691
    |||:::|||||
DB 391 -----ArgIleThrAla-----LeuGlyLeuGln-SerHisAla 401
QY 1692 ACATTTTAAGCTCTGACACTTTCGACCTTTTGTAGTGCTT-----CTGAGGG 1745
    |||:::|||||
DB 401 His-----ProArgGluIleMetGlnIleuValIleuValIleuGlnIle 416
QY 1746 ACTCGGCTGTGCTGGAGAA 1767
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DB 416 IleuAsnValCysThrIleuVal 423

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Search completed: September 22, 2005, 17:20:15
Job time : 115.96 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 15:59:25 ; Search time 433.035 Seconds
(without alignments)
6203.583 Million cell updates/sec

Title: US-10-705-757-1

Perfect score: 4789

Sequence: 1 gaggagagccggagagagc.....aataaaacccttgcttc 2623

Scoring table: BLOSUM62

Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+n2p.model -DEV=xlp
-Q/cgnt.1/USPTO.spool_p/US10705757/runat.22092005.115015.22129/app_query.faeca_1.5333
-DB=uniprot -QFMT=faetan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNIS-libs -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdd -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcr -NOR=ext -HEAPSIZES=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10705757_QCGN_1.1.980 @runat.22092005.115015.22129 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1670	34.9	313	1	P1M1_HUMAN
2	1659	34.6	313	1	P1M1_FELCA
3	1656	34.6	313	1	P1M1_BOVIN
4	1636	34.2	313	1	P1M1_RAT
5	1587	33.1	313	2	O8CFN8
6	1582	33.0	313	1	P1M1_MOUSE
7	1140	23.7	313	1	P1M1_COTJA
8	1133	23.6	313	1	P1M1_HUMAN
9	1129.5	23.6	313	1	P1M1_MOUSE
10	1128.5	23.6	313	1	P1M1_MOUSE
11	1116	23.3	313	2	O811X8
12	1105	23.1	313	1	P1M1_XENLA
13	1101	23.0	318	2	O66111
14	918	19.2	370	1	P1M2_MOUSE
15	889.5	18.6	311	2	O8R2P0
16	877.5	18.3	311	1	P1M2_HUMAN

17	854	17.8	310	2	O7ZVJ5	O7ZVJ5 brachydanio
18	851	17.8	310	2	O8JFW9	O8JFW9 brachydanio
19	846	17.7	310	1	P1M1_BRAPE	O9Y125 brachydanio
20	844	17.6	310	2	O6D152	O6D152 brachydanio
21	724.5	15.1	221	2	O8R1Z0	O8R1Z0 mus musculus
22	620	12.9	441	2	O20443	O20443 caenorhabditis
23	486	10.1	378	2	O8T3P1	O8T3P1 caenorhabditis
24	486	10.1	566	2	O17737	O17737 caenorhabditis
25	423	8.8	1383	1	PASK_MOUSE	O8EE66 mus musculus
26	421.5	8.8	134	2	O6P2J9	O6P2J9 homo sapien
27	403	8.4	125	2	O6Q2K5	O6Q2K5 canis familiaris
28	402	8.4	628	2	O9H093	O9H093 homo sapien
29	402	8.4	1398	2	O77268	O77268 drosophila
30	402	8.4	1398	2	O9W532	O9W532 drosophila
31	398	8.3	1107	2	O6C310	O6C310 yarrowia
32	397	8.3	661	1	ARK5_HUMAN	O60285 homo sapien
33	393.5	8.2	832	2	O963B6	O963B6 drosophila
34	391.5	8.2	658	2	O641K5	O641K5 mus musculus
35	391.5	8.2	1033	2	O8MLJ7	O8MLJ7 drosophila
36	391.5	8.2	1060	2	O9VBW0	O9VBW0 drosophila
37	391.5	8.2	1098	2	O7KRX7	O7KRX7 drosophila
38	391.5	8.2	1138	2	O7KRX3	O7KRX3 drosophila
39	390.5	8.2	631	2	O8C1C0	O8C1C0 mus musculus
40	390.5	8.2	950	2	O6NPA6	O6NPA6 drosophila
41	389	8.1	833	2	O7KRX5	O7KRX5 drosophila
42	389	8.1	905	2	O7KRX5	O7KRX5 drosophila
43	389	8.1	938	2	O9VBW8	O9VBW8 drosophila
44	389	8.1	1323	1	PASK_HUMAN	O96192 homo sapien
45	388	8.1	1075	2	O95U75	O95U75 drosophila

ALIGNMENTS

RESULT 1
P1M1_HUMAN
ID P1M1_HUMAN STANDARD; PRT; 313 AA.
AC P11309; O96RG3;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Proto-oncogene serine/threonine-protein kinase Pim-1 (BC 2.7.1.37).
GN Name=PIM1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90182681; PubMed=2205533; DOI=10.1016/0378-1119(90)90195-W;
RA Zakut-Houri R., Hazum S., Givol D., Teitelman A.;
RT "The cDNA sequence and gene analysis of the human pim oncogene.";
RT Gene 90:303-307(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
RA Zakut-Houri R., Hazum S., Givol D., Teitelman A.;
RT "The cDNA sequence and gene analysis of the human pim oncogene.";
RT Gene 54:105-111(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88217305; PubMed=3329709;
RA Domen J., von Lindern M., Hermans A., Breuer M., Groszfeld G., Berns A.;
RT "Comparison of the human and mouse PIM-1 CDNA: nucleotide sequence and immunological identification of the in vitro synthesized PIM-1 protein.";
RT Oncogene Res. 1:103-112(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=88115604; PubMed=3429489;
RA Wecker T.C., Nagarajan L., Ar-Rushdi A., Croce C.M.;
RT "Cloning and characterization of the human PIM-1 gene: a putative oncogene related to the protein kinases.";

RL J. Cell. Biochem. 35:105-112(1987).
 [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schaller G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Datchenko V., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uddin T.B., Tohiviyki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millar S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.U.M., Maria W.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RP SEQUENCE OF 1-302 FROM N.A.
 RX MEDLINE=21354098; PubMed=11460166; DOI=10.1038/35085588;
 RA Pasqualucci L., Neumeister P., Goossens T., Nandjangu G.,
 RA Chaganti R.S.K., Kupper R., Dalla-Favera R.,
 RT "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
 cell lymphomas.";
 RL Nature 412:341-346(2001).
 [7]
 RP CHARACTERIZATION.
 RX MEDLINE=88246418; PubMed=2837645;
 RA Teleman A., Anson R., Zakut-Houri R., Givol D.,
 RT "Identification of the human p1m-1 gene product as a 33-kilodalton
 cytoplasmic protein with tyrosine kinase activity.";
 RL Mol. Cell. Biol. 8:1498-1503(1988).
 [8]
 RP FUNCTION.
 RX MEDLINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4;
 RA Koike N., Maiba H., Taira T., Ariga H., Iguchi-Ariga S.M.M.,
 RT "Identification of heterochromatin protein 1 (HP1) as a
 phosphorylation target by p1m-1 kinase and the effect of
 phosphorylation on the transcriptional repression function of
 HP1(1).";
 RL FEBS Lett. 467:17-21(2000).
 [9]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE=22567470; PubMed=12680209;
 RA Ionov Y., Le X., Tungstun B.J., Sweetenham J., Sachs T., Ryder J.,
 RT "p1m-1 protein kinase is nuclear in Burkitt's lymphoma: nuclear
 localization is necessary for its biologic effects.";
 RL Anticancer Res. 23:167-178(2003).
 CC -1- FUNCTION: Thought to play a role in signal transduction in blood
 cells. May affect the structure or silencing of chromatin by
 phosphorylating HP1 gamma/CBX3.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBUNIT: Binds to RP9 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
 CC -1- TISSUE SPECIFICITY: Expressed primarily in cells of the
 hematopoietic and germ line lineages.
 CC -1- PTM: Autophosphorylated on tyrosine residues.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. P1M
 subfamily.
 CC -1- DATABASE: NMB=Atlas Genet. Cyrogenet. Oncol. Haematol.;
 WWW="http://www.infobiogen.fr/services/chronocancer/Genes/P1M1ID261.html".
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 or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; M27903; AAA60090.1; -;
 DR EMBL; M16750; AAA60089.1; -;
 DR EMBL; M54915; AAA36447.1; -;
 DR EMBL; M24791; AAA81553.1; -;
 DR EMBL; BC020224; AAH20224.1; -;
 DR EMBL; AF386792; AAK0871.1; -;
 DR PIR; J0327; TVHUP1.
 DR Genew; HGNC:8986; P1M1.
 DR H-InvDB; HIX0005835; -;
 DR MIM; 164960; -;
 DR GO; GO:0005737; Cytoplasm; TAS.
 DR GO; GO:0004674; Protein serine/threonine kinase activity; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR GO; GO:0004668; P:protein amino acid phosphorylation; TAS.
 DR InterPro; IPR011009; Kinase-like.
 DR InterPro; IPR000719; Prot. kinase.
 DR InterPro; IPR008271; Ser. thr. pkin. AS.
 DR Pfam; PF00069; Kinase; 1.
 DR ProDom; PD000001; Prot. kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
 Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 38 290
 FT NP BIND 44 52
 FT BINDING 67 67
 FT ACT SITE 167 167
 FT CONFLICT 15 16
 FT SEQUENCE 313 AA; 35685 MW; 35BA76D3688B9A3 CRC64;
 SQ

Alignment Scores:
 Score: 5.43e-83 Length: 313
 Percent Similarity: 1670.00 Matches: 313
 Best Local Similarity: 100.00% Conservative: 0
 Query Match: 34.87% Mismatches: 0
 DB: 1 Gaps: 0

US-10-705-757-1 (1-2623) x P1M1_HUMAN (1-313)

QY 351 ATGCTTGTGCAAAATCACTGCTGCGCACTGCGCGCGCTGCAACGACTG 410
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 DB 1 MetLeuLeuSerIylIeAmSerLeuAlaHisLeuArgAlaIaProCyAsnAspLeu 20
 QY 411 CACGCCCAACAGCTGCGCGCGCGCAAGAGAGAGCGCGCGAGTCGAGACAGG 470
 |||||
 DB 21 HisAlaThrIyLeuAlaProIyIyGluIyGluProLeuGlnSerIntyrgIVal 40
 QY 471 GGCCTGCTACTGGGAGCGCGCGCTTGGCTGCTGCTACTCAGAGATCCGCTCCGAC 530
 |||||
 DB 41 GlyProLeuLeuGlySerGlyIyPheGlySerValIySerGlyIleArgIalSerAsp 60
 QY 531 AACTTGGCGGTGGCGCATCAACACGCTGAGAGAGACCGGATTTCCGACTGGGAGAGCTG 590
 |||||
 DB 61 AsnLeuProValAlaIleIyHisIvalGluIyAspArgIleSerAspTrpGlyIleu 80
 QY 591 CCTAATGAGACTCGAGTGGCGCATGGAAGTGTCTGCGTGAAGAAGTGAAGTCGGGTTTC 650
 |||||
 DB 81 ProAsnGlyThrArgValaProMetGluValIalLeuLeuIyValaSerSerGlyIyPhe 100
 QY 651 TCCGGGCTATTAGGCTCTGAGCTGCTGAGAGAGCGCGAGAGTTCCTGCTGATCTG 710
 |||||
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluIyAspSerPheValLeuIleu 120
 QY 711 GAGAGCGCGAGCGCGGTGCAAGATCTTTCGACTTCATCAAGAGAGGAGGAGCGCTGCA 770
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Db      121  GluArgProGluProValGlnAspLeuPheAspHeileThrgluArgGlyAlaLeuGln 140
Qy      771  GAGAGACTGGCCCGCCACTTCTTTGGCAGGTGCTGGAGCCGCGGCGCACTGGCAAC 830
Db      141  GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
Qy      831  TGGGGGGTGTACACCGCGACATCAAGACGAAACATCCCTTATCGACTTCATCGCGG 890
Db      161  CysGlyValLeuHisAspGlnLeuAspGlnLeuAspGlnLeuLeuLeuLeuAspGln 180
Qy      891  GAGCTCAAGCTCATCGACTTCGGGTCGGGGCGCTGCTCAAGACACCGTCTACCGAC 950
Db      181  GluLeuLeuLeuLeuLeuLeuPheGlySerGlyAlaLeuLeuLeuLeuLeuLeuVal 200
Qy      951  TTGGATGGGACCGGAGTGTATAGCTTCGACAGTGGATCCGCTACCTCCATCATGGC 1010
Db      201  PheAspGlyThrArgValValTyrSerProGluLeuTrpLeuArgTyrHisArgTyrHisGly 220
Qy      1011  AGGTGGCGGCGAGCTGTGCTCCGCGGAGTCCGCTGATGATATAGTGTGGAGATATT 1070
Db      221  ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuLeuLeuLeuLeuLeuLeuLeu 240
Qy      1071  CCTTCGAGCATGACGAAAGATCATCATGAGGCGCGAGTTTCTTCAGGCGAGGATCTT 1130
Db      241  ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
Qy      1131  TCGAATGTACGATCTCATTAAGATGGTCTTGGCCCTGAGACCATGATAGGCCAAC 1190
Db      261  SerGluCysGlnHisLeuLeuLeuArgTyrCysLeuAlaLeuArgProSerArgPargProthr 280
Qy      1191  TTCGAGAAATTCGAAACATCATCATGAGTGTCTCCGCGCGCGAGAAATGCT 1250
Db      281  PheGluGluIleGlnHisAspTrpMetGlnHisPheAlaLeuLeuProGluGlnAla 300
Qy      1251  GAGATCCACCTCCACAGCTGTGCGCGCGCGCGCGCAAA 1289
Db      301  GluIleHisLeuHisSerLeuSerProGlyProSerIys 313

RESULT 2
PIM1_FELCA
ID      PIM1_FELCA      STANDARD;      PRT;      313 AA.
AC      095LTD;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN      Name=PIM1;
OS      Felis silvestris catus (Cat).
OC      Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Placentalia; Felidae; Felis.
OX      NCBI_TaxID=9685;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Fujino Y., Satoh H., Hiseue M., Maeda K., Ohno K., Tsujimoto H.;
RT      "The CDNA sequence of the feline pim-1 oncogene.";
RL      Submitted (OCT-2001) to the EMBL/GenBank/DBS databases.
CC      -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC      -1- SUBUNIT: Binds to Rps (By similarity).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC      -1- PTM: Autophosphorylated (By similarity).
CC      -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC      subfamily.
CC      -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.1sb-sib.ch/announce/
CC      or send an email to license@1sb-sib.ch).
CC      -----
CC      EMBL; AB073748; BAB71752.1; -.
CC      InterPro; IPR011009; Kinase_like.

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DR      InterPro; IPR000719; Prot kinase.
DR      InterPro; IPR008271; Ser_Ehr_pkin_AS.
DR      Pfam; PF00069; Kinase; 1.
DR      ProDom; PD000001; Prot kinase; 1.
DR      PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR      PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW      ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
KW      Serine/threonine-protein kinase; Transferase.
FT      DOMAIN      38      290      Protein kinase.
FT      NP_BIND      44      52      ATP (By similarity).
FT      BINDING      67      67      ATP (By similarity).
FT      ACT_SITE      167      167      Protein acceptor (By similarity).
SQ      SEQUENCE      313 AA; 35685 MW; C0BE26BD638E967 CRC64;

Alignment Scores:
Pred. No.:      2,16e-82      Length:      313
Score:      1659.00      Matches:      310
Percent Similarity:      99.68%      Conservative:      2
Best Local Similarity:      99.04%      Mismatches:      1
Query Match:      34.64%      Indels:      0
DB:      Gaps:      1

US-10-705-757-1 (1-2623) x PIM1_FELCA (1-313)

Qy      351  ATGCTCTTGTCCAAATCAACTGCTTGGCCACTGCGCGCGCGCTGCACAGACTTG 410
Db      1  MetLeuLeuSerIysHisSerLeuAlaHisLeuArgThrLabProCysAsnAspLeu 20
Qy      411  CAGCCACCAAGCTGCGCGCGCGCGCAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 470
Db      21  HisAlaThrIleLeuAlaProGlyLysGluLysGluProLeuGlnSerGlnTrpVal 40
Qy      471  GCGCCGCTACTGAGGAGCGCGCGCTTGGCTGCGGTACTCAGAGCATCCGCTTCGAC 530
Db      41  GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValAlaAsp 60
Qy      531  AACTCCCGCGTGGCCATCAACACGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
Db      61  AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyGluLeu 80
Qy      591  CCTAATGAGCAGCTGAGTGGCCATGAGAGAGTGTCTCTGTAAGAGAGAGAGAGAGAG 650
Db      81  ProAsnGlyThrArgValAlaProMetGluValIleLeuLeuLeuValSerSerGlyPhe 100
Qy      651  TCGGCGGTCAATAGGCTCTGAGACTGGTTCGAGAGAGCGCGAGCTTCTGATCTTG 710
Db      101  SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120
Qy      711  GAGAGCGCGAGCGCGGTGCAAGATCTTCTGACTTCATCAACGAAAGGAGAGAGAGAG 770
Db      121  GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
Qy      771  GAGGACTGGCGCGCGAGCTTCTTGGGAGGTGCTGAGAGCGCGTGGGAGCTGCCAAC 830
Db      141  GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
Qy      831  TGGGGGGTGTACACCGCGACATCAAGACGAAACATCCCTTATCGACTTCATCGCGG 890
Db      161  CysGlyValLeuHisAspGlnLeuAspGlnLeuAspGlnLeuLeuLeuLeuAspGln 180
Qy      891  GAGCTCAAGCTCATCGACTTCGGGTCGGGGCGCTGCTCAAGACACCGTCTACCGAC 950
Db      181  GluLeuLeuLeuLeuLeuPheGlySerGlyAlaLeuLeuLeuLeuLeuValTyrThrAsp 200
Qy      951  TTGGATGGGACCGGAGTGTATAGCTTCGACAGTGGATCCGCTACCTCCATCATGGC 1010
Db      201  PheAspGlyThrArgValValTyrSerProGluLeuTrpLeuArgTyrHisArgTyrHisGly 220
Qy      1011  AGGTGGCGGCGAGCTGTGCTCCGCGGAGTCCGCTGATGATATAGTGTGGAGATATT 1070
Db      221  ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuLeuLeuLeuLeuLeuLeuLeu 240

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Oy		CCTTTCGAGCATGCAGAAAGATATCATCAGGGGGCCAGGTTCCTTCAGGCAAGAAGGTCT	1130
Oy	1071	[]	
Db	241	PtPhegJinhAaPheJingJinIleIleIleArgJylgInvalPhePeArGlnArValSer	260
Oy	1131	TCAGAAATTCGACATCTCATTAAGATGTGTGTGGCCCTTGAGAACCATCAGATAGGCCAAC	1190
Db	261	SerGlucYsgJinhAaLeuIleArgTrpCySeuAlaLeuArGProSerArPaRigProser	280
Oy	1191	TTCGAGAAATTCGAGAACCATTCATGCATGATGCAGATGTTCTTCCTGGCCCCAGGAAC	1250
Db	281	PhegiJingJinIleGlnAsnHisProtTrpMetGlnArpValLeuLeuProGlingJinThra	300
Oy	1251	GAGATCCACCCTCCACAGCCTGTGTGGCGGGGGCCAGCAA	1289
Db	301	GluIleHisLeuHisSerLeuSerProGlyProSerTyrs	313
RESULT 3			
ID	PIM1_BOVIN	STANDARD:	PRT: 313 AA.
AC	Q9N0P9;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DE	05-JUL-2004 (Rel. 44, Last annotation update)		
Dt	Proto-oncogene serine/threonine-protein kinase pim-1 (BC 2.7.1.37).		
GN	Name=PIM1;		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovinae; Bos.		
OX	NCHI_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=21109090; PubMed=11182156; DOI=10.1016/S0165-2427(00)00259-2;		
RA	Wang Z., Petersen K., Weaver M.S., Magnuson N.S.;		
RT	"CDNA cloning, sequencing and characterization of bovine pim-1.";		
RL	Ver. Immunol. Immunopathol. 76:1177-195(2001).		
CC	-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.		
CC	-1- SUBUNIT: Binds to Rp9 (By similarity).		
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).		
CC	-1- PTM: Autophosphorylated (By similarity).		
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM		
CC	subfamily.		

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CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (see http://www.isb-sdb.ch/announce/		
CC	or send an email to license@isb-sdb.ch).		
DR	EMBL; AF259078; AAF67200.1; -.		
DR	HSSP; Q63450; IA06.		
DR	InterPro; IPR011009; Kinase_lke.		
DR	InterPro; IPR00719; Prot_Kinase.		
DR	InterPro; IPR008271; Ser_Thr_Pkin_AS.		
DR	Pfam; PF00069; Pkinase; 1.		
DR	ProDom; PD000001; Prot_kinase; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		
KW	ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;		
KW	Serine/threonine-protein kinase; Transferase.		
FT	DOMAIN 38..290		Protein kinase.
FT	NP_BIND 44..52		ATP (By similarity).
FT	BINDING 67..67		ATP (By similarity).
FT	ACT_SITE 167..167		Proton acceptor (By similarity).
SO	SEQUENCE 313 AA; 35629 MW; 9EF40229AB47AD47 CRC64;		
Alignment Scores:			
Pred. No.:	3,14e-82	Length:	313
Score:	1656.00	Matches:	309
Percent Similarity:	100.00%	Conservative:	4

Query Match:	98.72%	Mismatches:	0
DB:	34.58%	Indels:	0
	1	Gaps:	0
US-10-705-757-1 (1-2623) x PIM1_BOVIN (1-313)			
QY	351	ATGCTCTGTCCAAATCACTGGCTTGGCCCACTGGCGCGCGCCCTGCACGACCTG	410
DB	1	Mettuenuerlyvllleamserleuallhlleuylglaalaprocsesherpneu	20
QY	411	CACGSCCAAGCTGGCGCGCGCGCAAGAGAGGCCCTGAGTGCAGTACAGAGTG	470
DB	21	Hlelathrlhyrleuallaprogllylgulubprouleugluserglnlyglnval	40
QY	471	GGCCCGCTACTGGCGACGGCGGCTTGGCTCGGTACTACAGGACTCCGCTCCGAC	530
DB	41	GlyProleuenugllyserglylyrpheglyservaltyrserglylleargvalalaa	60
QY	531	AACTTGGCGGTGGCATCAACAACGTGGAAGAAGGACCGGATTTCCGATGGGAGAGCTG	590
DB	61	Asnuenprovalalalllelyvhlavaglnlyuabprgllleserabprrpelyglnleu	80
QY	591	CCTAATGGCACTCGAGTGGCCCAATGAAAGTGCTCTGCTGAAAGAAGTGAGCTCGGTTTC	650
DB	81	Prohanslyhrkxrgvalprometglnvalleuenuylyvvalserserglyphe	100
QY	651	TCCGCGCTCATTAAGCTCTCTGAGTGGTGTGAGAGGCCCAAGTTCGTCTGATCTGT	710
DB	101	Sercllyallleargyleuueaeprrpheglulnrgproabpserphevalleuileu	120
QY	711	GAGAGGCCCAAGCCGGTGCAGAAAGATCTCTTGACTTCACTCAACGGAAGAAGGACCCCTGCA	770
DB	121	Glnlrgprogluprovalglnaerleupheaprrhelethrghlvalargylalaleu	140
QY	771	GAGAGCTGGCCCGCAGACTCTTCTGGCAGGTGCTGAGGCGCCTGCGSCACTGSCACAA	830
DB	141	Glnlgluenuhlaargserpherhetrglnvalleuallalavalaarghlaocylhla	160
QY	831	TGCGGGGTGCTACACCGCAATCAAGACGAAACACTCTTATGCATCTAATGCGGCG	890
DB	161	Cyeglyallleuylhlaargabrrllelyabrglucanllleuileaderleuadnarggly	180
QY	891	GAGGTCAAGCTCATCGACTTCGGGTGGGGGGCGGTGTCAAGGACACCGTCTACAGGAC	950
DB	181	Glnleuylseuileaprrheglyserglyalaleuenuyabrrnvaltyrthaa	200
QY	951	TTCCGATGGGACCCGAGTGTATAGGCTCTGCAGAGTGATCCGCTACATCGCTACATGCG	1010
DB	201	Pheaprrlyhrkxrgvaltyrserproproglultrlleargtyrhlavargtyrhlav	220
QY	1011	AGGTGGCGGAGCTGTGCTCCCTGGGGATCTCTGTATGATATGTGTGTGAGATATT	1070
DB	221	Argserlalaavaltprserleuglylleuenuytrahpmetvalcygylaa	240
QY	1071	CCTTTCAGACATGACGAAGATATATAGGGCCGAGGTTTTCTCAGGAGAGGGTCTCT	1130
DB	241	Protheglnhlaargglnllyvalargglyglnvalphepheargglnargvalser	260
QY	1131	TCAGATGTGACAGATCTCATTTAGTGTGCTTGGCCCTGAGACATCAGATAGGSCAAC	1190
DB	261	Sercllyserglnhlaerlleargtyrpyaleuallaleuargproserabprrprouth	280
QY	1191	TTCCGAGAAATCCAGAACATCCATTCGATGTCAGAGATTTCTCTGCTCCGACGAAACTGCT	1250
DB	281	Phegllyglnllyleghlnaenhlaprottrpmetglnaerlalleuenuproglnglnlthla	300
QY	1251	GAGATCCAGCTCCACAGCTGTGCGCGGGGCCGACGCAA	1289
DB	301	GlnllehlseuhliserleuSERprogllyproserlyls	313

AC P26794;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Proto-oncogene serine/threonine-protein kinase Pim-1 (BC 2.7.1.37).
 GN Name=Pim1; Synonym=Pim-1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCBITaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=92319652; Pubmed=1620615;
 RA Miniglet D., Reeves R., Magnuson N.S.;
 RT "Characterization of the testes-specific pim-1 transcript in rat.";
 RL Nucleic Acids Res. 20:3183-3189(1992).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBUNIT: Binds to R9 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -1- PTM: Autophosphorylated (By similarity).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, X63675; CAA45214.1; --
 DR PIR, S26298; S26298.
 DR RGD, 3330; Pim1.
 DR InterPro, IPR0011009; Kinase like.
 DR InterPro, IPR000719; Prot kinase.
 DR InterPro, IPR008271; Ser_Thr_kin_AS.
 DR Pfam, PF00069; Pkinase; 1.
 DR ProDom, PD000001; Prot_kinase; 1.
 DR PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE, PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE, PS00108; PROTEIN_KINASE_ST; 1.
 KM ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
 KM Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 38 290
 FT NP_BIND 44 52 ATP (By similarity).
 FT BINDING 67 67 ATP (By similarity).
 FT ACT_SITE 167 167 Proton acceptor (By similarity).
 SQ SEQUENCE 313 AA; 35630 MW; D5757DA9F1821BP9 CRC64;
 Alignment Scores:
 Pred. No.: 3,876-81 Length: 313
 Score: 1636.00 Matches: 304
 Percent Similarity: 99.04% Conservative: 6
 Best Local Similarity: 97.12% Mismatches: 3
 Query Match: 34.16% Indels: 0
 DB: 1 Gaps: 0
 US-10-705-757-1 (1-2623) x PIM1_RAT (1-313)
 QY 351 ATGCTCTTGTCCAAATCACTGCTTGGCCACCTGCGCGCGCGCTTCGACGACCTG 410
 DB 1 MetLeuLeuSerIysIleAsnSerLeuAlaHisLeuAlaGAlaProCysAsnAspLeu 20
 QY 411 CAGCCACCAAGCTGGCGCGCGCGCAAGAGAGAGCGCTTGAGTGTGCGAGTCAAGTGG 470
 DB 21 HisAlaAsnIlybLeuAlaPProGlybGlybGlybGlybProLeuLeuIserGlnIyVal 40
 QY 471 GGGCGCTACTGGGCGAGCGCGCTTGGCTCGGTCTACTCAGGACATCCGCTTCGCG 530
 DB 41 GlyProLeuLeuGlybGlybGlybGlybGlybGlybSerValIySerGlyIleAlaValaAsp 60

QY 531 AACTGCGCGGTGACATCAAAACGATGAGAGACCGGATTTCCGACTGGGAGAGCTG 590
 DB 61 AsnLeuProValAlaIleuYbHisValGlybAspArgIleSerAspTrpGlybLeu 80
 QY 591 CCTAATGACACTGAGTGGCCATGAGAGTGGTCTCTGTAAGAAAGGTGAGCTGGGTTTC 650
 DB 81 ProAsnGlyThraArgAlaProMetGlyValAlaIleuLeuYbValSerSerGlyPhe 100
 QY 651 TCCGGGCTCATTTAGCTCTCTGCACTGGTTCGAGAGCCGACAGTTCCTGATCTCTG 710
 DB 101 SerGlyValAlaIleArgLeuLeuAspTrpPheGlybArgProAspSerPheValIleuLeu 120
 QY 711 GAGAGCGCGAGCGCGGTGCAAGATCTTCTGCACTTCATCAAGAAAGGGAGCGCTGC 770
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGlybArgGlybAlaLeuGln 140
 QY 771 GAGAGCTGGCGCGCGACTTCTTCTGCGAGGTGCTGAGAGCCGTCGCGGCACTGCCA 830
 DB 141 GluGlybLeuAlaArgSerPhePheTrpGlnValLeuGlybAlaValaArgHisGybHisAsn 160
 QY 831 TCGCGGGTGTACACCGGCAATCAAGACGAAATCTCTTATGCACTCAATTCGCGGC 890
 DB 161 CysGlyValLeuHisIleArgAspIleIySAspGlybAsnIleuLeuIleAspLeuAsnArgGly 180
 QY 891 GAGCTCAAGCTCATTCGCTTGGGTGGGGCGCTGCTCAAGACACCGCTTACAGGAC 950
 DB 181 GluLeuYbSerLeuIleAspPheGlybSerGlybAlaLeuYbAspThrValIyTrnAsp 200
 QY 951 TTCGATGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACATGCTTCACTGCG 1010
 DB 201 PheAspGlyThraArgAlaIySerProProGluTrpIleArgTrpHisArgGlybHisGly 220
 QY 1011 AGGTGCGCGGCACTGTGCTCTGCGGAGATCTGCTGTATGATATGGTGTGTGAGATATT 1070
 DB 221 ArgSerAlaAlaValAlaTrpSerLeuGlyIleLeuLeuIyAspMetValCysGlyAspIle 240
 QY 1071 CCTTGGACATGACCAAGACATGATCAGAGCGCGAGCTTCTTCTTCCGAGAGGGTCTCT 1130
 DB 241 ProPheGlnHisAspGluGluValIyGlybGlybValIyPheArgGlnAspValSer 260
 QY 1131 TCAGATGTCAAGATCTCATTTAGATGTCCTTGGCCCTGAGACCATCAATAGAGCCAC 1190
 DB 261 SerGlybGlybGlnHisIleuLeuArgTrpCysLeuSerLeuArgProSerAspArgProSer 280
 QY 1191 TTCGAAGAATTCAGAACCATTCATGATGATGCAAGATGTTCTCTGCGCCAGCAATGCT 1250
 DB 281 PheGlybGlybIleGlnAsnHisProTrpMetGlnAspValIleuLeuProGlnAlaTrnAla 300
 QY 1251 GAGATCCACCTCCACAGCGCTGTCCCGCGGCGCCAGCAAA 1289
 DB 301 GluIleHisLeuHisSerLeuSerProSerProSerIyS 313
 RESULT 5
 Q8CFN8 PRELIMINARY; PRT; 313 AA.
 ID Q8CFN8;
 AC Q8CFN8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 23, Last annotation update)
 DE Proximal integration site 1.
 GN Name=Pim1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBITaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain, and Eye;
 RX MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uddin T.B., Toohilyuki S., Garinai P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mallary S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A.C., Shvchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzywiński M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: BC042885; AAH42885.1; -
 DR EMBL: BC053019; AAH53019.1; -
 DR EMBL: BC055316; AAH55316.1; -
 DR MGD: MG1:97584; P1ML.
 DR GO: GO:0005524; P:ATP binding; IEA.
 DR GO: GO:0004674; P:Protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; P:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011009; Kinase_like.
 DR InterPro: IPR007719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR Prodom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KM ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SO SEQUENCE 313 AA; 35451 MW; 1294F16A03B7CD7 CRC64;

Alignment Scores:
 Pred. No.: 1,81e-78 Length: 313
 Score: 1587.00 Matches: 295
 Percent Similarity: 97.44% Conservative: 10
 Best Local Similarity: 94.25% Mismatches: 8
 Query Match: 33.14% Indels: 0
 DB: 2 Gaps: 0

US-10-705-757-1 (1-2623) x Q8CFN8 (1-313)

QY 351 ATGCTCTGTGCAAAATCAATGCTTGCACCTGGCGCGCGCTTGCACAGACCTG 410
 DB 1 MetLeuLeuSerYelLeuSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20
 QY 411 CAGCCACCAAGCTGGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
 DB 21 HisAlaThrIleuAlaProGlyArgIleuGluProLeuGluIleuArgIleuVal 40
 QY 471 GGGCCGCTACTGGGAGAGCGCGCGCTTGCCTGCTCTACTCAGGACCTCGCTCCGAC 530
 DB 471 GGGCCGCTACTGGGAGAGCGCGCGCTTGCCTGCTCTACTCAGGACCTCGCTCCGAC 530

DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValAlaAsp 60
 QY 531 AACTGCGCGGTGGCATCAACAGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
 DB 61 AsnLeuProValAlaIleLeuHisValGlyValAspArgIleSerAspTrpGlyIleu 80
 QY 591 CCTAATGGCACTGAGTGGCCCATGGAAGTGTCTCTGTGAAGAGAGAGAGAGAGAGAG 650
 DB 81 ProAsnGlyThrArgValProMetGluValValLeuLeuValValSerSerAspPhe 100
 QY 651 TCCGCGCTCATTAAGCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 710
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleu 120
 QY 711 GAGAGCGCGAGAGCGAG 770
 DB 121 GluArgProGluProValGluAspLeuPheAspPheIleTrpGluArgGlyAlaLeuGln 140
 QY 771 GAG 830
 DB 141 GluAspLeuAlaArgGlyPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn 160
 QY 831 TCGCGGCTGCTACACCGGAGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 890
 DB 161 CysGlyValLeuHisArgAspIleLeuAspGluAsnIleLeuIleAspLeuSerArgGly 180
 QY 891 GAGCTCAAGCTCATGAGCTTGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 950
 DB 181 GluIleLeuValLeuIleAspPheGlySerGlyAlaLeuLeuValAspThrValIleThrAsp 200
 QY 951 TTGATGGAGAGCCGAGTATATAGCCCTTCAGAGTGGATCCGTTACATCGTACATGAGC 1010
 DB 201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
 QY 1011 AGGTGGGCGGAGCTGTGCTGCTGGAGATCCGTCGTATGATATATATATATATATAT 1070
 DB 221 ArgSerAlaAlaValTrpSerIleuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
 QY 1071 CCTTCGAGCATGAGAGAGATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1130
 DB 241 PropheGluHisAspGluGluIleIleLeuGlyGlnValPhePheArgGlnThrValSer 260
 QY 1131 TCAGATGTCAGCATTCATTAAGATGTGCTTGGCCCTGAGACATCAGATAGGCCAACC 1190
 DB 261 SerGluCysGlnHisIleuIleLeuTyrCysLeuSerLeuArgProSerAspArgProSer 280
 QY 1191 TTCGAGGAATTCAGAACATTCATGATGAGATGCAAGATGTTCTCTGCGCCAGAACTGCT 1250
 DB 281 PheGluGluIleArgAsnHisIleProTrpMetGlnGlyAspLeuLeuProGlnAlaIleSer 300
 QY 1251 GAGATCCACCTCCACAGCCTGTGCGCGGAGGCCAGCAAA 1289
 DB 301 GluIleHisLeuHisSerLeuSerProGlySerSerIlys 313

RESULT 6
 P1ML MOUSE
 ID P06803; STANDARD; PRT; 313 AA.
 AC P06803;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Proto-oncogene serine/threonine-protein kinase pim-1 (BC 2.7.1.37).
 GN Name:Pim1; Synonyms:p1m-1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBT:Taxid=10090;
 OX [1]
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
 RA Selden G., Cuyper H.T., Boelens W., Robanus-Maandag E., Verbeek J.,
 RA Domen J., van Beveren C., Berns A.;
 RT "The primary structure of the putative oncogene pim-1 shows extensive


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RT  homology with protein kinases."
RL  Cell 46:603-611(1986).
RN  [2]
RP  INTERACTION WITH RP9.
RX  MEDLINE=20369540; PubMed=10931201;
RA  Maita H., Harada Y., Nagakubo D., Kiteaura H., Ikeda M., Tamai K.,
RA  Takehashi K., Ariga H., Iguchi-Ariga S.M.M.;
RT  "RAP-1, a novel target protein of phosphorylation by Pim-1 kinase."
RL  Eur. J. Biochem. 267:5168-5178(2000).
CC  -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC  -1- SUBUNIT: Binds to RP9.
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC  -1- PTM: Autophosphorylated (By similarity).
CC  -1- DISEASE: Frequently activated by provirus insertion in murine
CC  leukemia virus-induced T-cell lymphomas.
CC  -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC  subfamily.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC  or send an email to license@ebi.ac.uk).
CC  -----
DR  EMBL, M13945; AAA39930.1; -.
DR  PIR, A24169; TVMSPL.
DR  HSSP, Q63450; 1A06.
DR  MGD, MG1:97584; Pim1.
DR  InterPro, IPR011009; Kinase like.
DR  InterPro, IPR000719; Prot. kinase.
DR  InterPro, IPR008271; Ser_Thr_kin_AS.
DR  Pfam, PF00669; Pkinase; 1.
DR  ProDom, PD000001; Prot. kinase; 1.
DR  PROSITE, PS00107; PROTEIN KINASE ATP; 1.
DR  PROSITE, PS50011; PROTEIN KINASE DOM; 1.
DR  PROSITE, PS00108; PROTEIN_KINASE_ST; 1.
KW  ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
KW  Serine/threonine-protein kinase; Transferase.
FT  DOMAIN 38 290
FT  NP_BIND 44 52
FT  BINDING 67 67
FT  ACT_SITE 167 167
SQ  SEQUENCE 313 AA, 35536 MW, 79P477959DCBDC16 CRC64;
Alignment Scores:
Pred. No.: 3,39e-78 Length: 313
Score: 1582.00 Matches: 294
Percent Similarity: 97.12% Conservative: 10
Best Local Similarity: 93.93% Mismatches: 9
Query Match: 33.03% Indels: 0
DB: 1 Gaps: 0
US-10-705-757-1 (1-2623) x PIM1_MOUSE (1-313)
QY 351 ATGCTCTTGCAAAATCAACTGCTTGCCACCTGCGCGCCGCTTCGAAGACTG 410
DB 1 MetLeuLeuSerIySleAenSerLeuAlaHleuArgIlaArgProCyAaenAerLeu 20
QY 411 CAGGCCAAGAGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 470
DB 21 HlaAlaThrIyLeuAaProGlyIyGlnIyGlnIyGlnIyGlnIyGlnIyGlnIy 40
QY 471 GGGCGGCTACTGGGAGCGCGCGCTTGCTGCTGCTACTCAGAGCATCCGCTCCGAC 530
DB 41 GlyProLeuLeuGlySerGlyIyPheGlySerValIySerGlyIleArgValAlaAaP 60
QY 531 AACTGCGCGGCTGGCATCAACACGCTGGAAGAAGACCGGATTTCCGACTGGGAGACTG 590
DB 61 AenLeuProValAlaIleIyGlnIyGlnIyGlnIyGlnIyGlnIyGlnIyGlnIy 80
QY 591 CCAATGCGACTGCGAGTGGCCCATGAAGAGTGTCTCTGTAAGAAGAGTGGGTTTC 650

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DB 81 ProAenGlyThrArgValIyProMetGluValIyLeuLeuIySylSylAaSerSerAaPhe 100
QY 651 TCCGGCGCTATTAGGCTCTCTGAGCTGATCGAAGCGCCGACAGTTTCTGCTGATCTTG 710
DB 101 SerGlyValIleArgLeuLeuAaPTrpPheGluArgProAaPhePheValIleLeu 120
QY 711 GAGAGCGCGAGCGCGGAGCAAGATCTCTGACTTCATCGAGAAAGGGAGCGCTGGCA 770
DB 121 GluArgProGluProValGlnAaPheLeuAaPheIleThrGluArgGlyAlaLeuGln 140
QY 771 GAGAGCTGGCGCGCGAGCTCTCTGAGCTGATCGAAGCGCCGCTGCGACTCGACCAAC 830
DB 141 GluAaPheLeuAlaArgGlyPhePhePTrpGlnValIyLeuGluAlaIyArgIleCySHIaAa 160
QY 831 TGGCGGAGTGTACACCGCGACATCAAGAGCAAAACATCTTATTCGACTCAATCGCGC 890
DB 161 CyGlyValIyLeuIleAaPheIleIyAaPglAaSnIleLeuIleAaPheAaPheArgGly 180
QY 891 GAGCTCAAGCTATCGACTTCTGCGGCTGGGGCGCTGCTCAAGACACCGCTTACAGCGAC 950
DB 181 GluIleIySylLeuIleAaPhePheGlySerGlyAlaLeuLeuIyAaPTrpValIyThrAaP 200
QY 951 TTGATGAGGACCGGAGTGTATACCTCCAGAGTGTATCCGCTACCATCGCTACATGAC 1010
DB 201 PheAaPglIyThrArgValIyIySerProProGluIyIyArgIyIyIyArgIyIyIy 220
QY 1011 AGGTGCGCGGAGCTGTGCTCTGAGATCTCTGATGATATGATGTGTGAGATATT 1070
DB 221 ArgSerAlaIyAlaValIyPheSerLeuGlyIleLeuLeuIyIyAaPheValIyGlyIyAaP 240
QY 1071 CCTTTCAGAGTACGAGAAAGATCATCAGGGGCGCAGTTTCTTCAGGCGAGAGTCTT 1130
DB 241 ProPheGluIleAaPheGluIyIyIyIyGlyIyAlaPheAaPheArgIyIyIyValSer 260
QY 1131 TCAGATGTCAGCATCTCATTTAGATGATGCTTGCCCTGAGACCATCATGATAGCCAAC 1190
DB 261 SerGluCyAaGlnIleIyLeuIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 280
QY 1191 TTGAAAGAAATTCAGAACCATTCATGATGATGATGATGATGATGATGATGATGAT 1250
DB 281 PheGluGluIleIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 300
QY 1251 GAGATTCACCTTCACAGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1289
DB 301 GluIleIleIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 313
RESULT 7
PIM3_COTJA STANDARD; PRT; 323 AA.
ID PIM3_COTJA
AC G9P085;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (pim).
GN Name=PIM3; Synonym=pim-3;
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OC NCBI_TaxID=93934;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=20180111; PubMed=10713710; DOI=10.1038/nj.onc.1203355;
RA Richmann A., Yuan L., Breant C., Allitalo K., Koskinnen P.J.;
RT "Developmental expression of Pim kinases suggests functions also
RT outside of the hematopoietic system."
RL Oncogene 19:1215-1224(2000).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- PTM: Autophosphorylated.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.

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CC or send an email to license@isb-sib.ch).

DR EMBL; AJ130845; CAB62386.1; -
DR HSSP; Q63450; 1A06;
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR Prodom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KM ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KM Transferrase.
FT DOMAIN 40 291 Protein kinase.
FT NP_BIND 46 54 ATP (By similarity).
FT BINDING 69 69 ATP (By similarity).
FT ACT_SITE 168 168 Proton acceptor (By similarity).
SQ SEQUENCE 323 AA; 36597 MW; E2A4FA20B6F6396C CRC64;

Alignment Scores:

Pred. No.: 4.17e-54 Length: 323
Score: 1140.00 Matches: 209
Percent Similarity: 81.94% Conservative: 45
Best Local Similarity: 67.42% Mismatches: 52
Query Match: 23.80% Indels: 4
DB: 1 Gaps: 3

US-10-705-757-1 (1-2623) x PIM3_COTUA (1-323)

QY 351 ATGCTCTTGGCAAAATCAACTGCGCTTGGCCAGCGCGCGCGCTGCAACGACCTG 410
DB 1 MetLeuLeuSerIysPheGlySerLeuAlaHisIleCysSerProAlaSerMetAspHis 20
QY 411 CACGCCACCAAGCTGGCGCC-----GGCAGAGAGAGAGAGCCCTGAGTGCAGTAC 464
DB 21 LeuProValIleIleuProProValIleValIleGluIleuProPheAspLysValIle 40
QY 465 CAGGTGGGCGCGCTACTGGGACGCGCGCTTGGCGCTGCTACTACAGCATCCGCGTC 524
DB 41 GlnValGlySerValIleuGlySerGlyGlyPheGlyThrValIleGlySerArgThr 60
QY 525 TCCGACAACTTGGCGCGGCGCATCAACAGTGGAGAGAGAGCCGAGATTTCGACTGGAG 584
DB 61 AlaAspGlyLeuProValAlaValIleValIleValIleGluIleuValIleThrGluTrpGly 80
QY 585 GAGCTGCTTAAATGACCTGAGTGGCCAGTGAAGTGGTCTGCTGTAAGAAAGTGAAGCTG 644
DB 81 ThrIle---GlyGlyValMetValProLeuGluIleValLeuLeuLysValIleGlySer 99
QY 645 GGTTCCTCGCGCGCTCATAGGCTCTCGGACTGCTGAGAGGCGCCAGCACTTCGCTCG 704
DB 100 GlyPheArgGlyValIleIleValIleuLeuAspTrpTrpIleuArgProAspGlyPheLeuIle 119
QY 705 ATCTGGAGAGGCGCGGCGGAGTCAAGATCTTCACTTCAACGAGAAAGGAGGAGCC 764
DB 120 ValMetGluArgProGluIleuValIleAspLeuPheAspPheIleThrGlyLysGlyAla 139
QY 765 CTGCAAGAGAGCTGGCGCGCGCACTTCTTGGCAGGTGCTGAGAGCGCGCTGCGGCACTG 824
DB 140 LeuAspGluArgPheThrAlaArgGlyPhePheArgGlnValIleuGluAlaValAlaGlyHis 159
QY 825 CACAACTGGCGGCGGTGCTACACCGGACATCAAGAGAGAAACATCTTATCAACTCAAT 884
DB 160 TyrGlyCysGlyValValAlaHisArgAspIleIleLysAspGluAsnLeuValAspLeuArg 179

QY 885 CCGCGGAGACTCAAGCTCATCACTTGGGTCGGGGCGCTGCTCAAGACACCGTCTAC 944
DB 180 ThrGlyGluLeuIleValIleuLeuPheGlySerGlyAlaLeuLeuLysAspThrValIle 199
QY 945 ACGAATCTGATGGAGACCGGAGCTGATGAGCCCTCCAGACTGATCCGCTACCATGCTAC 1004
DB 200 ThrAspPheAspGlyThrArgValIleIleuSerProProGluTrpIleArgThrHisArgThr 219
QY 1005 CATGGCAGGTGGCGCGGAGCTGCGTCCCGGGGAGTCCGCTGATGATGATGGGTGGA 1064
DB 220 HisGlyArgSerAlaThrValIlePheLeuGlyValLeuLeuIleuValIleAspValCysGly 239
QY 1065 GATATTCCTTTGAGCATGACGACCAAGAGATCATCAAGGCGCGCGATTTCTTCAGCGAG 1124
DB 240 AspIleProPheGluGluAspGluIleuIleuLeuArgGlyAlaArgLeuIlePheArgArg 259
QY 1125 GTCTCTTCAAGATGTCAGCATCTCATTTAGATGTGCTGGCCCTGAGACCATCATATGAG 1184
DB 260 IleSerProGluCysGlnGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 279
QY 1185 CCAACCTTGAGAGAAATCCAGAACCATCATCATGAGAG--CAAGATGTTCTCGGCCAG 1241
DB 280 ProTrpLeuGluGlnIlePheAspHisGlnTrpMetHisLysSerGluValIleLysSer 299
QY 1242 GAAACTGTGAGATCCACTCCACGAGCGCTG 1271
DB 300 GluAspCysAspIleArgLeuArgThrLeu 309

RESULT 8
PIM3_HUMAN STANDARD; PRT; 326 AA.
ID PIM3_HUMAN
AC 086V6;
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN Name=PIM3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klauener R.D., Collins F.S., Wagner L., Scheiner C.F., Bhat N.K.,
RA Altshuler S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ushed T.B., Toshynki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,
RA Schnerch A., Schein J.B., Jones S.J.M., Maris M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP IDENTIFICATION FROM ESTS.
RX MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6;
RA Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.,
RT "Consistency checks for characterizing protein forms".
CC Comput. Biol. Chem. 27:29-35 (2003).
-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.


```

DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Proc_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding: Phosphorylation; Serine/threonine-protein kinase;
KW Transferase.
FT DOMAIN 40 293 Protein kinase.
FT NP BIND 46 54 ATP (By similarity).
FT BINDING 69 69 ATP (By similarity).
FT ACT SITE 170 170 Proton acceptor (By similarity).
SQ SEQUENCE 326 AA; 36002 MW; DD6CBP4635F851B CRC64;

Alignment Scores:
Pred. No.: 1,77e-53 Length: 326
Score: 1128.50 Matches: 213
Percent Similarity: 82.71% Conservative: 31
Best Local Similarity: 72.20% Mismatches: 44
Query Match: 23.56% Indels: 7
DB: Gaps: 5

US-10-705-757-1 (1-2623) x PIM3_RAT (1-326)

QY 351 ATGCTCTTTCACAAATCAACTGCTTGGCCCACTGGCGCGCGCC-----TGCAAC 404
DB 1 MetleuLeuSerIlybPheglYSerleuAlaHleu---CyeglyProglYglYValAsp 19
QY 405 GACCTGCACGCCCAACCAAGCTGGCGCGCGCGCAAG---GAGAAGAGACCCCTGAGTGCAG 461
DB 20 HleleuProValIlyleuAlaHleuGlnProAlaIlyAlaAspIlySerPheglYVal 39
QY 462 TACCAAGTGGCGCGCGCTACTGGGAGCGCGCGCTTGGCTTGCCTTACATCAAGCATCCG 521
DB 40 TyglInvalglYAlaValleuGlYserglYglYpHeglYthrValYtrAlaGlYserArg 59
QY 522 GTCTCCGACAACTTGGCGCGCTGCGCATCAACACCTGAGAGAGACCGGATTTCCGACTGG 581
DB 60 IleAlaAspIlyleuProValAlaValIlyHleValIlyValIlySerIlyValIlyThrGluTrp 79
QY 582 GGAAGAGCTGCCTAATGCACTGAGTGCCTGCAAGATGAGTGCCTGCAAGAGAGT--- 638
DB 80 GlYSerleu---GlYglYMetAlaValIProleuGlnValIlyleuAlaGlYValGlY 98
QY 639 ---AGCTGGGTTTCTCCGCGCTGATTAGGCTCTTGGACTGTTCGAGAGCGCGCAAGT 695
DB 99 AlaAlaGlYglYAlaArgIlyValIleArgLeuLeuAspTrpPheglYValGProAspGlY 118
QY 696 TTGCTCTGATCTCTGGAGAGAGCGCGAGCGGATGCAAGATCTTTCATCTTACATCAAGAA 755
DB 119 PheleuLeuValIleuGlnuArgProGluProAlaGlnAspLeuPheAspPheIleThrGln 138
QY 756 AGGAGAGCGCTGCAAGAGAGAGTGGCGCGAGCTTCTTGGGAGGAGTGCAGAGCGCTG 815
DB 139 ArgglYAlaIleuAspIlyProleuAlaArgArgPheHleAlaGlnIlyAlaIlaVal 158
QY 816 CGGCACTGCCCAACATGCGGAGTGTACACCGCGCATCAAGAGCAAGAAATCATCTTATC 875
DB 159 ArgHleCybHleAsnCybglYValIlaHleArgAspIleIlyAspIlyAsnIleuLeuVal 178
QY 876 GACCTCAATCGCGCGAGCTCAAGCTGATCGATTCGGGTCGGGGGCGCTGCAAGAGAC 935
DB 179 AspLeuArgSerIlyglYIleuIlyleuIleAspPheIlySerIlyAlaValIleuIlyAsp 198
QY 936 ACCGTCTACACGAGCTTCAGATGGGACCGAGTGTATGAGCCCTCAGAGTGCATCCGCTAC 995
DB 199 ThrValIlyThrAspPheAspIlyThrArgValIlySerProProGluTrpIleHglYtr 218
QY 996 CATGCTACCAAGAGAGTGGCGCGAGCTGTGCTCCCTGGGAGATCTGCTGTATGATATG 1055
DB 219 HleArgYtrHleglYArgSerAlaThrValIlyPserleuIlyValIleuLeuIlyrAspMet 238

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QY 1056 GTGNGTGAAGATATTCCTTTGAGCATGAGAGATGATCATGAGGCGCGAGTTTCTTC 1115
DB 239 ValCyglYAspIleProPheGlnGlnAspIlyGlnIleuArgIlyValPhePhe 258
QY 1116 AGCAGAGGCTCTCTTCAGAAATGTCAGATCTGATTAAGATGTGTGGCGCTGAGACCA 1175
DB 259 ArgArgArgIlySerProGluCyglYGlnGlnIleuIleGluTrpCybLeuSerleuAspPro 278
QY 1176 TCGATATGCGCAACTTCGAAAGATTCAGAACATCCATCATGATG 1220
DB 279 SerGluArgProSerleuAspIlyGlnIleAlaIleAspProTrpMet 293

RESULT 11
Q811X8 PRELIMINARY; PRT; 325 AA.
ID Q811X8;
AC Q811X8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KIDL.
GN Name=Pim3; Synonym=Kidl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu L.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ database.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AY026239; AKI6606.1; -.
DR HSSP: Q03656; 1Q99.
DR MGD: MGI:1355297; Pim3.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:Protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR011009; Kinase_Like.
DR InterPro: IPR007719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin__AS.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Proc_kinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding: Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 325 AA; 35931 MW; 77DBF8E20F41E3F4 CRC64;

Alignment Scores:
Pred. No.: 8,49e-53 Length: 325
Score: 1116.00 Matches: 212
Percent Similarity: 82.71% Conservative: 32
Best Local Similarity: 71.86% Mismatches: 43
Query Match: 23.30% Indels: 8
DB: Gaps: 6

US-10-705-757-1 (1-2623) x Q811X8 (1-325)

QY 351 ATGCTCTTTCACAAATCAACTGCTTGGCCCACTGGCGCGCGCC-----TGCAAC 404
DB 1 MetleuLeuSerIlybPheglYSerleuAlaHleu---CyeglyProglYglYValAsp 19
QY 405 GACCTGCACGCCCAACCAAGCTGGCGCGCGCGCAAG---GAGAAGAGACCCCTGAGTGCAG 461
DB 20 HleleuProValIlyleuAlaHleuGlnProAlaIlyAlaAspIlySerPheglYVal 39
QY 462 TACCAAGTGGCGCGCGCTACTGGGAGCGCGCGCTTGGCTTGCCTTACATCAAGCATCCG 521
DB 40 TyglInvalglYAlaValleuGlYserglYglYpHeglYthrValYtrAlaGlYserArg 59
QY 522 GTCTCCGACAACTTGGCGCGCTGCGCATCAACACCTGAGAGAGACCGGATTTCCGACTGG 581
DB 60 IleAlaAspIlyleuProValAlaValIlyHleValIlyValIlySerIlyValIlyThrGluTrp 79

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QY 582 GGAGAGCTGCTTAATGGCACTGAGAGTCCCATGAGAGTGGTCTCTGTAAGAAGTGG---- 638
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db GlySerLeu---GlyGlyValAlaValProLeuGlnValValLeuLeuArgGlyValGly 98
QY 639 ---AGCTCGGGTTTCTCCGGCTCATTTAGGCTCTGAGCTGTTTCAGAGGCCCGACAGT 695
    ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
    99 AlaAlaGlyGlyAlaArgGlyValIleArgLeuLeuAspTrpPheGlnArgProAspGly 118
QY 696 TTTCCTCTGATCTCTGGAGAGGCCCGGAGCCGCTGCAAGATCTTTCGATCTTCATCAGGAA 755
    ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db PheLeuLeuValLeuGlnArgProGlnProAlaGlnAspLeuPheAspPheIleTrpGln 138
QY 756 AGGGAGGCCCTGCAAGAGAGCTGGGCGCGGAGCTTCTTCGAGAGGTCGAGAGCCGCTG 815
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db ArgGlyValAlaLeuAspGlnProIleAspArgPhePheAlaGlnValLeuAlaVal 158
QY 816 CGGCACTGCGCAACTGCGGGGTGTACACCGGACATCAAGAGCAAAACATCTTATTC 875
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db ArgHisCysHisAsnGlyValValHisArgAspIleLeuAspGlnLeuLeuVal 178
QY 876 GACCTCAATCGCGGCGGAGCTCAAGCTCATGATCTGCGGGTCCGGGCGCTCGTCAAGAC 935
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db AspLeuArgSerGlyGlnLeuLeuValLeuAspPheGlySerGlyValAlaLeuLeuAsp 198
QY 936 ACCGTCACCGGACTTCGATCGAGCCCGAGTGTATAGCCCTCGAGAGTGGATCGGCTAC 995
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db ThrValValThrAspPheAspGlyThrArgValValSerProGlnTrpIleAspGly 218
QY 996 CATCGCTACCATGCAAGCTGCGGCGGAGCTGTGCTCCCTGGGAGCTCTGTATGATATG 1055
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db HisArgTrpHisGlyArgSerAlaThrValTrpSerLeuGlyValLeuLeuTrpAspMet 238
QY 1056 GTGTGTGAGATATTTCTTTCAGCATGACGAAGAATCATCAGGGCGGCGGCTTCTTC 1115
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db ValCysGlyAspIleProPheGlnGlnAspGlnGlnIleLeuArgGlyArgLeuPhePhe 258
QY 1116 AGGCAAGGGTCTCTTCAGAAATGTCAGCATCTAGATAGATGGTGGCTGAGAGCA 1175
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db ArgArgArgValSerProGlnCysGlnGlnIleGlnTrpCysLeuSerLeuAspPro 278
QY 1176 TCAGATAGGCCAAGCTTCGAAGAATTCAGAACATTCATGATGATG 1220
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db SerGlnArgProSerLeuAspGlyLeu---CysHisProTrpMet 292

RESULT 12
PIM3_XENLA STANDARD; PRT; 323 AA.
ID PIM3_XENLA O91822;
AC 091822;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Pim-1).
GN Name=PIM3; Synonyms=PIM1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_taxid=8335;
OX NCBI_taxid=8335;
RN 11
RP SEQUENCE FROM N.A., AND PHOSPHORYLATION SITES.
RA MEDLINE=9726766; Pubmed=909695; DOI=10.1074/jbc.272.16.10514;
RA Palaty C.K., Kaimar G., Tai G., Oh S., Amankwa L., Affolter M.,
RA Aebersold R., Pelech S.L.;
RT Identification of the autophosphorylation sites of the Xenopus laevis
RT Pim-1 proto-oncogene-encoded protein kinase."
RL J. Biol. Chem. 272:10514-10521(1997).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- PIM: Autophosphorylated.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC -1- CAUTION: Was originally (Ref.1) called Pim-1 but seems to
CC represent the pim-3 isoform.

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CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L29495; AAA85389.1; -.
DR InterPro: IPR011009; Kinase_1like.
DR InterPro: IPR00719; Prot Kinase.
DR InterPro: IPR008271; Ser thr_pkin_AS.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot Kinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferase.
FT DOMAIN 40 291 Protein kinase.
FT NP_BIND 46 54 ATP (By similarity).
FT BINDING 69 69 ATP (By similarity).
FT ACT_SITE 168 168 Proton acceptor (By similarity).
FT MOD_RES 4 4 Phosphoserine (by autocatalysis)
FT FT Phosphoserine (by autocatalysis).
FT MOD_RES 190 190 Phosphothreonine (by autocatalysis)
FT MOD_RES 205 205 Phosphothreonine (by autocatalysis)
FT FT
SQ SEQUENCE 323 AA; 36964 MW; AB4DD61E7A9A38F CRC64;

Alignment Scores:
Pred. No.: 3,37e-52 Length: 323
Score: 1105.00 Matches: 205
Percent Similarity: 80.25% Conservative: 47
Best Local Similarity: 65.29% Mismatches: 50
Query Match: 23.07% Indels: 12
DB: 1 Gaps: 5

US-10-705-757-1 (1-2623) x PIM3_XENLA (1-323)
QY 351 ATGCTCTGTTCCAAATATCACTGCTGCGCCACTGCGCGCGCGCTCGAAC----- 404
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db MetLeuLeuSerLeuPheGlySerLeuAlaHisIle-----CysAsnProSer 16
QY 405 -----GACCTGACGCGCACCAAGCTGGGCGCGCGGACG---GAGAAAGAGCCCGT 452
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db AsnMetGlnHisLeuProValIleValLeuGlnProValIleValAspArgLeuProPhe 36
QY 453 GAGTCGACGATACCAAGTGGGCGCGCTACTGCGAGCGGCGGCTCGGCTCGGCTACTCA 512
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db GlnValValIleGlnValGlySerValValAlaSerGlyGlyPheGlyThrValTyrSer 56
QY 513 GGCATCCGCGTCTCCGACAACTTCCCGGCTGCCATCAACACGTGGAAGAAGCCGGATT 572
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db AspSerArgIleAlaAspGlyGlnProValAlaValValHisValAlaValArgVal 76
QY 573 TTCGACTGGGAGAGCTGCTTAATGCACTGAGAGCCCATGAAGATGGTCTCGCTGAAG 632
    ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db ThrGlnTrpGlyThrLeu---AsnGlyValMetValProLeuGlnIleValLeuLeuVal 95
QY 633 AAGGTGAGCTCGGGTTTCTCCGGCGTCAATTAAGCTCTCTGAGCTGTTTCAGAGGCCCGAC 692
    ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db LysValProThrAlaPheArgGlyValIleAsnLeuLeuAspTrpTrpGlyArgProAsp 115
QY 693 AGTTTGTCTGATCTCTGGAGAGGCCCGGAGCCGCTGCAAGATCTTTCGATTCATCAGC 752
    ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db AlaPheLeuIleValMetGlnArgProGlnProValIleAspLeuPheAspTrpIleThr 135
QY 753 GAAAGGAGGCCCTGCAAGAAGAGCTGGCGCGGACGTTCTTCGAGAGTGTGAGAGGCC 812
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db GlnValGlyProLeuAspGlnAspThrAlaArgGlyPhePheArgGlnValLeuGlnAla 155

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Db 228 1leuLeuLeuYrAaerpMeVAlCyseUlYarPiLeRProRheGlnHnIsAaRAsGlnUleUleU 247
Qy 1098 AGGGGCCAGGTTTCTTCAAGCAGAGGGTCTCTTCAGAAATGTCAGCATCTCATTAAGATGG 1157
Db 248 LysGlyLysIleGlnTyrArgGyArGyAlSerAArgGluCyGlnHnIsleUleUleUtrP 267
Qy 1158 TGCTTGGCCCTGAGACCATCATGATGGCCCAACCTTCGAAAGAAATCCAGAACCATTCATGAG 1217
Db 268 CysLeuSerLyrAaRgProSerSerAaRgProSerLeuGlnGlnIleUleUlaHnIsProTrp 287
Qy 1218 ATG---CAAGATGTTCTCTCGCCAGAGAA 1244
Db 288 MetSerGlnAaRPaHnPhelUaAsPylsYs 297

RESULT 14
PIM2_MOUSE STANDARD; PRT; 370 AA.
ID PIM2_MOUSE 062070; 062071; 062072;
AC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-2 (EC 2.7.1.37).
GN Name=Pim2; Synonyms=Pim-2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95300786; PubMed=7781606;
RA van der Lugt N.M., Domen J., Verhoeven E., Linders K.,
RA van der Gulden H., Allen J., Berns A.;
RT "Proviral tagging in E mu-myc transgenic mice lacking the Pim-1 proto-
RT oncogene leads to compensatory activation of pim-2."
RL EMO J. 14:2536-2544 (1995).
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative Initiation;
CC Comment=3 isoforms, 1 (shown here), 2 and 3, are produced by
CC alternative initiation. Isoform 1 and isoform 2 initiate from
CC C TG codons;
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC -----
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CC CC send an email to license@isb-sib.ch).
CC -----
DR EMBL; L41495; AAA98922.1; -.
DR EMBL; L41495; AAA98923.1; -.
DR EMBL; L41495; AAA98924.1; -.
DR PIR; S55333; S55333.
DR HGSP; Q63450; 1A06.
DR MGD; MGI:97587; Pim2.
DR GO; GO:0005515; F:protein binding; IPT.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR GO; GO:0006916; F:anti-apoptosis; IDA.
DR GO; GO:0008637; P:apoptotic mitochondrial changes; IDA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR008719; Prot. Kinase.
DR InterPro; IPR008771; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SMO0220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR Alternative Initiation; ATP-binding; Phosphorylation;

```

KM	Setine/threonine-protein kinase; Transferase.
FT	Serine/threonine-protein kinase pim-2,
FT	CHAMIN 1 370 isoform 1.
FT	CHAMIN 26 370 serine/chreonine-protein kinase pim-2,
FT	isoform 1.
FT	CHAMIN 60 370 isoform 2.
FT	isoform 3.
FT	INIT MET 26 26 For isoform 2.
FT	INIT MET 60 60 For isoform 3.
FT	DOMAIN 91 345 Protein kinase.
FT	NP BIND 97 105 ATP (By similarity).
FT	BINDING 120 120 ATP (By similarity).
FT	ACT SITE 222 222 Proton acceptor (By similarity).
SQ	SEQUENCE 370 AA; 40059 MW; 128B70BFDD04DBEA CRC64;
 Alignment Scores:	
Pred. No.:	5,32e-42 Length: 370
Score:	918.00 Matches: 195
Percent Similarity:	62.44% Conservative: 51
Best Local Similarity:	49.49% Mismatches: 104
Query Match:	19.17% Indels: 44
DB:	Gaps: 9
 US-10-705-757-1 (1-2623) x PIM2_MOUSE (1-370)	
OY	153 GCTGGCGCGCTTCGCCGACATCCCGGCA-----GGCCTCAAGTTGTCTCCGACTCG 206
Dd	15 AlaserGIProPrpsrPserLeuProSerThrlEuAlaProPro--SerProGIySer 33
OY	207 CCTTGGGCTTCGCAGCGAGCACACGCCGACGCCAGCACGACAGCACAGCACC 266
Dd	34 ProAlaAlaLeuProArghAlaSerThr----- 42
OY	267 CAGGCAATAGCTTCGGACAAGCCCCGACTTCGCGTCCGCGACCTCC----TCTGGC 320
Dd	43 -----ProGYGLyleuSerglyPhesergly 51
OY	321 AGCTCCCTGGCGCGAATCTTGAGAGTTGATGCTCTTGTCCAAATCATCAGCTCGCC 380
Dd	52 LeuAsnmlLeArgSerThrsrSer-----MetleuTrlryS- 63
OY	381 CACTTGGCGGCGCGCCTTCGCAACGACTTCGACGCGACCAACGATCGGCGCCGCAAGAG 440
Dd	64 ProleuglnslYHIsrProSerProProValThlrProthrInPrProProGIyLyIysArp 83
OY	441 AAGAGACCCCTGAGATCGCATGAACAGTGGGCGCCGCTACTTGGCGAGCGGCGCTTGGC 500
Dd	84 ArgAlaAlaPheglIuAlaGlurYzArGrleuglyProleuIeuGlYylgIyglYPhesgly 103
OY	501 TCGGTCATCAAGGACATCCGCGTCGCGAACCACTTGCCGCGGAGGCATCAAAACGTGAG 560
Dd	104 ThrValPheAlaIYHIsrArgValThlrzsrPrgrArgInValAlaIlleYvalIIleSer 123
OY	561 AAGACCGGATTTCGACTGGGAGAGAGCTGCTCATATGCACTCGAGTGGCCCATAGAATG 620
Dd	124 ArgAsnArgrValIeuclYTrPrserThrValSerAspSerValThrycSProleuGlVal 143
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Dd	164 TrpPheGIuThrProGIuLyrPheMetLeuValIeuGIuThrPromePrAlaGIAsrP 183
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Dd	184 LeuPheAsprYrILethrGIuLYseLIyProleuGIyIuseryCSsarZArgSerPhePhe 203
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Dd	204 ThrGIuValValAlaAlaValGIuNHIsCYuNHIsValArgrGIyValIVIHIsArgAspRIle 223


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QY      1218 ATCAAGATGTTCTCTGCCCCAGAAACTGTGAGATCCACCTCCACAGCCTGTGCGCG 1277
      286 MetGlnSer-----ProAlaGluGluLysProIleAsnSerSerLysGlySerPro 302
QY      1278 GGGCCCGAGAAATAGCAGCCTTTCCTGGCAGGTCCTCCC 1316
      303 ThrProLeuPro-----TrpSerLeuLeuPro 311
Db
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Search completed: September 22, 2005, 17:14:39
Job time : 452.035 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 16:26:26 ; Search time 356.236 Seconds

(without alignments)
5993.731 Million cell updates/sec

Title: US-10-705-757-1

Perfect score: 4789

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 3653042

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1670	34.9	313	9	US-09-971-791-9
2	1670	34.9	313	14	US-10-081-119-18
3	1670	34.9	313	15	US-10-394-322A-52
4	1670	34.9	313	15	US-10-348-081-13
5	1670	34.9	313	16	US-10-664-421-1
6	1670	34.9	313	16	US-10-664-421-150
7	1670	34.9	313	16	US-10-664-421-150
8	1670	34.9	313	17	US-10-951-389-18
9	1670	34.9	313	17	US-10-951-406-18
10	1670	34.9	313	17	US-10-951-407-18
11	1670	34.9	313	18	US-10-977-087-18
12	1670	34.9	313	18	US-10-705-757-2
13	1670	34.9	313	18	US-10-941-635-1
14	1670	34.9	313	18	US-10-941-635-152
15	1657	34.6	313	16	US-10-620-052A-22
16	1636	34.2	313	9	US-09-971-791-8
17	1636	34.2	313	15	US-10-348-081-12
18	1636	34.2	313	18	US-10-705-757-4
19	1582	33.0	313	9	US-09-971-791-7
20	1582	33.0	313	15	US-10-348-081-14
21	1582	33.0	313	16	US-10-664-421-2
22	1582	33.0	313	16	US-10-377-268-10
23	1582	33.0	313	18	US-10-705-757-6
24	1582	33.0	313	18	US-10-941-635-2
25	1362	28.4	253	16	US-10-620-052A-71
26	1149.5	24.0	455	9	US-09-971-791-5
27	1144	23.9	374	15	US-10-425-114-54275
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32	1133	23.7	326	9	US-09-971-791-2
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35	1133	23.7	326	16	US-10-618-941-82
36	1129.5	23.6	326	15	US-10-348-081-6
37	1129.5	23.6	326	16	US-10-377-268-14
38	1129.5	23.6	326	18	US-10-705-757-11
39	1129.5	23.6	326	18	US-10-941-635-6
40	1128.5	23.6	326	15	US-10-348-081-10
41	1128.5	23.6	326	18	US-10-705-757-9
42	1116	23.3	325	16	US-10-664-421-6
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44	1105	23.1	323	15	US-10-348-081-11
45	1105	23.1	323	16	US-10-664-421-8

ALIGNMENTS

RESULT 1
US-09-971-791-9
Sequence 9, Application US/09971791
Patent No. US20020115120A1
GENERAL INFORMATION:
APPLICANT: Rosanna Kapeller-Libermann
APPLICANT: Laura A. Rudolph-Owen
APPLICANT: Kyle MacBeth
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 35800/238856
CURRENT APPLICATION NUMBER: US/09/971, 791
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 09/644, 450
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/237, 543
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 313

TYPE: PRF
ORGANISM: Homo sapiens
US-09-971-791-9

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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Percent Similarity:	100.00%	100.00%	100.00%	0	0	0
Best Local Similarity:	100.00%	100.00%	100.00%	0	0	0
Query Match:	34.87%	34.87%	34.87%	0	0	0

US-10-705-757-1 (1-2623) x US-09-971-791-9 (1-313)

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QY 471 GGCCTGCTACTGGGCAAGCGCGGCTTCGCTCGCTCTACTCAGGCACTCGCGCTCCGAC 530
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Db 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerApe 60
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QY 711 GAGAGCGCGAGAGCGGTGGCAAGATCTTGAATTCACCGAAGGAGAGAGAGAGAGAGAG 770
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QY 771 GAGAGCTGGCGCGGAGCTTCTTCTGGCAGAGTCTGAGAGCGCGCGCGCACTGCCAACA 830
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RESULT 2

US-10-081-119-18
 ; Sequence 18, Application US/1008119
 ; Publication No. US20030045491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reinhard, Christoph
 ; APPLICANT: Jefferson, Anne B.
 ; APPLICANT: Chan, Vivien W.
 ; TITLE OF INVENTION: Target in Cancer
 ; TITLE OF INVENTION: Target in Cancer
 ; FILE REFERENCE: 16932.002
 ; CURRENT APPLICATION NUMBER: US/10/081,119
 ; PRIOR FILING DATE: 2002-02-21
 ; PRIOR APPLICATION NUMBER: 60/289,813
 ; PRIOR FILING DATE: 2001-02-21
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 18
 ; LENGTH: 313
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 US-10-081-119-18

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Best Local Similarity:	100.00%	100.00%	100.00%	0	0	0
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US-10-705-757-1 (1-2623) x US-10-081-119-18 (1-313)

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Db 21 HisAlaThrIleuLeuAlaProGlyLysGlyGlyProLeuLeuSerGlnTrgInVal 40
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QY 471 GGCCTGCTACTGGGCAAGCGCGGCTTCGCTCGCTCTACTCAGGCACTCGCGCTCCGAC 530
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Db 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerApe 60
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QY 531 AACTGCGCGGTGGCCATCAAAACGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
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Db 61 AsnLeuProValAlaIleLysHisValGlnLysAspArgIleSerApeTrpGlyGlnLeu 80
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/ Sequence 52, Application US/10394322A
/ Publication No. US20030232391A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNEIS PHARMACEUTICALS, INC.
/ APPLICANT: Prescott, John C.
/ TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
/ FILE REFERENCE: 39750-0006 US
/ CURRENT APPLICATION NUMBER: US/10/394,322A
/ CURRENT FILING DATE: 2003-03-20
/ PRIOR APPLICATION NUMBER: US 60/366,892
/ PRIOR FILING DATE: 2002-03-21
/ NUMBER OF SEQ ID NOS: 70
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 52
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-394-322A-52

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Score: 1670.00 Matches: 313
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.87% Indels: 0
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QY      711 GAGAGCCCGAGCGGTGCAAGATCTCTTCGACTTCATCAGGAAAGGAGGAGCCCTGCA 770
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QY      771 GAGAGCTGGCCCGAGCTTCTTCTGGAGTGTCTGAGGCGGTGCGGCACTGCGCAAC 830
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DB      141 GluGlnleuulaargserPhePhePetrpGlnValleuGlnlavalArgghlsCyshlsAsn 160
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DB      161 CyseglyvalleuuhlsargaprllelyasprGlnasnlleuuleasprleuAsnArggly 180
QY      891 GAGCTCAAGCTCATGACCTTCGGGTCGGGGGCGCTGCAAGACACCGTCTACACGAGAC 950
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DB      181 GlnuenuylseuileahpnegllyserglyalaueuenuybaaprhvaltyrthrAsp 200
QY      951 TTCAGATGGACCCGAGTGTATAGCCCTTCAGAGTGAATCCGCTACATCCGCTACCATAGGC 1010
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DB      201 PheapgllythrargvaltyrserProbioluptrileargtyrhlsargtyrhlsGly 220
QY      1011 AGCTGGCGGCGAGTCTGGTCCCTGGGAGATCCTGCTGTATGATATGATGTGTGTGAAGATTT 1070
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DB      221 ArgserilaalavaltrpserleuglylleuenuytraspmetvalcyseglyaspIle 240
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DB      241 ProPheglunhlsaprglulgulileleargglylnvalPhePheargglylnargvalSer 260
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DB      261 SerGlucyseglnhlsleuileargtrpCyseuulaaleuargProseraapargProthr 280
QY      1191 TTGGAAGAAATCCGAACCATTCATGATGCAAGATGTTCTCTGCCCGAGAAATGCT 1250
      |||
DB      281 PheglulgulileglnaahnlsprotPmetGlnaspValleuProglngluthrAla 300
QY      1251 GAGATCCACCTCCACAGCCTGTGGCGGGGCCGAGCAA 1289
      |||
DB      301 GluilehlsleuuhlsSerleuSerProglyProserlys 313

RESULT 4
US-10-348-081-13
/ Sequence 13, Application US/10348081
/ Publication No. US20040038246A1
/ GENERAL INFORMATION:
/ APPLICANT: KORN, Marcus
/ APPLICANT: MOELLER, Guenter
/ APPLICANT: SCHNEIDER, Rudolf
/ APPLICANT: TSCHANK, Georg
/ TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
/ FILE REFERENCE: DE42002/0004 US NP
/ CURRENT APPLICATION NUMBER: US/10/348,081
/ CURRENT FILING DATE: 2003-01-21
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 13
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-348-081-13

Alignment Scores:

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Db	181	GIuLeuLybLeuIIeAspPheGlySerGlyAlaLeuLeuLybAspThrValIlyThrAsp	200
QY	951	TTTCAGTGGACCCCGAGTGTATAGCCCTTCCAGAGTGAATCCGATCCATCCGATCCATGAC	1010
Db	201	PheAspGlyIlyThrArgValIlySerProGlnIlyTrpIleArgIyHLeArgIyHLeGly	220
QY	1011	AGGTGGCGGCGAGTGGTCCCTGGGGATCCCGTGTATGATATGATGGTGGAGATATT	1070
Db	221	ArgSerAlaAlaValIlyPheSerLeuGlyIleLeuLeuLybAspMetValCysGlyAspIle	240
QY	1071	CCTTTCAGCATGACGAAGAATCATCAGGCGCGATTTTCTTCAGGACAGAGGTCTCT	1130
Db	241	ProPheGlnIlybAspGlnGlnIlyIleIleArgIyGlnValIlePheAspGlnAlaGlyAlaSer	260
QY	1131	TCAGAAATGACGATCTCATTAAGATGGAGCTTTGGCCCTGAGACCATTCAGATAGGCGAAC	1190
Db	261	SerGlnCysGlnHLeuIleArgIlyTrpCysLeuAlaLeuArgProSerbAspArgProThr	280
QY	1191	TTTCGAAGAATTCAGAAACCATTCATGATGCAAGATGTTCTCTGCCCCAGAAACTGCT	1250
Db	281	PheGlnGlnIlyIleGlnAsnHLeuProIlyPheGlnAspValIleLeuLeuProGlnGlnIlyThrAla	300
QY	1251	GAGATCCACCTTCCACAGGCTGTCCGCGGGGCCACGAA	1289
Db	301	GlnIleHLeuHLeuSerLeuSerProGlyProSerIlyb	313

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RESULT 6
US-10-664-421-150
/ Sequence 150, Application US/10664421
/ Publication No. US20040142864A1
/ GENERAL INFORMATION:
/ APPLICANT: BREMER, RYAN
/ APPLICANT: IBRAHIM, PRAHMA
/ APPLICANT: KUMAR, ABHINAV
/ APPLICANT: MANDIVAN, VALSAN
/ APPLICANT: MILBURN, MICHAEL V.
/ TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
/ FILE REFERENCE: 039363/0703
/ CURRENT APPLICATION NUMBER: US/10/664,421
/ CURRENT FILING DATE: 2003-09-16
/ PRIOR APPLICATION NUMBER: 60/412,341
/ PRIOR FILING DATE: 2002-09-20
/ PRIOR APPLICATION NUMBER: 60/411,398
/ PRIOR FILING DATE: 2002-09-16
/ NUMBER OF SEQ ID NOS: 169
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 150
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-664-421-150

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Alignment Scores:

Pred. No.:	2,43e-94	length:	333
Score:	1670.00	Matches:	333
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	34.87%	Indels:	0
DB:	16	Gaps:	0

US-10-705-757-1 (1-2623) x US-10-664-421-150 (1-313)

Oy	35	ATGCTCTTGGCAAAATCAACTCGCTGTGGCCACTGGGGCGCGCCCTGGAAAGACTG	410
Db	1	MetLeuLeuSerLysIleIenSerLeuAlaHsIleAlaGAlaAlaProCysAsnAspLeu	20
Oy	411	CAGCCCAACAAGCTGGCGCCCGCAAGAAAGAGACCTCGAGTCGCAATACCAAGTG	470
Db	21	HsAlaIhrIhrIleuAlaProGlyIyrGAluIyrGAluProLeuGlnSerGlnIyrGlnVal	40
Oy	471	GGCCCGCTACTGGGCAAGCGCGGCTTCGCGCTGCTACTACAGGCAATCCGCGTTCGGAC	530

Db	41	GlyProLeuLeuGlySerGlyGlyPheGlySerValItyrSerGlyIleArgValSerAsp	60
Qy	531	AACTTGCCTGGTGCATTCAAACACGTGAGAGAGACCGGATTTCCGACTGGGGAGACTG	590
Db	61	AsnLeuProValAlaIleItyrHisIleValGlnIlyAspArgIleSerAspTrpGlyGlnLeu	80
Qy	591	CCPAAATGGACATCGAGTGGCCCATGGAAGTGGTCCCTGCTGAAGAAAGTACGAGCTCGGGTTCC	650
Db	81	ProAsnGlyThrArgValProMetGlnValValLeuLeuIlybIyValSerSerGlyPhe	100
Qy	651	TCCGGCGCTCATTAAGCTCTCGGACCTGGTTCGAGAGGCCGACATTTCTGTCCTGATCTCG	710
Db	101	SerGlyValIleArgLeuLeuAspTrpPheGlnArgProAspSerPheValIleuIleu	120
Qy	711	GAGAGGCCCGGACGCCGTGTGCAGAGATCTTGTGACTTCATCACGAAAGGGAGCCCTTGCA	770
Db	121	GlnArgProGlnProValGlnAspLeuPheAspPheIleThrGlnArgGlyAlaLeuGln	140
Qy	771	GAGAGAGCTGGCCGCGACGTTCTTGTGACAGGTGTGAGAGCCGGCGGGACCTGCGACAAAC	830
Db	141	GlnGlnLeuAlaArgSerPhePheTrpGlnValIleuGlnAlaValArgHisCysHisAsn	160
Qy	831	TGCGGGGTGTCTACACCGCGACATCAAGAGACGAAACATCTTATGCACTTCAATCGCGGC	890
Db	161	CysGlyValLeuHisIleArgAspIleItyrAspGlnAsnIleLeuIleAspLeuAsnArgGly	180
Qy	891	GAGCTCAAGCTCATGCACTTCGGGTCCGGGGCGCTGCTCAAGAGACCCGTCTACCGGAC	950
Db	181	GlnLeuIysLeuIleAspPheGlySerGlyAlaLeuLeuIysAspThrValItyrThrAsp	200
Qy	951	TTTGATGGAGACCCGAGTGTATAGCCCTCCAGAGTGAATCCGCTACCATTCGTCACATGCGC	1010
Db	201	PheAspGlyThrArgValItyrSerProProGlnTrpIleArgIlyThrAspGlyTrpHisGly	220
Qy	1011	AGGTCCGCGGACGTCTGTGCTCCCTGGGAGCTCTGTGTATGATATGATGTGTGAGATATT	1070
Db	221	ArgSerHisIleValItyrPserLeuGlyIleLeuLeuItyrAspMetValCysGlyAspIle	240
Qy	1071	CCTTTCGAGCATGACGAAAGATATATCAAGGGCCAGGTTTCTTCAGGACGAGGGTCTCT	1130
Db	241	ProPheGlnHisAspArgGlnIleIleItyrGlyValIlePhePheArgGlnArgValSer	260
Qy	1131	TCAGAAATGTACAGATCTCATTAAGTGTGTGGCCCTGAGACCATCAGATAGAGCCAAAC	1190
Db	261	SerGlnCysGlnHisIleuIleArgItyrCysLeuAlaLeuArgProSerAspArgProThr	280
Qy	1191	TTTCGAGAAATTCAGAAACATTCATGAGATGAGATGTTCTCTGCCACGAAATGTCT	1250
Db	281	PheGlnGlnIleGlnAsnHisProTyrMetGlnAspValIleLeuProGlnGlnIleThrAla	300
Qy	1251	GAGATTCACCTCCACAGCTGTGTCCGGGGCCCAAGCAA	1289
Db	301	GlnIleHisLeuHisSerLeuSerProGlyProSerIys	313

RESULT

US-10-377-268-9
: Sequence 9, Application US/10377268
: Publication No. US20040171062A1
: GENERAL INFORMATION:
: APPLICANT: HIRTH, KLAUS-PETER
: APPLICANT: MILBURN, MICHAEL VANCE
: TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS

// CURRENT APPLICATION NUMBER: US/10/377,268
 // PRIOR APPLICATION NUMBER: 2003-02-28
 // PRIOR FILING DATE: 2003-01-02
 // PRIOR APPLICATION NUMBER: 60/437,929
 // PRIOR FILING DATE: 2003-01-02
 // PRIOR APPLICATION NUMBER: 60/360,651
 // PRIOR FILING DATE: 2002-02-28
 // PRIOR APPLICATION NUMBER: 60/411,398
 // PRIOR FILING DATE: 2002-09-16
 // PRIOR APPLICATION NUMBER: 60/412,341
 // PRIOR FILING DATE: 2002-09-20


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Db      141  GUGLULEULHARSGERPHENETPGGLNValleuclulalalaAghIscYshIaen 160
Qy      831  TGGGGGGTGTACACCCGACATCAGAGAGAAACATCTTATCGACTCAATCGGAC 890
Db      161  CysgIyValleuHIsarGarpIlelysaRgIubsnIleuHleapleuAenAsgIy 180
Qy      891  GAGCTCAAGCTCATCGACTTCGGGTGGGGGGCGTGTCAAGGACACCGCTACAGGAC 950
Db      181  GILUeulYLeuHleapRhegIysergIyAlaleuLeuYsaRptnValTyrtHAsp 200
Qy      951  TTCGATGGGACCCGAGTGTATAGCCCTCAGAGTGATCCGCTACCATCGCTACATGCG 1010
Db      201  PheasRgIyThrtArgValTyrsErProrogIutPrIleArgTyrtHAsgTyrtHsgIy 220
Qy      1011 AGGTGGGCGGAGCTGTGTCCTCGGGGATCTGTCTGTATATATGTGTGTGAATATT 1070
Db      221  ArgserAlaIvalaItrpserleuGlyIleleuLeuTyraRmetValCysgIyAapRle 240
Qy      1071  CCTTGGAGCATGACGAGATCATAGAGGGGCGAGTTTCTTCAAGGAGAGGTCTCT 1130
Db      241  ProPhegluHIsarPgluIleIleArgIyGlnValPheRheArgGlnArgValser 260
Qy      1131  TCAGAAATGCAGCATCTCATTAAGTGTGCTTGCCCTGAGACCATCAGATTAGGCGCAAC 1190
Db      261  SerGIuCyseIlnHleuHleatrgTPrCyseuAlaleuArgProserAapArgProtrH 280
Qy      1191  TTGGAAGAATCCAGAACCATCCATGATGATGATGATGATGATGATGATGATGATGATGAT 1250
Db      281  PhegluGluIleGlnsnHIsarProtrPmetGlnAapRValleuLeuProglngIutnAla 300
Qy      1251  GAGATCCACCTCCACAGCCTGTGGCGGGGCCAGCAAA 1289
Db      301  GIUIleHleuHIsarLeuSerProglYProserIys 313

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RESULT 9

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US-10-951-406-18
; Sequence 18, Application US/10951406
; Publication NO. US20050059630A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951.406
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081.119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289.813
; PRIOR FILING DATE: 2001-02-21
; SOFTWARE: Paaseq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-406-18

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Alignment Scores:

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Pred. No.: 2 42e-94 Length: 313
Score: 1670.00 Matches: 313
Percent Similarity: 100.00% Conservatave: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.87% Indels: 0
DB: 17 Gaps: 0

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US-10-705-757-1 (1-2623) x US-10-951-406-18 (1-313)

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Qy      351  ATGCTTTGTCAAAATCAATCGCTTGTCCACATGCGCGCGCGCTGACAGACTG 410
Db      1  MetLeuLeuSerTyrlleAenSerleuAlaHleuAlaArgAlaIarProCyAaenAapRleu 20

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Qy      411  CAGCGCACAAAGTGGCGCCCGGCAAGAGAACCCCTGAGTCCAGTACAGTAC 470
Db      21  HIsaIethrIyLeuHlaIarProglYlYsgIuYgIuProlouHIsarGlnTyrtGlnVal 40
Qy      471  GGCCCGCTACTGGGACAGCGGCGCTTCGGCTCGGTCTACTCAGGACATCCGCTCGAC 530
Db      41  GYProleuLeuHIsarGlyserGlyPheglYserValTyserGIyIleArgValserAap 60
Qy      531  AACTGCCGGTGGCCATCAACACGTGAGAAAGAACCCGATTTCCAGCTGGGGAGAGCTG 590
Db      61  AenLeuProValAlaIleIyshIsValGIuYsaRArgIeserAapRptgIyGluLeu 80
Qy      591  CCTAATGGGACATCGACTGCCCATNGAAGTGCCTCTGAAAGGTGAGCTCGGGTTTC 650
Db      81  ProAenGIyThrtArgValPrometGluValleuLeuYsaRValserSerGIyPhe 100
Qy      651  TCCGCGGTCAATPAGCTCTGTGACTGTTCAAGAGGCCGACAGTTTCTGTGATCTTG 710
Db      101  SerGIyValIleArgleuLeuAapRtrPhegluArgProAapserPheValleuIleu 120
Qy      711  GAGAGGCCGAGCGGATGCAAGATCTTTCGACTTCATACGGAAGGAGGAGCTTGCAA 770
Db      121  GluArgProgluProValGlnAapRleuPheAapRheIleThrgIuArgIyAlaleuGln 140
Qy      771  GAGGAGCTGGCCCGGAGCTTCTTTCGAGAGCTGTGAGGCGCGTGGGACCTGGCAAC 830
Db      141  GUGLULEULHARSGERPHENETPGGLNValleuclulalalaAghIscYshIaen 160
Qy      831  TGGGGGGTGTACACCCGACATCAGAGAGAAACATCTTATCGACTCAATCGGAC 890
Db      161  CysgIyValleuHIsarGarpIlelysaRgIubsnIleuHleapleuAenAsgIy 180
Qy      891  GAGCTCAAGCTCATCGACTTCGGGTGGGGGGCGTGTCAAGGACACCGCTACAGGAC 950
Db      181  GILUeulYLeuHleapRhegIysergIyAlaleuLeuYsaRptnValTyrtHAsp 200
Qy      951  TTCGATGGGACCCGAGTGTATAGCCCTCAGAGTGATCCGCTACCATCGCTACATGCG 1010
Db      201  PheasRgIyThrtArgValTyrsErProrogIutPrIleArgTyrtHAsgTyrtHsgIy 220
Qy      1011 AGGTGGGCGGAGCTGTGTCCTCGGGGATCTGTCTGTATATATGTGTGTGAATATT 1070
Db      221  ArgserAlaIvalaItrpserleuGlyIleleuLeuTyraRmetValCysgIyAapRle 240
Qy      1071  CCTTGGAGCATGACGAGATCATAGAGGGGCGAGTTTCTTCAAGGAGAGGTCTCT 1130
Db      241  ProPhegluHIsarPgluIleIleArgIyGlnValPheRheArgGlnArgValser 260
Qy      1131  TCAGAAATGCAGCATCTCATTAAGTGTGCTTGCCCTGAGACCATCAGATTAGGCGCAAC 1190
Db      261  SerGIuCyseIlnHleuHleatrgTPrCyseuAlaleuArgProserAapArgProtrH 280
Qy      1191  TTGGAAGAATCCAGAACCATCCATGATGATGATGATGATGATGATGATGATGATGATGAT 1250
Db      281  PhegluGluIleGlnsnHIsarProtrPmetGlnAapRValleuLeuProglngIutnAla 300
Qy      1251  GAGATCCACCTCCACAGCCTGTGGCGGGGCCAGCAAA 1289
Db      301  GIUIleHleuHIsarLeuSerProglYProserIys 313

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RESULT 10

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US-10-951-477-18
; Sequence 18, Application US/10951477
; Publication NO. US20050063974A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951.477

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Db 1 MetleuLeuSerlyslleAenSerleuAlahleuAargAlaalaProCyAaenAAspLeu 20
QY 411 CAGGCCCAACAGCTGGGGCCCGGCAAGAAAGAGCCCTGGAGTGGCACTACAGAGT 470
Db 21 HleAlaThrlyseuAlaProGlyLysGlnLysGlnProleuGlnSerGlnTyGlnVal 40
QY 471 GGCCCGCTACTGGGCAAGCGGCGCTTGGCTCGGTACTACAGGACATCCGGTCTCCGAC 530
Db 41 GlyProleuLeuGlySerGlyGlyPheGlySerValTySerGlyLeuAargValSerAsp 60
QY 531 AACTGGCGGTGGCCATCAACACGTGAGAAAGAGCCGGAATTCGACTGGAGAGAGCTG 590
Db 61 AenleuProValAlaAlaIleLysHleValGlnLysAerArgIleSerAerTrpGlyGlnLeu 80
QY 591 CTTAAATGGCACTGAGAGTGGCCCAATGAGAGTGTCTCTGTAAGAAAGAGTGGAGTTC 650
Db 81 ProAenGlyThrArgValProMetGlnValValLeuLysLysValSerSerGlyPhe 100
QY 651 TCCGCGCTCATTAAGGCTCTGAGTGGTTCGAGAGGCGCGAGTTTCGCTGATCTG 710
Db 101 SerGlyValIleAargLeuLeuAerTrpPheGlnAargProAerSerPheValLeuLeu 120
QY 711 GAGAGCGCCGAGCGCGTGAAGATCTTCTGACTTCAACGAAAGGAGGAGCCCTGCAA 770
Db 121 GluAargProGlnProValGlnAerPheAerPheIleThrGlnAargGlyAlaLeuGln 140
QY 771 GAGAGCTGGCGCGGAGCTTCTTGGCAGAGTGTCTGAGAGCGCGTGGCACTGGCACAC 830
Db 141 GlnGlnLeuAlaAargSerPhePheTrpGlnValLeuGlnAlaValAargHscYshAsn 160
QY 831 TGGCGGGTGTCTACACCGCGCATCAACAGAAAGAAATCTCTTAATCGACTTCGAGCG 890
Db 161 CysGlyValLeuHleAargAerIleLysAerGlnAenIleLeuIleAerAaAaAargGly 180
QY 891 GAGCTCAAGCTCATCGACTTCGAGTTCGAGGCGCGTCTCAAGGACACCGTCTACACGAC 950
Db 181 GlnLeuLysLeuIleAerPheGlySerGlyAlaLeuLysLysAerTrpValTyTrnAer 200
QY 951 TTGAGATGGGACCCGAGTGTATAGCCCTCGAGAGTGCATCCGCTACCATGGCTAGC 1010
Db 201 PheAerGlyThrArgValTySerProGlnTrpIleAargTyHscAargTyHscGly 220
QY 1011 AGGTGGCGGAGCTGTGGTCTCTGGGAGTCTGTGATGATATAGTGTGGAGATATT 1070
Db 221 AargSerAlaAlaAlaIlePheSerLeuGlyIleLeuLysTyAerPheValCysGlyAerPhe 240
QY 1071 CCTTTCGAGCATGACGAAGATCATCAAGGCGCGAGTTTCTTCAAGGAGAGGCTCTCT 1130
Db 241 ProPheGlnHleAerGlnGlnIleIleAargGlyGlnValPheAerAargGlnAargValSer 260
QY 1131 TCGAATGTGACATCTCATTAATGAGTGTGGCTTGGAGCCATGACATGATAGGCCAAC 1190
Db 261 SerGlnCysGlnHleAerIleAargTyCysLeuAlaLeuAargProSerAerAerProThr 280
QY 1191 TTGGAAGAATTCGAACATCATCAAGATGATGATGATGATGATGATGATGATGATGAT 1250
Db 281 PheGlnGlnIleGlnAenHleAerProTrpMetGlnAerAlaLeuLysProGlnGlnTrnAla 300
QY 1251 GAGATCCACTTCACAGCTGTGCGCGGCGCGCCAGCAAA 1289
Db 301 GlnIleHleAerHleAerSerLeuSerProGlyProSerTySer 313

RESULT 12
US-10-705-757-2
; Sequence 2, Application US/10705757
; Publication No. US20040146942A1
; GENERAL INFORMATION:
; APPLICANT: GRUNENTHAL, GMBH
; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
; FILE REFERENCES: 029310, 5281805
; CURRENT APPLICATION NUMBER: US/10/705, 757
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/EP02/05234

; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: DE 101 23 055.9
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-705-757-2
Alignment Scores:
Pred. No.: 2,42e-94 Length: 313
Score: 1670.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34,87% Indels: 0
DB: 18 Gaps: 0
US-10-705-757-1 (1-2623) x US-10-705-757-2 (1-313)
QY 351 ATGCTCTTGTCAAAATCAATCGCTTGGCCACCTGGCGCGCGCCCTGCAACGACTG 410
Db 1 MetleuLeuSerlyslleAenSerleuAlahleuAargAlaalaProCyAaenAAspLeu 20
QY 411 CAGGCCCAACAGCTGGGGCCCGGCAAGAAAGAGCCCTGGAGTGGCACTACAGAGT 470
Db 21 HleAlaThrlyseuAlaProGlyLysGlnLysGlnProleuGlnSerGlnTyGlnVal 40
QY 471 GGCCCGCTACTGGGCAAGCGGCGCTTGGCTCGGTACTACAGGACATCCGGTCTCCGAC 530
Db 41 GlyProleuLeuGlySerGlyGlyPheGlySerValTySerGlyLeuAargValSerAsp 60
QY 531 AACTGGCGGTGGCCATCAACACGTGAGAAAGAGCCGGAATTCGACTGGAGAGAGCTG 590
Db 61 AenleuProValAlaAlaIleLysHleValGlnLysAerArgIleSerAerTrpGlyGlnLeu 80
QY 591 CTTAAATGGCACTGAGAGTGGCCCAATGAGAGTGTCTCTGTAAGAAAGAGTGGAGTTC 650
Db 81 ProAenGlyThrArgValProMetGlnValValLeuLysLysValSerSerGlyPhe 100
QY 651 TCCGCGCTCATTAAGGCTCTGAGTGGTTCGAGAGGCGCGAGTTTCGCTGATCTG 710
Db 101 SerGlyValIleAargLeuLeuAerTrpPheGlnAargProAerSerPheValLeuLeu 120
QY 711 GAGAGCGCCGAGCGCGTGAAGATCTTCTGACTTCAACGAAAGGAGGAGCCCTGCAA 770
Db 121 GluAargProGlnProValGlnAerPheAerPheIleThrGlnAargGlyAlaLeuGln 140
QY 771 GAGAGCTGGCGCGGAGCTTCTTGGCAGAGTGTCTGAGAGCGCGTGGCACTGGCACAC 830
Db 141 GlnGlnLeuAlaAargSerPhePheTrpGlnValLeuGlnAlaValAargHscYshAsn 160
QY 831 TGGCGGGTGTCTACACCGCGCATCAACAGAAAGAAATCTCTTAATCGACTTCGAGCG 890
Db 161 CysGlyValLeuHleAargAerIleLysAerGlnAenIleLeuIleAerAaAaAargGly 180
QY 891 GAGCTCAAGCTCATCGACTTCGAGTTCGAGGCGCGTCTCAAGGACACCGTCTACACGAC 950
Db 181 GlnLeuLysLeuIleAerPheGlySerGlyAlaLeuLysLysAerTrpValTyTrnAer 200
QY 951 TTGAGATGGGACCCGAGTGTATAGCCCTCGAGAGTGCATCCGCTACCATGGCTAGC 1010
Db 201 PheAerGlyThrArgValTySerProGlnTrpIleAargTyHscAargTyHscGly 220
QY 1011 AGGTGGCGGAGCTGTGGTCTCTGGGAGTCTGTGATGATATAGTGTGGAGATATT 1070
Db 221 AargSerAlaAlaAlaIlePheSerLeuGlyIleLeuLysTyAerPheValCysGlyAerPhe 240
QY 1071 CCTTTCGAGCATGACGAAGATCATCAAGGCGCGAGTTTCTTCAAGGAGAGGCTCTCT 1130
Db 241 ProPheGlnHleAerGlnGlnIleIleAargGlyGlnValPheAerAargGlnAargValSer 260

US-10-705-757-1 (1-2623) x US-10-941-635-152 (1-313)

QY 351 ATGCTTTTGCAGAAATCAACTGCTTGCSCACCTGCGCGCGCCCTGCAAGCACTG 410
 DB 1 MetLeuLeuSerLysIleAenSerLeuLhIleuLrgLlAlaProCybAaAaPheU 20
 QY 411 CAGGCCCAAGCTGGCGCGCGCGAGAGAAAGAGAGCCCTGAGTGCAGTACAGCTG 470
 DB 21 HleAlThrlYsLeuAlaProGlyLysGlyLeuPheLeuProLeuGlnSerGlnYglVal 40
 QY 471 GGGCCGCTACTGGGCGAGCGCGCTTGCCTGCTGCTACTCAGGCACTCGCGCTCCGAC 530
 DB 41 GlyProLeuLeuGlnSerGlyGlyPheGlySerValYlSerGlyIleArgValSerAaP 60
 QY 531 AACTTGGCGGTGGCCATCAAAACAGTGAAGAGAGCCGAGATTTCCGACTGGAGAGCTG 590
 DB 61 AaLeuProValAlaIleYbHleValGlyLysAaAaPrgIleSerAaPTrpGlyGlyLeu 80
 QY 591 CTTAATGGCACTGAGTGGCCCAATGAAGTGGCTCTGCTGAAGAAAGTGAAGCTGGCTTC 650
 DB 81 ProAaAaGlyThrlArgValIleProMetGlyValIleuLeuYbYsValSerSerGlyPhe 100
 QY 651 TCGCGGCTCATTTAGGCTCTGCACTGCTGAGAGCGCGAGAGCTTTCCTGATCTGCTG 710
 DB 101 SerGlyValIleArgLeuLeuAaPTrpPheGlyLysProAaPserPheValIleuLeu 120
 QY 711 GAGAGCCCGAGCGCGTGAAGATCTTGTGCACTTCACTCAAGAAAGGAGCGCTGCA 770
 DB 121 GluArgProGlyProValGlnAaPhePheAaPheIleThrlGlyAaGlyAlaLeuGln 140
 QY 771 GAGAGCTGGCGCGCGAGCTTCTTGTGCAAGTGTGAGAGCGCGCTGCGCACTGCGCAAC 830
 DB 141 GluGlyLeuAlaArgSerPhePheTrpGlnValIleuGlyAlaValArgHleCybHleAaP 160
 QY 831 TGGCGGCTGTACACCGCGCATCAAGAGAGAAACATCTTATCCGACTCATTCGCGGCG 890
 DB 161 CybGlyValIleuHleAaAaPTrpIleLysAaPTrpIleuLeuIleAaPLeuAaAaGly 180
 QY 891 GAGCTCAAGCTCACTGCACTTCCGAGTGGAGCGCTGCTCAAGAGACACCTGCTACACGAG 950
 DB 181 GluLeuYbLeuIleAaPheGlySerGlyAlaLeuLeuYbAaPTrpValYlYlThrlAaP 200
 QY 951 TTGAGTGGAGCCGAGTGTATAGCTTCCAGAGTGAATCCGCTACATCCGCTACATGCG 1010
 DB 201 PheAaPTrpThrlArgValYlYlSerProProGlyTrpIleArgYlHleAaGlyYlHle 220
 QY 1011 AGGTGGCGGAGCTGCTGCTCCGAGGAGCTGCTGCTGATATAGTATGCTGTGAGATAT 1070
 DB 221 ArgSerAlaAlaValIlePheSerLeuGlyIleuLeuYlAaPTrpMetValCybGlyAaPTr 240
 QY 1071 CCTTTCAGAGTGAAGAGATCATCAAGAGGCGCAGAGTTTCTTCAAGAGAGGAGTCT 1130
 DB 241 PhePheGlnHleAaPTrpGlyIleIleArgGlyGlnValIlePhePheAaGlnAaGlySer 260
 QY 1131 TCAAGATGTGAGCATCTCATTAAGTGTGCTTGGCCCTGAGACCATCAATAGAGCCAAC 1190
 DB 261 SerGlyCybGlnHleuIleArgTrpCybLeuAlaLeuArgProSerAaPArgProThr 280
 QY 1191 TTGGAAGAAATCCAGAACATCCATGATGCAAGATGTTCTCCGCGCCCAAGAACTGCT 1250
 DB 281 PheGlnIleuIleGlnAaPTrpMetGlnAaPValIleuLeuProGlnGlyThrlAla 300
 QY 1251 GAGATTCACCTCCACAGCTGTGCGCGGCGCGCAGCAAA 1289
 DB 301 GluIleHleuHleuHleuSerLeuSerProGlyProSerYs 313

RESULT 15

US-10-620-052A-22

Sequence 22, Application US/10620052A

Publication No. US20040126784A1

GENERAL INFORMATION:

APPLICANT: HitcoBnI, YasumiChI

APPLICANT: Jenkins, Yonchu
 APPLICANT: Markovtsov, Vadim
 APPLICANT: Rigel Pharmaceuticals, Inc.
 TITLE OF INVENTION: Modulators of Cellular Proliferation
 FILE REFERENCE: 021044-004010US
 CURRENT APPLICATION NUMBER: US/10/620,052A
 CURRENT FILING DATE: 2003-07-14
 PRIOR APPLICATION NUMBER: US 60/395,443
 PRIOR FILING DATE: 2002-07-12
 NUMBER OF SEQ ID NOS: 78
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 22
 LENGTH: 313
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: PIM1 oncogene serine threonine kinase
 US-10-620-052A-22

Alignment Scores:

Pred. No.: 1,53e-93 Length: 313
 Score: 1657.00 Matches: 311
 Percent Similarity: 99.36% Conservative: 2
 Best Local Similarity: 99.36% Mismatches: 0
 Query Match: 34,60% Indels: 0
 DB: 16 Gaps: 0

US-10-705-757-1 (1-2623) x US-10-620-052A-22 (1-313)

QY 351 ATGCTTTTGCAGAAATCAACTGCTTGCSCACCTGCGCGCGCCCTGCAAGCACTG 410
 DB 1 MetLeuLeuSerLysIleAenSerLeuLhIleuLrgLlAlaProCybAaAaPheU 20
 QY 411 CAGGCCCAAGCTGGCGCGCGCGAGAGAAAGAGAGCCCTGAGTGCAGTACAGCTG 470
 DB 21 HleAlThrlYsLeuAlaProGlyLysGlyLeuPheLeuProLeuGlnSerGlnYglVal 40
 QY 471 GGGCCGCTACTGGGCGAGCGCGCTTGCCTGCTGCTACTCAGGCACTCGCGCTCCGAC 530
 DB 41 GlyProLeuLeuGlnSerGlyGlyPheGlySerValYlSerGlyIleArgValSerAaP 60
 QY 531 AACTTGGCGGTGGCCATCAAAACAGTGAAGAGAGCCGAGATTTCCGACTGGAGAGCTG 590
 DB 61 AaLeuProValAlaIleYbHleValGlyLysAaAaPrgIleSerAaPTrpGlyGlyLeu 80
 QY 591 CTTAATGGCACTGAGTGGCCCAATGAAGTGGCTCTGCTGAAGAAAGTGAAGCTGCGCTTC 650
 DB 81 ProAaAaGlyThrlArgValIleProMetGlyValIleuLeuYbYsValSerSerGlyPhe 100
 QY 651 TCGCGGCTCATTTAGGCTCTGCACTGCTGAGAGCGCGAGAGCTTTCCTGATCTGCTG 710
 DB 101 SerGlyValIleArgLeuLeuAaPTrpPheGlyLysProAaPserPheValIleuLeu 120
 QY 711 GAGAGCCCGAGCGCGTGAAGATCTTGTGCACTTCACTCAAGAAAGGAGCGCTGCA 770
 DB 121 GluArgProGlyProValGlnAaPhePheAaPheIleThrlGlyAaGlyAlaLeuGln 140
 QY 771 GAGAGCTGGCGCGAGCTTCTTGTGCAAGTGTGAGAGCGCGCTGCGCACTGCGCAAC 830
 DB 141 GluGlyLeuAlaArgSerPhePheTrpGlnValIleuGlyAlaValArgHleCybHleAaP 160
 QY 831 TGGCGGCTGTACACCGCGCATCAAGAGAGAAACATCTTATCCGACTCATTCGCGGCG 890
 DB 161 CybGlyValIleuHleAaAaPTrpIleLysAaPTrpIleuLeuIleAaPLeuAaAaGly 180
 QY 891 GAGCTCAAGCTCACTGCACTTCCGAGTGGAGCGCTGCTCAAGAGACACCTGCTACACGAG 950
 DB 181 GluLeuYbLeuIleAaPheGlySerGlyAlaLeuLeuYbAaPTrpValYlYlThrlAaP 200
 QY 951 TTGAGTGGAGCCGAGTGTATAGCTTCCAGAGTGAATCCGCTACATCCGCTACATGCG 1010
 DB 201 PheAaPTrpThrlArgValYlYlSerProProGlyTrpIleArgYlHleAaGlyYlHle 220

```
QY 1011 AGGTCGGCGGCACTGTGTCCTGGGGATCTGCTGTATGATATGTTGTGTGAGATATT 1070
    |||||
Db 221 ArgSerIaIaIaValTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
    |||||
QY 1071 CTTTCAGCATGACGAAAGATCATTCAGGGGCCAGGTTTCTTCAGGCAGAGGTCCTCT 1130
    |||||
Db 241 ProPheGluHisAspGluGluIleLeuArgGlyGlnValPhePheArgGlnArgValSer 260
    |||||
QY 1131 TCAGAAATGTCAGCATCTCATTAAGATGGTGGCTGGCCCTGAGACCATCAGATAGGCCAAC 1190
    |||||
Db 261 SerGluCysGlnHisLeuIleArgTyrCysLeuHisLeuArgProSerAspArgProThr 280
    |||||
QY 1191 TTGGAAGAAATCCAGAACCATTCATGAGATGCAAGATGTTCTCTGCCCCAGAAACTGCT 1250
    |||||
Db 281 PheGluGluIleGlnAsnHisProTyrMetGlnAspValLeuLeuProGlnGluThrAla 300
    |||||
QY 1251 GAGATCCACCTCCACAGCCTGTGCGCGGGGCCAGCMAA 1289
    |||||
Db 301 GluIleHisLeuHisSerLeuSerProGlyProSerIys 313
    |||||
```

Search completed: September 22, 2005, 17:46:35
Job time : 374.236 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 15:57:45 ; Search time 342.494 Seconds

(without alignments)
5924.037 Million cell updates/sec

Title: US-10-705-757-1

Perfect score: 4789
Sequence: 1 gaggagagcccgagagagc.....aataaaacccttgcttc 2623

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ n2p.model -DEV=xlp
-Q/cgn2.1/USPRO.epool_p/US10705757/runat_22092005_115014_22122/app_query.fasta_1.5333
-DB=A.Geneseq -QMT=fastran -SUFFIX=n2p.xsg -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNIT5-bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPRM=prc -NOR=ext -HEA=SIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10705757_QCGN_1_1_753_@runat_22092005_115014_22122 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A.Geneseq_16Dec04:.*
1: geneseqp19808:.*
2: geneseqp19908:.*
3: geneseqp20008:.*
4: geneseqp20018:.*
5: geneseqp20028:.*
6: geneseqp20038:.*
7: geneseqp20038:.*
8: geneseqp20048:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1670	34.9	313	5	ABP54943 Human P1m
2	1670	34.9	313	5	ABG33017 Human PRO
3	1670	34.9	313	6	AAO19788 Human P1M
4	1670	34.9	313	7	ABU61613 Human P1M
5	1670	34.9	313	7	ABR62939 Human P1M
6	1670	34.9	313	7	ABR62939 Human ser
7	1670	34.9	313	7	ADP45083 Human PRO
8	1670	34.9	313	8	ADO19690 Human PRO
9	1670	34.9	313	8	ADR88370 Human P1M
10	1670	34.9	313	8	ADP24227 PRO polyp

11	1657	34.6	313	2	AAW08139 Human CYT
12	1657	34.6	313	3	AAV87959 Human CR7
13	1657	34.6	313	8	AD157202 Human P1M
14	1657	34.6	313	8	ADN03170 Human P1M
15	1636	34.2	313	5	ABG33016 Rat prote
16	1636	34.2	313	6	AAO19789 Rat P1M
17	1636	34.2	313	7	ABR62938 Rat berin
18	1582	33.0	313	5	ABG33015 Mouse pro
19	1582	33.0	313	6	AAO19790 Murine PI
20	1582	33.0	313	7	ABR62940 Mouse ser
21	1582	33.0	313	7	ADN97347 Murine PI
22	1582	33.0	313	8	ADR88371 Mus muscu
23	1362	28.4	253	8	AD157241 P1M1 domi
24	1296.5	27.1	257	8	AAV33942 Rat prote
25	1294.5	27.0	254	8	ADK71853 Human Kin
26	1149.5	24.0	455	5	AAE23836 Rat K1D-1
27	1149.5	24.0	455	5	ABG33013 Rat prote
28	1149.5	24.0	455	7	ADE55366 Rat Prote
29	1145	23.9	382	8	ADO20314 Human PRO
30	1145	23.9	382	8	ADP55593 Human PRO
31	1140	23.8	323	8	ADR88376 Colunlix
32	1135	23.7	326	2	AAV06886 HWHHJ20 P
33	1133	23.7	326	4	AAE23834 Human HKI
34	1133	23.7	326	5	ABG33011 Human ser
35	1133	23.7	326	5	ABR62932 Human pro
36	1133	23.7	326	7	ADJ96625 Human cal
37	1133	23.7	326	8	ADL97960 Human P1M
38	1129.5	23.6	326	6	AAO19792 Murine PI
39	1129.5	23.6	326	7	ABR62933 Mouse pro
40	1129.5	23.6	326	8	ADO60032 CRH 61gna
41	1129.5	23.6	326	8	ADR88375 Mus muscu
42	1129.5	23.6	326	5	AAO20524 Protein B
43	1128.5	23.6	326	6	AAO19791 Rat P1M3
44	1128.5	23.6	326	7	ABR62936 Rat prote

ALIGNMENTS

RESULT 1
ABP54943
ID ABP54943 standard; protein; 313 AA.
XX
AC ABP54943:
XX
DT 13-JAN-2003 (first entry)
XX
DE Human P1m1.
XX
KW P1m1; tyrosine threonine kinase; TTK; protein kinase; enzyme;
KW mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;
KW human; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200266444-A1.
XX
PD 06-SEP-2002.
XX
PF 21-FEB-2002; 2002WO-US005278.
XX
PR 21-FEB-2001; 2001US-0271254P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Reinhard C, Jefferson AB, Chan VW;
XX
DR WPI, 2002-698650/75.
XX
DR N-PSDB; ABV73989.
XX
PT Reducing growth of cancer cells comprises reducing Tyrosine Threonine
PT Kinase (TTK) activity; useful in diagnosing and treating disorders with
PT abnormal expression levels and activity of TTK, such as lung, colon,

XX Sequence 313 AA:
 SQ Alignment Scores:
 Pred. No.: 7.05e-113 Length: 313
 Score: 1670.00 Matches: 313
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.87% Indels: 0
 DB: Gaps: 0
 US-10-705-757-1 (1-2623) x ABG3017 (1-313)
 QY 351 ATGCTCTTTCACAAATCAACTGGCTTGGCCACCTGGCGCGCGCCCTGCAAGCACTG 410
 DB 1 MetLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20
 QY 411 CACGCCACCAAGCTGGCGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
 DB 21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGlnSerGlnTyrGlnVal 40
 QY 471 GGGCGGCTACTGGGCGAGCGCGGCTTGGCTCGGCTACTGAGCATCCGGCTCCGAC 530
 DB 41 GlyProLeuGlnSerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
 QY 531 AACTGGCGGCTGGCATCAACAACGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
 DB 61 AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTyrGlyGluLeu 80
 QY 591 CCTAATGGCACTGAGTGGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 650
 DB 81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
 QY 651 TCCGGGCTCAATTAGGCTCTGAGACTGGTTCGAAGAGAGAGAGAGAGAGAGAGAGAG 710
 DB 101 SerGlyValIleArgLeuLeuAspTyrPheGluArgProAspSerPheValLeuIleLeu 120
 QY 711 GAGAGCGCGAGCGCGGCGCAAGATCTCTGACTTCACTCAAGAGAGAGAGAGAGAGAG 770
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgValAlaLeuGln 140
 QY 771 GAGGAGCTGGCGCGAGCTTCTTCTGGCAGAGTGTGAGAGAGAGAGAGAGAGAGAGAG 830
 DB 141 GluGluLeuAlaArgSerPhePheTyrGlnValLeuGlnAlaValArgHisCysHisAsn 160
 QY 831 TGGGGGCTGTACACCGCGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 890
 DB 161 CysGlyValLeuHisArgAspIleLysAspGluAsnIleLeuIleAspLeuAsnArgGly 180
 QY 891 GAGCTCAAGCTCATGCACTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 950
 DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200
 QY 951 TTTCGATGGAGCCGAGTGTATAGCCCTCAGAGTGTGATCCGCTACCATCGCTACATGGC 1010
 DB 201 PheAspGlyThrArgValTyrSerProProGluTyrIleArgTyrHisArgTyrHisGly 220
 QY 1011 AGGTGGCGGCACTGGGTCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1070
 DB 221 ArgSerAlaIleValTyrSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
 QY 1071 CCTTGGAGAGATGAGAGAGATCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1130
 DB 241 ProPheGluHisIleAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
 QY 1131 TCAGAAATGTCAGCATCTCATTAAGTGTGCTTGGCCCTGAGACCATCAGATAGAGCAAC 1190
 DB 261 SerGluCysGlnHisIleLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProThr 280
 QY 1191 TTTCGAGAAATCCAGAAACATCATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1250
 DB 281 PheGluGluIleGlnHisAsnHisProTyrMetGlnAspValLeuLeuProGlnGluThrAla 300

QY 1251 GAGATCCAGCTCCAGACGCTGTGGCGGCGCGCCGCAAA 1289
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313
 RESULT 3
 ID AA019788 standard; protein; 313 AA.
 AC AA019788;
 XX 11-AUG-2003 (first entry)
 DT
 DE Human PIM1 kinase.
 KW Human; PIM1 kinase; PIM3 kinase; pain; analgesic.
 OS Homo sapiens.
 PN WO200293173-A2;
 PD 21-NOV-2002.
 PF 13-MAY-2002; 2002WO-EP005234.
 PR 11-MAY-2001; 2001DE-01023055.
 PA (CHEP) GRUENENTHAL GMBH.
 PI Weihe E, Schaefer MK;
 DR WPI; 2003-120715/11.
 DR N-PSDB; ABZ69186.
 PT Method for identifying analgesics, useful particularly for treating
 PT chronic pain, by screening compounds for interaction with PIM-1 or -3
 PT kinase, or related compounds.
 PS Claim 1; Fig 1B; 97pp; German.
 CC The present invention relates to a method of identifying pain-regulating
 CC compounds, involving screening candidate compounds for interaction with
 CC PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
 CC useful for treating chronic pain, particularly of neuropathic or
 CC inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
 CC neurodegenerative diseases). The present sequence is human PIM1 kinase
 XX
 SQ Sequence 313 AA:
 Alignment Scores:
 Pred. No.: 7.05e-113 Length: 313
 Score: 1670.00 Matches: 313
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.87% Indels: 0
 DB: Gaps: 0
 US-10-705-757-1 (1-2623) x AA019788 (1-313)
 QY 351 ATGCTCTTTCACAAATCAACTGGCTTGGCCACCTGGCGCGCGCCCTGCAAGCACTG 410
 DB 1 MetLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20
 QY 411 CACGCCACCAAGCTGGCGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
 DB 21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGlnSerGlnTyrGlnVal 40
 QY 471 GGGCGGCTACTGGGCGAGCGCGGCTTGGCTCGGCTACTGAGCATCCGGCTCCGAC 530
 DB 41 GlyProLeuGlnSerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
 QY 531 AACTGGCGGCTGGCATCAACAACGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
 DB 61 AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTyrGlyGluLeu 80

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QY 591 CCTATGCACTGAGTGGCCATGGAAGTGTCTGTGAAGAAAGGAGCTCGGGTTTC
DB 81 PtoAenGlyThrArgValProMetGluValValLeuLeuLeuValSerSerGlyPhe
QY 651 TCCGGGCGTATTAGGCTCTGAGTGGTTCGAGAGGCCGACAGTTCCTCGATCCG
DB 101 SerGlyValIleArgLeuLeuLeuAspIlePheGluArgProAspSerPheValLeuIleLeu
QY 711 GAGAGGCCGAGCCGGTGCAGAACTCTTTCGACTTCACCGGAAAGGGAGCCCTGCAC
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln
QY 771 GAGAGCTGGCCGCGAGCTTCTTTCGAGAGTGTCTGAGAGCCGTCGGGACCTCCACAC
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValValLeuGluAlaValArgHisCysHisAsn
QY 831 TCCGGGGTGTACACCCGACATCAAGAGAGAAACATCTTATCGACTCAATCCGCGC
DB 161 CysGlyValLeuLeuHisArgAspIleLeuAspGluAsnIleLeuIleAspLeuAsnArgGly
QY 891 GAGCTCAAGCTCATCCACTTCGGGTGGGGGGCCCTGTCAAGACACCGTCTACAGGAC
DB 181 GluLeuLeuSerLeuIleAspPheGlySerGlyAlaLeuLeuLeuAspThrValTyThrAsp
QY 951 TTCGATGGAGCCCGAGTGTATAGCCCTCCAGAGTGTCCGATCCATCGCTACATGGC
DB 201 PheAspGlyThrArgValTySerProPheGluTrpIleArgTyHisArgTyHisGly
QY 1011 AGGTGGCGGCGAGTGTGTCTGCTGCGGAGATCTCTGTATGATATGATGTGTGAGATATT
DB 221 ArgSerAlaIleValIlePheSerLeuGlyIleLeuLeuTyArgPheValCysGlyAspIle
QY 1071 CCTTTGAGAGTATGACGAAGATCATCAAGGGGCGCAGGTTTCTTCAGCGAGAGGTTCT
DB 241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer
QY 1131 TCAGAAATGTCAGCATCTCATTAGATGGTCTTGGCCCTGAGACCATCAGATAGCCCAAC
DB 261 SerGluCysGlnHisLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProTrp
QY 1191 TTGGAAGAAATCCAGAACCATTCATGGATGATGATGTTCTCTGCCCCAGAAACTGCT
DB 281 PheGluGluIleGlnIleAsnHisProTrpMetGlnAspValLeuLeuProGlnGluTrpAla
QY 1251 GAGATCCACTCCACAGACCTGTGCGCGGGGCCCAAGCAA 1289
DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerLeu 313

```

RESULT 4

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ID ABU61613 standard; protein; 313 AA.
XX
AC ABU61613;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human PIM1 protein.
XX
KW Human; tyrosine threonine kinase; TTK; cancer; cytosolic;
KW mitotic checkpoint gene; PIM1.
XX
OS Homo sapiens.
XX
PN US2003045491-A1.
XX
PD 06-MAR-2003.
XX
PF 21-FEB-2002; 2002US-00081119.
XX
PR 23-FEB-2001; 2001US-0289813P.
XX
PA (REIN/) REINHARD C.

```

```

PA (JEFF/) JEFFERSON A B.
PA (CHAN/) CHAN V W.
PI Reinhard C, Jefferson AB, Chan VW;
DR WPI; 2003-456566/43.
DR N-PSDB; ACA62265.
XX
PT Detecting cancer in a subject, by comparing expression levels of tyrosine
PT threonine kinase polypeptide or polynucleotide in a subject cell and a
PT normal cell, where an increase in the expression level in the test cell
PT is indicative of cancer.
XX
PS Disclosure; Page 34-35; 79pp; English.
XX
CC The invention relates to detecting cancer (other than ovarian cancer) in
CC a subject, comprising comparing the expression levels of tyrosine
CC threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or
CC polynucleotide in a test cell obtained from the subject and in a normal
CC non-cancer cell, where an increase in the expression level of TTK protein
CC or nucleic acid in the test cell compared to that in the normal cell,
CC indicates the presence of cancer other than ovarian cancer. Also included
CC are reducing growth of a cancerous cell (by contacting a cancerous cell
CC with an amount of an agent effective to reduce TTK polypeptide activity
CC in the cell), an assay for identifying a candidate agent that reduces
CC growth of a cancerous cell (comprising: (i) detecting the activity of a
CC TTK polypeptide in the presence of a candidate agent; and (ii) comparing
CC the activity of TTK polypeptide in the presence of a candidate agent
CC relative to TTK polypeptide activity in the absence of the candidate
CC agent), identifying an agent that reduces TTK activity (comprising: (i)
CC contacting a cancerous cell displaying elevated expression of a TTK-
CC encoding polynucleotide with a candidate agent; and (ii) determining the
CC effect of the candidate agent on TTK polypeptide activity) and assessing
CC the prognosis of a cancerous disease other than ovarian cancer in a
CC subject (comprising: (i) detecting expression of TTK encoding
CC polynucleotide in a test cancer cell of a subject; and (ii) comparing a
CC level of expression of TTK-encoding polynucleotide in the test cancer
CC cell with a level of expression of the polynucleotide in a control non-
CC cancer cell, where the level of expression of TTK in the test cancer cell
CC relative to the level of expression in the control non-cancer cell is
CC indicative of the prognosis of the cancerous disease). The methods are
CC useful for detecting cancer (other than ovarian cancer) in a subject,
CC reducing growth of cancerous cells, identifying a candidate agent that
CC reduces growth of a cancerous cell, identifying an agent that reduces TTK
CC activity and assessing the prognosis of a cancerous disease other than
CC ovarian cancer. The methods are also useful for determining the ability
CC of a subject to respond to a particular therapy e.g. as a basis of
CC rational therapy. The present sequence represents a closely related
CC protein to human TTK, in this case human PIM1 (not defined)
XX
SQ Sequence 313 AA;
XX

```

Alignment Scores:

```

Pred. No.: 7.05e-113 Length: 313
Score: 1670.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.87% Indels: 0
DB: 7 Gaps: 0

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US-10-705-757-1 (1-2623) x ABU61613 (1-313)

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QY 351 ATGCTCTGTCCAAATCAACTCGATTGGCCACTTGGCGCGCGCTTCAGACACTG 410
DB 1 MetLeuLeuSerIleLeuAsnSerLeuAlaHisLeuArgAlaIleProCysAsnAspLeu 20
QY 411 CACGCCACCAAGCTGGCGCCGCGCAAGAGAGAGAGCCCTGAGTGTGAGTACAGAGTG 470
DB 21 HisAlaThrIleLeuAlaProGlyIleGluValGluProLeuGlnSerGlnTyArgIleVal 40
QY 471 GGGCCGCTACTGGGCGCGCGGCTTGGCTGTCTACTCAGGACATCCGGCTCTCCGAC 530
DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTySerGlyIleArgValSerAsp 60

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QY 531 AACTGGCGGTGGCCATCAACAGTGGAGAAAGACCCGATTTCCGACTGGGAGAGCTG 590
DB 61 AsnLeuProValAlaIleValSHISValGluLysAspArgIleSerAspTrpGlyGluLeu 80
QY 591 CCTAATGACATCGAGTGGCCATGATGAGTGGTCTCTGAGAAAGAGTACGCGGTTTC 650
DB 81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
QY 651 TCCGGCGCTCATTAGGCTCTCGAGCTGGTTGAGAGGCCGACAGTTTCGTCGATCTTG 710
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
QY 711 GAGAGGCCGACCGCGGTGCAAGATCTTGTGACTTCATCAAGAAAGGAGCCCTGCA 770
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 771 GAGAGCTGGCCGCGACCTTCTTGGCAGAGTGGTGGAGGCCGCGGACCTGCGACAAC 830
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCySHISAsn 160
QY 831 TGGCGGGGTGTACACCCGACATCAAGAGACGAAACATCCTTATCGACTTCGCGGC 890
DB 161 CyGlyValLeuHisArgAspIleValAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY 891 GAGCTCAAGCTCATCGACTTCGCGGTGGGGGCGCTGCTCAAGACACCGTCTACACGAC 950
DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValIyrThrAsp 200
QY 951 TTCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACATCCATCGATGGC 1010
DB 201 PheAspGlyThrArgValIyrSerProGluTrpIleArgIyrHisAspGlyrHisGly 220
QY 1011 AGGTCCGCGGCACTGTGGTCTCTGGGAGATCTCTGTATGATATGTTGTGAGATATT 1070
DB 221 ArgSerAlaIleValTrpSerLeuGlyIleLeuLeuLysAspMetValCyGlyAspIle 240
QY 1071 CCTTTCGAGCATGACGAAAGATCATACAGGGGCCAGGTTTCTTCAGGCAAGAGGTTCT 1130
DB 241 ProPheGluHisAspGluGluIleIleArgGlyAlaLeuPheAspArgGlnArgValSer 260
QY 1131 TCAGAAATGTCAGATCTCATTAAGTGGTGGTGGCCCTGAGACCATCAGATAGGCCAAC 1190
DB 261 SerGluCySerGlnHisLeuIleArgTrpCyLeuAlaLeuArgProSerAspArgProthr 280
QY 1191 TTGGAAGAAATCCAGAACATCCATGAGATGATGTTCTCTGCCCCAGAAACTGCT 1250
DB 281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGluGlnThrAla 300
QY 1251 GAGATCCACTCCACAGCTGTGGCGGGGCCGACGAAA 1289
DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerIyrS 313

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RESULT 5
ABR62939
ID ABR62939 standard, protein; 313 AA.

AC ABR62939,
DT 04-DEC-2003 (first entry)
DE Human serine/threonine protein kinase PIM-1.
KW Human, PIM-1; protein kinase; enzyme.
OS Homo sapiens.
XX
PN M02003060130-A2.
XX
PD 24-JUL-2003.
XX
PF 20-JAN-2003; 2003M0-BP000492.
XX

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PR 19-JAN-2002; 2002EP-00001401.
XX (AVET ) AVENTIS PHARMA DEUT GMBH.
PA
XX
PI Korn M, Mueller G, Schneider R, Tschank G;
XX WPI; 2003-598536/56.
PT New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
PT agent for identifying anti-type 2 diabetes mellitus drugs, or for
PT treating insulin resistance or type 2 diabetes mellitus.
XX
PS Example 2; Page 40; 40pp; English.
XX
XX The present sequence is the protein sequence of the human
XX serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins
XX are the paralogs of novel human and murine PIM-3 proteins (see ABR62932
XX and ABR62933) of the invention, which are therefore expected to be
XX involved in cancer and cell growth regulation. PIM-3 is also involved in
XX the development of insulin resistance and type 2 diabetes mellitus. The
XX invention relates to the use of PIM-3 nucleic acids and proteins in:
XX screening assays for compounds that modulate insulin resistance or type 2
XX diabetes mellitus; detection assays for detecting insulin resistance or
XX type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
XX forensic biology); predictive medicine (e.g. diagnostic or prognostic
XX assays, monitoring clinical trials, pharmacogenomics); and for the
XX preparing a medicament for the treatment of insulin resistance or type 2
XX diabetes mellitus.
XX
SQ Sequence 313 AA;
XX
XX Alignment Scores:
XX Pred. No.: 7.05e-113 Length: 313
XX Score: 1670.00 Matches: 313
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 34.87% Indels: 0
XX DB: 7 Gaps: 0

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US-10-705-757-1 (1-2623) x ABR62939 (1-313)

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QY 351 ATGCTCTTGTCCAAATCAACTGCTGGCCACCTGGCGGCGGCGCTGCAAGCACTG 410
DB 1 MetLeuLeuSerIyrHisLeuSerLeuAlaHisLeuArgAlaIleProCyAsnAspLeu 20
QY 411 CACGCCACCAAGCTGGCGGCGGCGGCAAGAGAGAGACCCCTGAGTTCGACATCAGAGTG 470
DB 21 HisAlaThrIleValLeuAlaProGlyLysGluLysGluProLeuGluSerGlnIyrGlnVal 40
QY 471 GGGCGGCTACTGGGCGAGCGGCGCTTGGCTCGGTCTACTCAGGATCCGCGTCCGAC 530
DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValIyrSerGlyIleArgValSerAsp 60
QY 531 AACTGGCGGTGGCCATCAACAGTGGAGAAAGACCCGATTTCCGACTGGGAGAGCTG 590
DB 61 AsnLeuProValAlaIleValSHISValGluLysAspArgIleSerAspTrpGlyGluLeu 80
QY 591 CCTAATGACATCGAGTGGCCATGATGAGTGGTCTCTGAGAAAGAGTACGCGGTTTC 650
DB 81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
QY 651 TCCGGCGCTCATTAGGCTCTCGAGCTGGTTGAGAGGCCGACAGTTTCGTCGATCTTG 710
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
QY 711 GAGAGGCCGACCGCGGTGCAAGATCTTGTGACTTCATCAAGAAAGGAGCCCTGCA 770
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 771 GAGAGCTGGCCGCGACCTTCTTGGCAGAGTGGTGGAGGCCGCGGACCTGCGACAAC 830
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCySHISAsn 160

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QY 831 TCGGGGTCCTACACCGCATCAAGACGAAAAACCTTATCGACCTCAATCGCGGC 890
|||
DB 161 CysgLYValLeuHlaArgAspIleYsAbpGluAaHlleuLeuLeuAsnArgGly 180
QY 891 GAGCTCAAGCTCATCGACTTCGGGTCGGGGCCCTCTCAAGACACCGCTTACACGAC 950
|||
DB 181 GluLeuLeuLeuLeuAspPheGlySerGlyAlaLeuLeuLeuAspThrValTyrThrAsp 200
QY 951 TTCGATGGGACCGGACGTATACGCTCCAGAGTGAATCGGACCATCGCTACCATGGC 1010
|||
DB 201 PheAspGlyThrArgValTyrSerProProGluTyrIleArgTyrHisArgTyrHisGly 220
QY 1011 AGCTCCGCGCATGTCGTCTCCCTGGGGATCTCGCTGTATGATATGAGTGTGAGATATT 1070
|||
DB 221 ArgSerAlaAlaValTyrPheSerLeuGlyIleLeuLeuTyrAspMetValCysgLYAspIle 240
QY 1071 CCTTTCGAGCATGACGACGACGATCATCGAGGGCCAGGTTTCTTTCGAGGACGAGGTCCT 1130
|||
DB 241 ProPheGluHlaAspArgGluIleIleArgGlyGluValPhePheArgGluArgValSer 260
QY 1131 TCAGATGTCAGCATCTCATTTAGATGGTGTGGCTGGCCCTGAGACCATCAGATGGCCAAC 1190
|||
DB 261 SerGluCysGluHlaSerLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProThr 280
QY 1191 TTCGAAAGAAATCCAGAACCATTCATGATGACGATGTTCTCTGCGCCGACGAAACTGCT 1250
|||
DB 281 PheGluGluIleGluHlaHlaSerProTyrMetGluAspValLeuLeuProGluGluThrAla 300
QY 1251 GAGATCCAGCTCCACAGCCTGTGTGGCGGGGCCACGCAA 1289
|||
DB 301 GluIleHlaSerLeuSerLeuSerProGlyProSerIlys 313
RESULT 6
ADE55368
ID ADE55368 standard; protein; 313 AA.
XX
AC ADE55368;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein AAA60089, SEQ ID NO 1183.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN MO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002MO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; AAA60089.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 313 AA;
XX
Alignment Scores:
Pred. No.: 7 05e-113 Length: 313
Score: 1670.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.87% Indels: 0
DB: 7 Gaps: 0
US-10-705-757-1 (1-2623) x ADE55368 (1-313)
QY 351 ATGCTCTTGTCCAAATCAACTGCTGCCACCTGCGCGCGCCCTGACGACGCTG 410
|||
DB 1 MetLeuLeuSerLysIleHlaHlaSerLeuAlaHlaSerLeuAlaProCysAaHlaSerLeu 20
QY 411 CACGCCACCAAGCTGGCGCGCCGCGCAAGAGAGAGCCCTGAGTGGCAGTCCAGCTG 470
|||
DB 21 HlaIaThrLysLeuAlaProGlyLysGluSerGluProLeuGluSerGluIleVal 40
QY 471 GGCCTGCTACTGGGCGAGCGCGCTTGGCTGCTTACTACGAGCATCCGCTCCGAC 530
|||
DB 41 GlyProLeuLeuGlySerIleGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
QY 531 AACTGCGCGTGGGACCATCAACACGCTGAGAGACCGGATTTCCGACTGGGAGAGCTG 590
|||
DB 61 AsnLeuProValAlaIleIleYsHisValGluYsAspArgIleSerAspTrpGlyIleu 80
QY 591 CCTAATGGCACTCGAGTGGCCATGGAAGTGTCTGCTGGAAGAAGTGAGCTCGAGTTTC 650
|||
DB 81 ProAsnGlyThrArgValProMetGluValIleuLeuYsValSerSerGlyPhe 100
QY 651 TCCGCGCTATAGAGCTCTCGACTGCTTCGAGAGCCCGGACAGTTCTCTCGATCCG 710
|||
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleu 120
QY 711 GAGAGCGCGGACCGGATGCAAGATCTTTCGAGCTTTCGAGGAGCGGCTGCGGACTGCCAAC 770
|||
DB 121 GluArgProGluProValGluHlaSerPheAspPheIleThrGluArgGlyAlaLeuGlu 140
QY 771 GAGAGCTGGCGCGAGCTTCTTTCGAGGAGTGTCTGAGGAGCGGCTGCGGACTGCCAAC 830
|||
DB 141 GluGluLeuAlaArgSerPhePheTrpGluValLeuGluAlaValArgIleCysHisAsn 160
QY 831 TCGGGGTCCTACACCGCATCAAGACGAAAAACCTTATCGACCTCAATCGCGGC 890
|||
DB 161 CysgLYValLeuHlaArgAspIleYsAbpGluAaHlleuLeuLeuAsnArgGly 180

QY	891	GAGCTCGAAGCTCATGACTTGGGGATCGGGGCGCTGCTCGAAGACACCGCTTACACGGAC	950
Db	161	GIUUEUyVLEuIILeAspPheGlyGergIyALeUeUyVAspThValTyTThzAsp	200
QY	951	TTGCAATGGGACCCGAGTGATGATGAGCCCTCAGAGTGAGATCCGTCACATGGTACCAATGCC	1010
Db	201	PheAspGlyThzAspValTySerProGlnTrpIleArgTyThzAspTyThzIleGly	220
QY	1011	AGGTGGGCGGCGAGTGTGGTCCCTGGGGATCCCTGCTGTATGATATGATGTGTGAGATATT	1070
Db	221	ArgSerIILeALeValTrpSerIleuGlyIleUeUeUyThzPheMeValCyGGLyAspIle	240
QY	1071	CCTTTGCAAGCATGACGAAAGAGATCATCAAGGGGCGAGTTTCTTCCAGGACAGGGTCTCT	1130
Db	241	ProPheGlnThzAspGlyGlnIleIleArgGlyGlnValPhePheArgGlnArgValSer	260
QY	1131	TCAGAAATGTCAGCATCTCATTTAGATAGAGTGGCTGGCCCTGGAGACCATGACGATAGGCCAAC	1190
Db	261	SergIuCyGlnThzAspIleArgTrpCyUeUeALeUeArgProSerAspArgProThr	280
QY	1191	TTGCAAGAAATTCAGAACCATTCATGATGCAAGATGTTTCTTCTGCCCCAGAAACTGCT	1250
Db	281	PheGlnGlyIleGlnAspIleAspProIleTrpMetGlnAspValIleUeUeProGlnIuThzAla	300
QY	1251	GAGATCCACCTTCACACAGCCTGTGCGCGGGGCCACAGCAA	1289
Db	301	GIUIIeHILeUHIserIeUserProGlyProSerTyS	313
RESULT 7			
ADPF5083	ID	ADPF5083 standard; protein; 313 AA.	
XX	AC	ADPF5083;	
XX	DT	12-FEB-2004 (first entry)	
XX	XX	Human kinase PIM1.	
KM	XX	Human; protein kinase; enzyme; inhibitor; PIM1.	
XX	OS	Homo sapiens.	
PN	XX	MO2003081210-A2.	
PD	XX	02-OCT-2003.	
XX	XX	20-MAR-2003; 2003MO-US008725.	
PF	XX	21-MAR-2002; 2002US-0366892P.	
PR	XX	(SUNE-) SUNE81S PHARM INC.	
PA	XX	Prescott JC, Braisted A;	
P1	XX	WPI; 2003-065136/80.	
DR	XX		
XX	XX		
CC	CC	The present invention relates to a method for identifying a ligand (L),	
CC	CC	which binds to an inactive conformation of target protein kinase (T). The	
CC	CC	method involves contacting inactive conformation of (T), which contains	
CC	CC	or is modified to contain a reactive group at or near a binding site of	
CC	CC	interest, with one or more ligand candidates capable of covalently	
CC	CC	bonding to the reactive group thus forming a kinase-(L) conjugate (C).	
CC	CC	The method is useful for identifying protein kinase inhibitors that	
CC	CC	preferentially bind to inactive conformation of a target protein kinase.	
CC	CC	The present sequence is a protein kinase which may be modified via an	

CC amino acid substitution, for use in the method of the invention.

SQ Sequence 313 AA;

Alignment Scores:

Pred. No.:	7.05e-113
Score:	1670.00

Percent Similarity:	100.00%	conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match:	34.87%	Indels:	0
DR:	7	Gaps:	0

HS-10-705-757-1 (1-2623) v ADE45083 (1-313)

OY	351	ATGCTCTTGTCCAAATAACTCGCTTGGCCCACTCGCGCGCGCGCCCTTGCAACGACTG	410
Db	1	MetLeuLeuSerValLeaSnSerLeuAlaHsLeuAlaAlaProCysAsnAspLeu	20
OY	411	CACCCCAACCAAGCTGCGCGCGGCAAGAGAAGAGCCCTGAGAGTCCAGATCCAGAGTG	470
Db	21	HisLeaThrIySLeuAlaProGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly	40
OY	471	GAGCCGCTACTGGGCAAGCGCGCGCTTCGGCTCGGCTCTACAGGCATCCGCGTCTCCGAC	530
Db	41	GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp	60
OY	531	AACCTTGCOCGGGGGCATCAAAACAGGTGGAGAAGACCGGATTTCCGATCGAGGGAGAGCTG	590
Db	61	AsnLeuProValAlaIleLysHisIleValGlyLysAsnAspGlyIleSerAspTrpGlyLysLeu	80
OY	591	CCTAATGGCACTCGAGTGCCTCCATGGAAGATGAGTCTCGTCTGAAGAAGATGAGCTCGGATTC	650
Db	81	ProAsnGlyThrArgValProMetGlyValIleLeuLeuLysLysValSerSerGlyLys	100
OY	651	TTCGGCGGCTAATGAGCTCTCGGAGATCGGTTCGAGAGGCCCGGACAGTTTCGTCTGATCTCTG	710
Db	101	SerGlyValIleArgLeuLeuAspTrpPheGlyLysArgProAspSerPheValLeuLeuLeu	120
OY	711	GAGAGGCCCGGACCGCGTGCAAGATCTCTTCACATTCATACGGAAGAGGGAGCCCTGCA	770
Db	121	GlyLysArgProGlyLysProValGlyLysAspLeuPheAsnPheIleThrGlyLysGlyLysLeuGly	140
OY	771	GAGAGAGTGGCGCGGACGCTTCTTTCGGCAGGTGTCTGAGGCCGCTGCGGCACTGCCAAC	830
Db	141	GlyGlyLysLeuAlaArgSerPhePheTrpGlyValIleGlyLysAlaValArgHisCysHisAsn	160
OY	831	TGCGGGGGGTGCACACCGGACATCAAGAGAGCAAAACAATCCTTATTCGACTCAATGGCGGC	890
Db	161	CysGlyValLeuHisAsnArgAspIleLysAsnGlyLysAsnIleLeuIleAsnLeuAsnArgGly	180
OY	891	GAGCTCAAGCTCATGACTTTCGGGTCGGGGGCGCTGCTCAAGAGACACCGGTCTACACGAGC	950
Db	181	GlyLeuLysLeuIleAsnPheGlySerGlyLysAlaLeuLeuLysAsnThrValTyrThrAsp	200
OY	951	TTCCATATGGAGACCCGAGAGTATAGGCCCTCCAGAGTGCATCCGCTACCATCGCTACATAGC	1010
Db	201	PheAsnGlyThrArgValTyrSerProGlyLysIleArgGlyHisAsnGlyHisGly	220
OY	1011	AGGTCCGCGGAGCTGAGTCCCTCGGAGATCCTGCTGATATGATATAGAGTGTGAGAGATTT	1070
Db	221	ArgSerHisAlaValIlePheSerLeuGlyIleLeuLeuLysArgPheMetValCysGlyLysPhe	240
OY	1071	CCTTTTCAGACATGACGAAGAGATCATACAGGGGCGAGGTTTTCTTCAGGACAGAGGCTCTCT	1130
Db	241	ProPheGlyHisAsnArgGlyLysIleIleArgGlyLysIleValPhePheArgGlyHisValSer	260
OY	1131	TCGAAATATGCAAGCTCATTAAGATGGGCTTGGCCCTGAGACCATCAGATAGAGCCAAAC	1190
Db	261	SerGlyLysGlyHisIleLeuIleArgTrpCysLeuAlaLeuArgProSerAsnArgProThr	280
OY	1191	TTCCAGAGAAATCCAGAACCATCATCGATGATGCAAGATGTTCTCTGCGCCAGAGAACTGCT	1250
Db	281	PheGlyLysIleGlyHisAsnHisAsnTrpMetCysHisAsnValLeuLeuProGlyLysIleHisAla	300

QY 1251 GAGATCCACCTGCAGACCTGTGCGCGG66CCAGCAA 1289
 ID ADO19690 standard; protein; 313 AA.
 DB 301 GluileHisLeuHisSerLeuSerProGlyProSerLys 313

RESULT 8

AD019690
 AD019690:
 AD019690:
 12-AUG-2004 (first entry)

Human PRO polypeptide #308.
 Human PRO polypeptide #308.

Human; PRO; immune related disorder; systemic lupus erythematosus;
 rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 myeloma; scleroderma; Sjogren's syndrome; vasculitis; sarcoidosis;
 autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 diabetes mellitus; renal disease; demyelinating disease;
 central nervous system; peripheral nervous system;
 demyelinating polyneuropathy; Guillain-Barre syndrome;
 chronic inflammatory demyelinating polyneuropathy.

Homo sapiens.

MO2004043361-AA2.

27-MAY-2004.

06-NOV-2003; 2003MO-US035268.

08-NOV-2002; 2002US-0425235P.

(GETH) GENENTECH INC.

Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM,

Wood WI, Wu TD;

MP1, 2004-42067/39.

N-PSDB; ADO19689.

Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 treating an immune related disorder such as systemic lupus erythematosus,
 rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 spondyloarthritis.

Claim 7; SEQ ID NO 616; 1731pp; English.

The invention relates to human PRO polypeptides and the polynucleotides
 encoding them. The polypeptides and polynucleotides are useful for
 treating and diagnosing immune related disorders in mammals. The immune
 related disorders include systemic lupus erythematosus, rheumatoid
 arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 mellitus, immune-mediated renal disease, demyelinating diseases of the
 central or peripheral nervous system, demyelinating polyneuropathy,
 Guillain-Barre syndrome and chronic inflammatory demyelinating
 polyneuropathy. This sequence represents a human PRO polypeptide of the
 invention.

Sequence 313 AA:

Alignment Scores:

Pred. No.: 7.05e-113 Length: 313
 Score: 1670.00 Matches: 313
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.87% Indels: 0
 DB: 8 Gaps: 0

US-10-705-757-1 (1-2623) x ADO19690 (1-313)

QY 351 ATGCTCTTGTCACAAATCAACTCGTTGCCCACTGCGCGCGCCCTGCAACGACTG 410
 DB 1 MetLeuLeuSerLysIleHisSerLeuAlaHisLeuAlaIleProCysAlaMetLeu 20
 QY 411 CAGGCCACCAAGCTGGCGCCCGGCAAGAGAAAGAGCCCTTGAGTCGACATCAAGGTG 470
 DB 21 HisAlaThrLysLeuAlaProGlyLysGlyLysProLeuGluSerGlnTyrGlnVal 40
 QY 471 GGGCCGCTACTGGGCAAGGGGCGGCTTCGGCTCGGTCTACTCAGGCACTCCGCTCCGAC 530
 DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerMet 60
 QY 531 AACTTGCCGCTGGCCATCAACACGTTGAGAAAGACCCGATTCGACTGCGGAGAGCTG 590
 DB 61 AsnLeuProValAlaIleLysHisValGlyLysAspArgIleSerMetProLysLeu 80
 QY 591 CCTAATGGCACTCGAGTGGCCCATGGAAAGTGTCTCTGTGAAGAGTGAAGTCCGAGTTTC 650
 DB 81 ProAlaGlyThrArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
 QY 651 TCCGCGCTCATTAAGCTCTCGACTGCTTCGAGAGAGCCCGACAGTTTCTCTGATCTCG 710
 DB 101 SerGlyValIleArgLeuLeuMetProPheGluArgProMetSerPheValLeuLeu 120
 QY 711 GAGAGCCCGAGCCGCTGCAAGATCTCTTCGACTTCATCAACGAAAGGAGGACCTGCA 770
 DB 121 GluArgProGluProValGlnMetLeuPheMetPheIleThrGluArgLysAlaLeuGln 140
 QY 771 GAGAGCTGGCCCGAGCTTCTTCTGGCAGGTGTGTGAAGCCGTCGCGACTCCACAAAC 830
 DB 141 GluGluLeuAlaArgSerPheMetProGlnValLeuGluAlaValArgIleCysHisAsn 160
 QY 831 TGGCGGGTCTACACCGGCACTCAAGACGAAACATCTTAATGACTCAATGGCGGC 890
 DB 161 CysGlyValLeuHisArgMetLysAspArgLysAlaHisLeuIleAspLeuMetArgLys 180
 QY 891 GAGCTCAAGCTCATGCACTTCGAGTCCGAGGCGCGCTGCAAGACACCGTCTTACAGGAC 950
 DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrMet 200
 QY 951 TTGCATGGAGCCCGAGTGTATGCTTCGACAGTGGATTCGCTTACCATCGTCAATGGC 1010
 DB 201 PheAspGlyThrArgValTyrSerProProGluTyrIleArgTyrHisArgTyrHisGly 220
 QY 1011 AGTGGCGGCGAGTGTGCTTCCTGGGAGTCCGCTGATGATGATGTGTGAGAGATAT 1070
 DB 221 ArgSerAlaAlaValTyrSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
 QY 1071 CCTTCGAGCATGACGAAGATCATCAAGGCGCCAGTTTCTTCAGGCAAGGCTTCT 1130
 DB 241 ProPheGluHisAspGluGluIleLeuArgGlyGlnValPhePheArgGlnArgValSer 260
 QY 1131 TCAGAAATGCAGCATCTCATTAAGATGTGTGCTTCGCTGAGACCATCAATAGGCCAAC 1190
 DB 261 SerGluCysGlnHisLeuLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProThr 280
 QY 1191 TTCGAAAGAAATCCAAACCATTCATGAGATGCAAGATGTTCTCTCCCGCAGAAACTGT 1250
 DB 281 PheGluGluIleGlnHisMetProThrMetGlnAspValLeuLeuProGlnGluThrAla 300
 QY 1251 GAGATCCACCTGCAGACCTGTGCGCGG66CCAGCAA 1289
 DB 301 GluileHisLeuHisSerLeuSerProGlyProSerLys 313

RESULT 9

AD88370
 AD88370 standard; protein; 313 AA.

AD88370:
 AD88370:
 18-NOV-2004 (first entry)

US-10-705-757-1 (1-2623) x ADO19690 (1-313)

DE Human PIM 1 protein.
 XX Molecular scaffold; nuclear hormone receptor; TNF receptor;
 KM G-protein coupled receptor; methyl transferase; ligase; PIM; human.
 OS Homo sapiens.
 PN US2004171062-A1.
 XX
 PD 02-SEP-2004.
 XX
 PF 28-FEB-2003; 2003US-00377268.
 XX
 PR 28-FEB-2002; 2002US-0360651P.
 PR 16-SEP-2002; 2002US-0411398P.
 PR 20-SEP-2002; 2002US-0412341P.
 PR 02-JAN-2003; 2003US-0437929P.
 XX
 PA (PLEX-) PLEXIKON INC.
 XX
 PI Hirth K, Milburn MV;
 DR WPI, 2004-642017/62.
 XX
 PT Designing a ligand binding to a target molecule, comprises identifying as
 PT molecular scaffold compounds binding to members of a molecular family,
 PT detecting orientation of scaffolds at a binding site of target, and
 PT synthesizing ligand.
 XX
 PS Disclosure; SEQ ID NO 9; 186pp; English.
 XX
 CC The present invention relates to a method of designing a ligand binding
 CC to a target molecule. The method involves identifying as molecular
 CC scaffold compounds binding to members of a molecular family, detecting
 CC orientation of scaffolds at a binding site of target, and synthesizing
 CC ligand. The invention is useful for designing drug products and for
 CC designing ligand binding to target molecules such as nuclear hormone
 CC receptor, TNF receptors, G-protein coupled receptors, methyl
 CC transferase, ligases, etc. The present sequence is the human PIM 1
 CC protein. This sequence is used to illustrate the method of invention.
 XX
 SQ Sequence 313 AA;
 Alignment Scores:
 Pred. No.: 7.05e-113 Length: 313
 Score: 1670.00 Matches: 313
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.87% Indels: 0
 DB: 8 Gaps: 0
 US-10-705-757-1 (1-2623) x ADR88370 (1-313)
 QY 351 ATGCTCTTGTCCAAATCAACTGCTTGCACCTGCGCGCGCCCTGCAAGACTG 410
 DB 1 MetIeuLeuSerIySileAenSerIeuAlHieIeuAlrgAlaIaIaProCySaNaApleu 20
 QY 411 CAGGCCCAAGCTGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
 DB 21 HieAlaThrIyLeuAlaIaProGlyIyGluIyGluIyProIeuGluSerGlnIyrgIVal 40
 QY 471 GGGCCGCTACTGGCGCGCGCGCGCTTGGCTCGCTCACTACAGCATCCCGCTCCGAC 530
 DB 41 GlyProIeuLeuGlySerGlyIyGlyIyPheGlySerValIySerGlyIleAryValSerAsp 60
 QY 531 AACTTGGCGGTGCGCATCAACAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
 DB 61 AsnIeuProValAlaIleIyBhIeValGluIyAspArgIleSerSerIyPglIyGluIeu 80
 QY 591 CTTAATGGCACTCGAGTGGCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 650
 DB 81 ProAenGlyThraIyrgValIyPrometGluValIleValIeuLeuIyBhIeValSerSerGlyPhe 100

QY 651 TCCGGCGCTAATPAGGCTCTGAGCTGGTTGAGAGCGCGAGACTTTCGTCGATGCTG 710
 DB 101 SerGlyValIleIeArgIeuIeuAspIyPheGluIyArgProIeAspSerPheValIleIeu 120
 QY 711 GAGAGGCCCGAGCGCGGTGCAAGATCTCTTGACTTCATCAGGAAAGGAGCGCTGCAA 770
 DB 121 GluArgProGluProValGlnAerIeuPheAspPheIleThrGluIyrgIyAlaIeuGln 140
 QY 771 GAGAGAGTGGCGCGCGAGCTTCTTCTGGAGGTCTGAGAGCGCTGCGGCACTGCACAC 830
 DB 141 GluIleuAlaIySerPhePheIyrgIyValIeuGluIyAlaIyArgIleCyBhIeAsn 160
 QY 831 TGGCGGCTGTACACCGCGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 890
 DB 161 CyegIyValIeuIleIeArgIleIyBhIeValIyGluIyAsnIleIeuIleAspIeAsnArgGly 180
 QY 891 GAGCTCAAGCTCATCGACTTCGCGGTGCGGCGCGCTGCAAGAGACCGCTCAACGAGAC 950
 DB 181 GluIeuIyLeuIleAspPheGlySerGlyAlaIeuIeuIyAspIyThrValIyTrIyAsp 200
 QY 951 TTGATGGAGACCGAGTGTATACCTCCAGAGTGAATCCGCTACATCGCTACATGCGC 1010
 DB 201 PheAspGlyThraIyrgValIySerProIeGluIyTrIleArgIyIleAspIyIleGly 220
 QY 1011 AGGTGCGCGCGAGCTGTCGTCCTGGGAGATCCTGTATGATATGAGTGTGAGATATT 1070
 DB 221 ArgSerAlaIleAlaIyPheSerIeuGlyIleIeuIyIyAspIyValIyGlyIyAspIle 240
 QY 1071 CCTTTCGAGCATGACCAAGAGATCATCAGAGGCGCAGATTTCTTCAAGCGAGAGTCTCT 1130
 DB 241 ProPheGluIleIeAspIyGluIleIleIeArgIyGlnValPheIeAspIyGlnValSer 260
 QY 1131 TCGAATGTCAAGATCTCATTAATGATGATGCTGCGCTGAGACCATCAATAGGCCAAC 1190
 DB 261 SerGluIyGlnIleIeAspIyIleAspIyIyPheIyAlaIeuIyArgProIeAspArgProThr 280
 QY 1191 TTGGAAGAATCCAGAACCATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1250
 DB 281 PheGluIyGlnIleIeAspIyIleAspIyIyPheIyAlaIeuIyArgProIeAspArgProThr 300
 QY 1251 GAGATCCACCTCCAGAGCTGTGCGCGGCGCGAGAGAA 1289
 DB 301 GluIleIleIeuIleIeSerIeuSerProGlyProIeSerIyS 313
 RESULT 10
 ADP24227
 ID ADP24227 standard; protein; 313 AA.
 XX
 AC ADP24227;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE PRO polypeptide SEQ ID NO:1405.
 XX
 KM PRO: antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KM osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KM antiscabetic; hepatotropic; respiratory; gene therapy; immune system.
 XX
 OS Unidentified.
 XX
 PN WO2004041170-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WO-US034312.
 XX
 PR 01-NOV-2002; 2002US-0423394P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
 PI Wu TD;
 XX

DR WPI; 2004-419628/39.
 DR N-PSDB; ADP24226.
 XX
 PT New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 XX
 PS Claim 7; SEQ ID NO 1405; 2940bp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteoprotective, antidiabetic, dermatological, antipeptic, antiallergic,
 CC antiseptic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 CC
 XX
 SO Sequence 313 AA:
 Alignment Scores:
 Pred. No.: 7.05e-113 Length: 313
 Score: 1670.00 Matches: 313
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.87% Indels: 0
 DB: 8 Gaps: 0
 US-10-705-757-1 (1-2623) x ADP24227 (1-313)
 QY 351 ATGCTCTGTCCAAATCAACTCGCTGCCACCTGGCGCGCGCCCTCAAGACGCTG 410
 DB 1 MetleuLeuSerIySIIeAsenSerIeUAlHISleuRgAlAlaPProCySaMaAbpLeu 20
 QY 411 CACGCCAACAAAGCTGGCGCGCGCGCAAGAGAGAGAGCCCTGAGTGCAGTACCAAGTG 470
 DB 21 HIsAlaIeThIySleuAlaPProGIIySgIIuSgIuPProleuGIIuSerGIIuYrGIIuVal 40
 QY 471 GGGCCGCTACTGGCGAGCGCGCGCTTGGCTCGGTCTACTCAGGACCTCGCTCCGAC 530
 DB 41 GlyPProleuLeuGIIySerGIIyPheGIIySerValIySerGIIyIleArgValISerAsp 60
 QY 531 AACCTGGCGGTGGCGCATCAACAGTGGAGAGAGACCGGATTTCCGACTGGGAGAGCTG 590
 DB 61 AsnleuPProValAlAlaIleYbHISValGIIuYbAbpRgIIeSerAbpIIPGIIyGIIuLeu 80
 QY 591 CCTAATGGCACTCGAGTCCCATGAGAGTGTCTGCTGAAGAAGTGAAGCTCGGGTTTC 650
 DB 81 ProAsnGIIyThIyRgValIPrometGIIuValIleuLeuIleYbValISerSerGIIyPhe 100
 QY 651 TCCGGCGCTCAATAGGCTCTCGACTGGTTCGAGAGGCCGACAGTTTCGTCGATCTCTG 710
 DB 101 SerGIIyAlIleArgIleuLeuAspIIPrPheGIIuArgProAspSerPheValIleuLeu 120

QY 711 GAGAGCCGAGACCGGATGCAAGATCTTGCATTCATCAGGAAAGGGAGCCCTGCAA 770
 DB 121 GluArgPProGIIuPProValGIIuAsPProleuPheAsPheIleThGIIuArgGIIyAlaIleuGIIu 140
 QY 771 GAGAGCTGGCCCGGACCTTCTTGGCAGGTGCTGAGAGCCGTGGCGACTGCCAAGC 830
 DB 141 GluGIIuLeuAlaIArgSerPhePheIIPrGIIuValIleuGIIuAlaValAlArgHISCySHISaAn 160
 QY 831 TGGCGGGTGTCAACCGGACATCAAGAGGAAACATCTTATGACCTCAATGCGCGC 890
 DB 161 CySgIIyValIleuHISArgSPrIleYbAsPrgIuAsnIleuIleAsPProleuAsnRgGIIy 180
 QY 891 GAGCTCAAGCTCATGCACTTCGAGTGGGGGCGCTGCTCAAGACACCGTCTTACGAGAC 950
 DB 181 GluLeuYbIleuIleAsPProleuGIIySerGIIyAlaIleuLeuYbAsPProIyThIyRgAsp 200
 QY 951 TTGATGGGACCCGAGTGTATAGCCCTCCAGAGTGATCCGTACCATGCTTACATGGC 1010
 DB 201 PheAspGIIyThIyRgValIySerPProGIIuIIPrIleArgTyrHISArgTyrHISgIIy 220
 QY 1011 AGTGGCGGCGAGTGTGTGCTGGGGAATCCTGCTGTAATGATAGTGTGGAATATT 1070
 DB 221 ArgSerAlaAlaValIySerIeUgIIyIleuLeuIyTAsPProValCySgIIyAspIle 240
 QY 1071 CCTTTCAGCATGACGAAGAAGATCATCAGGGGCCAGGTTTCTTCCAGCAGAGGCTCTCT 1130
 DB 241 PProPheGIIuHISAsPrgIuGIIuIleIleArgGIIyGIIuValIleuPheArgGIIuRgValISer 260
 QY 1131 TCAGAAATGCACATCTCAATGATGTGTGGCCCTGAGACCATCAGATAGGCCAAC 1190
 DB 261 SerGIIuCySgIIuHISleuIleuIleArgTyrCySleuAlaIleuArgPProSerAspRgProItr 280
 QY 1191 TTCGAAGAAATCCAGAACCATCATGAGATGGAAGTTCCTGCTGCCAGGAAACTGCT 1250
 DB 281 PheGIIuGIIuIleGIIuAsnHISProItrPmetGIIuAsPProleuPProGIIuIuIuAla 300
 QY 1251 GAGATCCACCTCAACAGCTGTGGCGGGGCCAGCAAA 1289
 DB 301 GluIleHISleuHISerIeUAsPProGIIyPProSerIyS 313
 RESULT 11
 ID AAM08139
 AA AAM08139 standard; protein; 313 AA.
 AC AAM08139;
 XX 11-MAR-1997 (first entry)
 DT
 XX Human cytokine response protein CR7.
 DE
 KW Cytokine response protein; CR7; interleukin-2; IL-2;
 KW ligand-stimulated gene expression; diagnosis; therapy; proto-oncogene;
 KW p1m1; protein kinase; lymphoma.
 OS Homo sapiens.
 XX
 PN MO9639427-Al.
 PD 12-DEC-1996.
 XX
 PF 05-JUN-1996; 96MO-US009194.
 XX
 PR 05-JUN-1995; 95US-00461379.
 PR 05-JUN-1995; 95US-00462337.
 PR 05-JUN-1995; 95US-00462390.
 PR 05-JUN-1995; 95US-00463074.
 PR 05-JUN-1995; 95US-00463081.
 PR 05-JUN-1995; 95US-00465585.
 XX
 PA (DART-) DARTMOUTH COLLEGE.
 XX
 PI Smith KA, Beadling C;

XX WPI; 1997-043062/04.
 DR N-PSDB; AAT43382.
 XX
 PT Cytokine response proteins and genes - used in the detection and therapy
 of diseases caused by a mutation in the CR coding region.
 XX
 PS C1a1m 15; Page 32-33; 81bp; English.
 CC
 CC Cytokine response proteins CR1-CR8 (AAM08133-40) are encoded by genes
 (see also AAT43376-83) isolated from a cDNA library. 6 genes (CR1, 2, 3, 5, 6, 8) are
 induced human T-cell blast cDNA library. 6 genes (CR1, 2, 3, 5, 6, 8) are
 novel. CR7 is a serine/threonine protein kinase involved in T-cell
 lymphomagenesis. The CR7 gene is identical to the putative proto-oncogene
 CC lym-1, which is over-expressed in about 50% of Mv1-induced T-cell
 CC lymphomas. Recombinant CR7 polypeptides can be produced e.g. as GST
 CC fusions for use as immunogens and as diagnostic and therapeutic agents
 XX
 SQ Sequence 313 AA;
 Alignment Scores:
 Pred. No.: 6 24e-112 Length: 313
 Score: 1657.00 Matches: 311
 Percent Similarity: 99.36% Conservative: 0
 Best Local Similarity: 99.36% Mismatches: 2
 Query Match: 34.60% Indels: 0
 DB: Gaps: 0
 US-10-705-757-1 (1-2623) x AAM08139 (1-313)
 QY 351 ATGCTCTTGTCCAAATCAACTGCTTCCACCTGCGCGCGCGCTTCCGAAAGACTG 410
 DB 1 MetleuenuerlyrlyleuanserleuAlhileuakrglyAlaArglaCybanaApleu 20
 QY 411 CAGCCCAAGCTGCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
 DB 21 HsAlaThrlyrleuAlaProglyLygLyglulysglulProleuglSerGlnTyrGlnVal 40
 QY 471 GGGCCGCTACTGGGAGCGCGCGCTTGGCTCGCTACCTGAGAGAGAGAGAGAGAGAG 530
 DB 41 GlyProleuenuerlyserglyrlypneglyserValTyrserglylyleuValSerAsp 60
 QY 531 AACTGCGCGTGGCCATCAAAACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
 DB 61 AenleuProvalAlaileuylhileuAlaGululysAspArglyleuSerAspTrpGlyleu 80
 QY 591 CCTAATGGCACTGAGTGGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 650
 DB 81 ProAenGlyThyrArgValPrometGluValleuenuerlyserSerGlyPhe 100
 QY 651 TCGGCGGTCAATTGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 710
 DB 101 SerGlyValleuAlaileuAerPheTrpPheGluArgProAspSerPheValleuileu 120
 QY 711 GAG 770
 DB 121 GluArgProgluProvalGlnAspPhePheleuThrcylulrGlyAlaAleGln 140
 QY 771 GAG 830
 DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValleuGlnAlaValArgHisCybHsAan 160
 QY 831 TGGGCGGTGTACACCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 890
 DB 161 CybGlyValleuAlaileuArgPheTrpPheGluAsnHileuileuAspPheuAnaArgGly 180
 QY 891 GAGCTCAAGCTCATGACTTGGGCGCGCGCGCTGCTCAAGAGAGAGAGAGAGAGAG 950
 DB 181 GluLeuLeuLeuileuAspPheGlyserGlyAlaLeuLeuLeuysAspThrValTyrThrAsp 200
 QY 951 TTGATGGAG 1010
 DB 201 PheAspGlyThyrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220

QY 1011 AGGTCGCGCGAGTGTGCTTCCCTGGGAGATCTGCTGATGATATGAGTGTGAGATATT 1070
 DB 221 ArgSerAlaAlaValTrpSerleuGlyleuLeuenuThrAspPheValCybGlyAspPile 240
 QY 1071 CCTTTCGAGCAGTACGAGAGAGATCATCAGGAGCGAGATTTCTTTCAGCAGAGAGTCT 1130
 DB 241 ProPheGlnHlsAspPheGlnGluileuileuArgGlyGlnValPhePheArgGlnArgValSer 260
 QY 1131 TCGAATGTACGATCTCATTTAATGTGCTTGGCCCTGAGACCATCATGATAGCCCAAC 1190
 DB 261 SerGlyCybGlnHlsleuileuArgTyrCybLeuAlaLeuArgProSerAspArgProthr 280
 QY 1191 TTGGAAGAAATCCAGAACCATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1250
 DB 281 PheGlnGluileuileuAsnHlsProTrpMetGlnAspValleuenuProGlnGluTrpAla 300
 QY 1251 GAGATCCACTCCACAGAGCTGTGCGCGGAGCCAGCAAA 1289
 DB 301 GluileuHlsleuHlsSerleuSerProGlyProSerlyr 313
 RESULT 12
 AAY87959
 ID AAY87959 standard; protein; 313 AA.
 XX
 AC AAY87959;
 XX
 DT 18-SEP-2000 (first entry)
 XX
 DE Human CR7 protein.
 XX
 KW CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic;
 immunosuppressive; antimicrobial; therapy; cell proliferation; treatment;
 cell differentiation; cancer; immune disease; rheumatologic disease;
 KW transplant rejection; anti-infective; CR7.
 OS
 XX Homo sapiens.
 XX
 PN US6057427-A.
 XX
 PD 02-MAY-2000.
 XX
 XX
 PF 05-JUN-1996; 96US-00652446.
 XX
 PR 20-NOV-1991; 91US-00796066.
 PR 10-AUG-1993; 93US-00104736.
 PR 27-OCT-1994; 94US-00330108.
 PR 05-JUN-1996; 96WO-US008992.
 XX
 PA (DART-) DARTMOUTH COLLEGE.
 XX
 PI Beadling C, Smith KA;
 PI
 DR WPI; 2000-338623/29.
 DR N-PSDB; AAA39677.
 XX
 PT Novel antibody or antibody fragment which selectively binds to a
 polypeptide encoded by cytokine response gene 2.
 XX
 PS Example IV; Col 111-114; 66bp; English.
 PS
 CC This invention describes a novel isolated antibody or antibody fragment
 (I) which selectively binds to a polypeptide encoded by cytokine response
 gene 2 (CR2) and modulates CR2 activity. The products of the invention
 CC have cytostatic, anti-allergic, immunosuppressive and antimicrobial
 activity. The antibodies are useful as therapeutic agents for regulating
 CC cellular proliferation and differentiation and for treating all kinds of
 CC cancer, immune diseases such as allergic, autoimmune, and rheumatologic
 CC diseases, transplant rejection, and as anti-infectives for fighting
 CC viral, bacterial, parasitic and fungal infections. This sequence
 CC represents the human CR7 protein described in the invention
 XX
 SQ Sequence 313 AA;

Alignment Scores:

Pred. No.: 6,24e-112 Length: 313
 Score: 1657.00 Matches: 311
 Percent Similarity: 99.36% Conservative: 0
 Best Local Similarity: 99.36% Mismatches: 2
 Query Match: 34.60% Indels: 0
 DB: 3 Gaps: 0

US-10-705-757-1 (1-2623) x AAY87959 (1-313)

```

QY 351 ATGCTTTGTCCAAATCAACTGCTTGCCCACTGCGCGCGCGCTTCCGATCGAAGCACTG 410
DB 1 MetLeuLeuSerIyIleAsnSerIleuAlaHleuAlaArgAlaCysAsnAspLeu 20
QY 411 CACGCCAACCAAGCTGGCGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
DB 21 HleAlaThrIyLeuAlaProGlyIySGIyIySGIyIySGIyIySGIyIySGIyIySGIyIy 40
QY 471 GGGCGGCTACTGGCGCGCGCGCGCTTCCGCTGCTGATCAAGAGAGAGAGAGAGAGAGAGAG 530
DB 41 GlyProLeuLeuSerIyIySGIyIySGIyIySGIyIySGIyIySGIyIySGIyIySGIyIy 60
QY 531 AACTTCCGCTGCGCATCAAAACGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
DB 61 AsnLeuProValAlaIleIySHleValGluIyAspArgIleSerAspTrpGlyIyIleu 80
QY 591 CCTAATGGCACTGAGTGGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 650
DB 81 ProAsnGlyIyThrArgValIyProMetGluValIyLeuLeuIyIyValSerSerGlyPhe 100
QY 651 TCGGGGCTACTTGGGCTTCCGATCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 710
DB 101 SerGlyValIleArgIyLeuLeuAspTrpPheGluArgProAspSerPheValIleuIleu 120
QY 711 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 770
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyIyAlaLeuGln 140
QY 771 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 830
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValIleGlnIyAlaValIyArgHisCysHisAsn 160
QY 831 TGGGGGGTGTACACGCGGAGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 890
DB 161 CysGlyValIleuAlaArgAspIleIyAspGlyIyAsnIleuIleAspLeuAsnArgGly 180
QY 891 GAGCTCAAGCTCATGCACTTGGGAGTGGGCGCGCTGCAAGAGAGAGAGAGAGAGAGAGAG 950
DB 181 GluLeuIyLeuIleAspPheGlySerGlyIyAlaLeuLeuIyAspPheIyIyTrpAsp 200
QY 951 TTGCGATGGAGCCGAGTGTATAGCCCTCCAGAGTGCATCCGCTACCATCCATCCATGCC 1010
DB 201 PheAspGlyIyThrArgValIyIySerProGluIyTrpIleArgIyIyHisArgIyIySGIy 220
QY 1011 AGATCGCGCGAGCTGCTGCTTCCGCTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1070
DB 221 ArgSerIleAlaValIyIySerIyIyIyLeuLeuIyIyAspMetValIySGIyIyAspIle 240
QY 1071 CCTTTCGAGCATGCAAGAGAGATCATCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1130
DB 241 ProPheGluIyIyAspGluIyIyIleIleArgGlyIyGlnIyAlaPhePheArgGlnIyValSer 260
QY 1131 TCGAATGTCAAGCATCTTCAATTAAGTGTGCTGGCCCTGAGAGAGAGAGAGAGAGAGAG 1190
DB 261 SerGluIySGIyIyHisIyLeuIleArgIyIyCysIyLeuAlaLeuArgProSerAspArgProTrp 280
QY 1191 TTGGAAGAATCAAGAGAGATCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1250
DB 281 PheGluIyIyIleGlnAsnHisAspTrpIyMetGlnAspAlaIyLeuLeuProGlnIyIyTrpAla 300
QY 1251 GAGATCCACCTCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1289
  
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DB 301 GluIleHleuHleuSerLeuSerProGlyProSerIyS 313

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RESULT 13
ADIS7202
ID ADIS7202 standard; protein; 313 AA.
XX
XX
AC ADIS7202;
XX
XX
DT 22-APR-2004 (first entry)
XX
XX
DE Human PIM1 protein SEQ ID NO:22.
XX
XX
KW cell cycle arrest; CK2-specific siRNA molecule; short interfering RNA;
KW CK2 inhibition; PIM1-specific siRNA molecule; PIM1 inhibition;
KW Hbo1-specific siRNA molecule; Hbo1 inhibition; cyostatic; gene therapy;
KW cancer; proliferative disorder; human; PIM1.
XX
OS Homo sapiens.
XX
PN MO200400754-A2.
XX
PD 22-JAN-2004.
XX
XX
PF 14-JUL-2003; 2003WO-US022164.
XX
XX
PR 12-JUL-2002; 2002US-0395443P.
XX
PA (RIGE-) RIGEL PHARM INC.
PI Hitoshi Y, Jenkins Y, Markovtsov Y;
PI
PI
DR MPI; 2004-122975/12.
DR N-PDB; ADIS7201.
XX
XX
PT Identifying a compound that modulates cell cycle arrest, useful for
PT developing therapeutic reagents for treating cancer comprising contacting
PT a cell comprising a target polypeptide with the compound.
XX
XX
PS Claim 1, SEQ ID NO 22; 180pp; English.
XX
XX
CC The present invention describes a method for identifying a compound (C)
CC that modulates cell cycle arrest. The method comprises contacting a cell
CC comprising a target polypeptide with the compound (C), where the target
CC polypeptide encoded by the complement of a nucleic acid that hybridises
CC under stringent conditions to a nucleic acid encoding a polypeptide
CC having an amino acid sequence selected from 18 148-1408 amino acid
CC sequences (SEQ ID NO: 2-36, even numbers only). Also described: (1)
CC modulating cell cycle arrest in a subject; (2) a CK2-specific short
CC interfering RNA (siRNA) molecule comprising the sequence: (I)
CC AACATGATTAAGATCCAGT, where the siRNA molecule is from 21-30 nucleotide
CC base pairs in length; (3) inhibiting expression of a CK2 gene in a cell;
CC (4) a PIM1-specific siRNA molecule comprising the sequence: (II)
CC AAATTCGAGAGACTGTC, where the siRNA molecule is from 21-30 nucleotide
CC base pairs in length; (5) inhibiting expression of a PIM1 gene in a cell;
CC (6) an Hbo1-specific siRNA molecule comprising the sequence: (III)
CC AACTGACGAGCGTGAATTT, where the siRNA molecule is from 21-30 nucleotide
CC base pairs in length; and (7) inhibiting expression of an Hbo1 gene in a
CC cell. (C) has cyostatic activity, and can be used in gene therapy. The
CC method is useful for identifying a compound (C) that modulates cell cycle
CC arrest. Compounds that modulate cell cycle arrest are useful for
CC developing therapeutic reagents for treating cancer and other
CC proliferative disorders. The present sequence represents human PIM1,
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 313 AA;
XX
  
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Alignment Scores:

Pred. No.: 6,24e-112 Length: 313
 Score: 1657.00 Matches: 311
 Percent Similarity: 99.36% Conservative: 0
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 Query Match: 34.60% Indels: 0
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US-10-705-757-1 (1-2623) x AD157202 (1-313)

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 ADN03170 standard; protein; 313 AA.
 XX ADN03170
 AC ADN03170;
 XX

DT 29-JUL-2004 (first entry)
 XX
 DE Human P1M-1 polypeptide.
 XX
 KM Human; P1M-1; antisense oligonucleotide; phosphorothioate linkage;
 KM 2'-O-methoxyethyl sugar moiety; 5-methylcytosine;
 KM hyperproliferative disorder; cancer; cytostatic.
 OS Homo sapiens.
 XX
 PN US2004092463-A1.
 XX
 XX 13-MAY-2004.
 PD
 XX
 PF 11-NOV-2002; 2002US-00292849.
 XX
 XX 11-NOV-2002; 2002US-00292849.
 PR
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Watt AT;
 PT
 DR WPI; 2004-374981/35.
 DR N-PSDB; ADN03035.
 XX
 PT New compound that modulates P1M-1 expression, useful in treating an
 PT animal having a disease or condition, i.e. hyperproliferative disorder.
 XX
 PS Claim 1; SEQ ID NO 4; 51pp; English.
 XX
 CC The invention relates to a compound targeted to a nucleic acid molecule
 CC encoding the human P1M-1 polypeptide. The compound is an antisense
 CC oligonucleotide that specifically hybridizes with the nucleic acid and
 CC inhibits expression of the polypeptide. The antisense oligonucleotide
 CC comprises at least one modified internucleoside linkage i.e. a
 CC phosphorothioate linkage, at least one modified sugar moiety, preferably
 CC a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase
 CC comprising a 5-methylcytosine. The antisense compounds are useful for
 CC modulating the expression of the human P1M-1 polypeptide and in
 CC preparation of a composition for treating hyperproliferative disorders,
 CC e.g. cancer. This sequence represents the human P1M-1 polypeptide of the
 CC invention.
 XX
 SQ Sequence 313 AA:
 Alignment Scores:
 Pred. No.: 6,24e-112 Length: 313
 Score: 1657.00 Matches: 311
 Percent Similarity: 99.36% Conservative: 0
 Best Local Similarity: 99.36% Mismatches: 2
 Query Match: 34,60% Indels: 0
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 QY 471 GGGCCGCTACTGGGCAAGCGCGCGCTTGGCTGGCTCTACTCAGGCACTCCGCTCCGAC 530
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GenCore version 5.1.6
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Run on: September 22, 2005, 16:26:26 ; Search time 176.828 Seconds
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Searched: 1826521 seqs, 407012169 residues

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1668	68.3	313	15 US-10-348-081-12	Sequence 18, Appl
3	1668	68.3	313	18 US-10-705-757-4	Sequence 4, Appl
4	1636	67.0	313	9 US-09-971-791-9	Sequence 9, Appl
5	1636	67.0	313	14 US-10-081-119-18	Sequence 18, Appl
6	1636	67.0	313	15 US-10-394-322A-52	Sequence 52, Appl
7	1636	67.0	313	15 US-10-348-081-13	Sequence 13, Appl
8	1636	67.0	313	16 US-10-664-421-1	Sequence 1, Appl
9	1636	67.0	313	16 US-10-664-421-150	Sequence 150, App
10	1636	67.0	313	16 US-10-377-268-9	Sequence 9, Appl
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12	1636	67.0	313	17 US-10-951-406-18	Sequence 18, Appl
13	1636	67.0	313	17 US-10-951-477-18	Sequence 18, Appl
14	1636	67.0	313	18 US-10-977-087-18	Sequence 18, Appl
15	1636	67.0	313	18 US-10-705-757-2	Sequence 2, Appl
16	1636	67.0	313	18 US-10-941-635-1	Sequence 1, Appl
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18	1623	66.4	313	16 US-10-620-052A-22	Sequence 22, Appl
19	1584	64.8	313	9 US-09-971-791-7	Sequence 7, Appl
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21	1584	64.8	313	15 US-10-664-421-2	Sequence 2, Appl
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23	1584	64.8	313	18 US-10-705-757-6	Sequence 6, Appl
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44	1104	45.2	323	15 US-10-348-081-11	Sequence 11, Appl
45	1104	45.2	323	16 US-10-664-421-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
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; Sequence 8, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle MacBeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971,791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237,543
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 313

TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-971-791-8

Alignment Scores:

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Score:	1668.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
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US-10-705-757-3 (1-1302) x US-09-971-791-8 (1-313)

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RESULT 2

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 ; Sequence 12, Application US/10348081
 ; Publication No. US20040038246A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KORN, Marcus
 ; APPLICANT: MUELLER, Guenter
 ; APPLICANT: SCHNEIDER, Rudolf
 ; APPLICANT: TSCHAN, Georg
 ; TITLE OF INVENTION: PIV-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
 ; FILE REFERENCE: DEAY2002/0004 US NP
 ; CURRENT APPLICATION NUMBER: US/10/348,081
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 12
 ; LENGTH: 313
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-10-348-081-12

Alignment Scores:

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Score:	1668.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	68.28%	Indels:	0
DB:	15	Gaps:	0

US-10-705-757-3 (1-1302) x US-10-348-081-12 (1-313)

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QY 304 TCGGGGCTATTAGACTCTTGGACTGGTGTGAGAGGCGCATAGTTTCGCTGATCTTG 363
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Db 101 SerGlyValIleArgLeuLeuAspTrpPheGlnArgProAspSerPheValIleuIleu 120

QY 364 GAGAGCTGGCCCGGAGCTTCTTCTGGCAGTGTCTGAGGCGCTGCGGCAATTGCCAACA 483
    |||
Db 121 GlnArgProGlnProValGlnAspLeuPheAspPheIleThrGlnArgGlyAlaLeuGln 140

QY 424 GAGAGCTGGCCCGGAGCTTCTTCTGGCAGTGTCTGAGGCGCTGCGGCAATTGCCAACA 483
    |||
Db 141 GlnGlnLeuAlaArgSerPhePheTrpGlnValIleuGlnIleValArgHsCySHAsn 160

QY 484 TCGGGGGTTCCTCCACCGCGCATCAAGAGAGAGAACTTAAATCCAGTCAACCGCGGC 543
    |||
Db 161 CysGlyValLeuHleAspArgIleYsAspGlnAsnIleuLeuIleAspLeuAsnArgGly 180

QY 544 GAATCTAAATCATCGACTTCGAGTGGGGGCGCTGCTCAAGGACACAGTCTTACAGCGAC 603
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Db 181 GluLeuYleuLeuIleAspPheGlySerGlyAlaIleuLeuYsAspThrValIYrThrAsp 200
QY 604 TTTGACGGAACCCGAGTGTACAGTCTCTCCAGAGTGAATTCGTAACCATCGCTACCAAGC 663
Db 201 PheAspGlyThrArgValIYrSerProGluTrpIleArgTYrHisArgTYrHisGly 220
QY 664 AGTGGCGTCTGTCTTGGTCCCTGGGAGATCTGTCTATGACATGCTGTCCGAGATAT 723
Db 221 ArgSerIAlaValIYrPserLeuGlyIleLeuLeuYrAspMetValCYsGlyAspIle 240
QY 724 CCATTGAGCAGCAGAAAGATCGTCAAGGCGCAAGTGTACTTAAAGCAAGGATCTCT 763
Db 241 ProPheGluHisAspGluGluIleValysGlyGlnValIYrPheArgGlnArgValSer 260
QY 784 TCAGAAATGTCAACATCTTATTAGTGTGCTGTCTCTGAGACCATCGAACCGGCTCTC 843
Db 261 SerGluCYsGlnHisLeuIleAspIleArgTrpCYsLeuSerLeuArgProSerAspArgProSer 280
QY 844 TTTGAAGAATCCAGAACCATTCGTGTGATGACAGATTTCTCTGCGCCGAGGCAACGCGC 903
Db 281 PheGluGluIleGlnHisAspTrpMetGlnAspValLeuLeuProGlnIAlaThrAla 300
QY 904 GAGATTCATCTGACAGCCTGTGACCATCAACCCAGCAA 942
Db 301 GluIleHisLeuHisSerLeuSerProSerProSerIYs 313

RESULT 3
US-10-705-757-4
; Sequence 4, Application US/10705757
; Publication No. US20040146942A1
; GENERAL INFORMATION:
; APPLICANT: GRUNERTHAL GMBH
; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
; FILE REFERENCE: 029310.52818US
; CURRENT APPLICATION NUMBER: US/10/705,757
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/EP02/05234
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: DE 101 23 055.9
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-705-757-4

Alignment Scores:
Pred. No.: 2,126-111 Length: 313
Score: 1668.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Beet Local Similarity: 100.00% Mismatches: 0
Query Match: 68,288 Indels: 0
Gaps: 0

US-10-705-757-3 (1-1302) x US-10-705-757-4 (1-313)

QY 4 ATGCTCTTGTCAAGATCAACTCCCTGGCCACCTGGGCGAGCCCTTGCACAGACG 63
Db 1 MetLeuLeuSerYAlaIleAspSerLeuAlaHisLeuArgAlaIAspProCYsAsnAspLeu 20
QY 64 CAGCGCAACAAGCTGGCGCGCGGCAAGAGAGAGAGCCCTGAGTGTGACAGTGTG 123
Db 21 HisAlaAsnYleuAlaPArgIYrGlyGluYleuGluProLeuHisSerGlnIYrGlnVal 40
QY 124 GGGCCGCTGTGGGACGCGGTGGCTTGGCTCGGTCTAATCGGGCATCCGCGTCCGAC 183
Db 41 GlyProLeuLeuHisSerGlyGlyPheGlySerValIYrSerGlyIleArgValAlaAsp 60
QY 184 AACCTGCGGTGCGCATCAAGACGTGAGAGAGACCGGATTCGACATGGGGGAACTG 243

Db 61 AsnLeuProValAlaIleIYrHisValGluYAspArgIleSerAspTrpGlyGluLeu 80
QY 244 CCCAAGCGACCCGAGTGTCCCATGAGATGTCTCTCTGAAGAGAGTGAACCTCGGCTTC 303
Db 81 ProAsnGlyThrArgValIYrPrometGluValIleuLeuYsValSerSerGlyPhe 100
QY 304 TCGGGCGTCAATTGACTTCTGAGCTGTTCGAGAGGCGCGATGTTTCGTCGATCCG 363
Db 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleuLeu 120
QY 364 GAGAGCCCGCAACCCGTGCAAGACTCTTCACTTATCACTTCAACGAGGAGAGGCTTCAG 423
Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 424 GAGAGCTGGCCCGAGCTTCTTCTGAGAGTCTGAGGCGCTGCGGCAATTGCCAAC 483
Db 141 GluGluLeuAlaArgSerPhePheTrpGlnValIleuGlnAlaValArgHisCYsHisAsn 160
QY 484 TGGGGGTTCTCCACCGGCACATCAAGACGAGAACATCTTATTCGACCTGAACCGGCGC 543
Db 161 CYsGlyValLeuHisAspAspIleYsAspGluAsnIleuLeuIleAspLeuAsnArgGly 180
QY 544 GAACCAAACTCATGACTTCGGGTGCGGGGCGCTGTCGAAGGACACAGTCTACAGGAC 603
Db 181 GluLeuYleuLeuIleAspPheGlySerGlyAlaIleuLeuYsAspThrValIYrThrAsp 200
QY 604 TTTGACGGAACCCGAGTGTACAGTCTCTCCAGAGTGAATTCGTAACCATCGCTACCAAGC 663
Db 201 PheAspGlyThrArgValIYrSerProGluTrpIleArgTYrHisArgTYrHisGly 220
QY 664 AGTGGCGTCTGTCTTGGTCCCTGGGAGATCTGTCTATGACATGCTGTCCGAGATAT 723
Db 221 ArgSerIAlaValIYrPserLeuGlyIleLeuLeuYrAspMetValCYsGlyAspIle 240
QY 724 CCATTGAGCAGCAGAAAGATCGTCAAGGCGCAAGTGTACTTAAAGCAAGGATCTCT 763
Db 241 ProPheGluHisAspGluGluIleValysGlyGlnValIYrPheArgGlnArgValSer 260
QY 784 TCAGAAATGTCAACATCTTATTAGTGTGCTGTCTCTGAGACCATCGAACCGGCTCTC 843
Db 261 SerGluCYsGlnHisLeuIleAspIleArgTrpCYsLeuSerLeuArgProSerAspArgProSer 280
QY 844 TTTGAAGAATCCAGAACCATTCGTGTGATGACAGATTTCTCTGCGCCGAGGCAACGCGC 903
Db 281 PheGluGluIleGlnHisAspTrpMetGlnAspValLeuLeuProGlnIAlaThrAla 300
QY 904 GAGATTCATCTGACAGCCTGTGACCATCAACCCAGCAA 942
Db 301 GluIleHisLeuHisSerLeuSerProSerProSerIYs 313

RESULT 4
US-09-971-791-9
; Sequence 9, Application US/09971791
; Patent No. US2002015120A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Kyle MacBeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971,791
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-791-9

Alignment Scores:

Pred. No.:	4,25e-109	Length:	313
Score:	1636.00	Matches:	304
Percent Similarity:	99.04%	Conservative:	6
Best Local Similarity:	97.12%	Mismatches:	3
Query Match:	66.97%	Indels:	0
DB:	9	Gaps:	0

US-10-705-757-3 (1-1302) x US-09-971-791-9 (1-313)

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QY 4 ATGCTTTGTCCAAAGATCAACTCCCTGGCCCACTGGCGGCGAGCCCTTTCACGACCTG 63
DB 1 MetLeuLeuSerlyIleAenSerleuAlaHleuAArgAlaAlaProCyAaenAerleu 20
QY 64 CACGCCAACAGCTGGCGCGCGGCAAGAGAGAGAGCCCTGGAGTGGCACTGACGAGT 123
DB 21 HleAlaThrLyseuAlaProGlyLygLuLygLuProleuGlusSerGlnVal 40
QY 124 GGGCCGCTGTGGGAGCGGTGGCTTGGCTCGCTACTCGGGCAATCCGGCTGGCGGAC 183
DB 41 GlyProleuLeuLySerGlyLygPneGlySerValTySerGlyIleAArgValSerAap 60
QY 184 AACTGCCGCTGGCCATCAAGACGTCGAGAGAGAGACCGGATTTCCGACTGGGGGAACTG 243
DB 61 AenLeuProValAlaIleLyshIleValGluLyshAArgIleSerAapTrpGlyIleu 80
QY 244 CCCAAGCGGACCCGAGTGGCCATGAGAGTGTCTCTGCAAGAGTGAAGTTCGGGCTTC 303
DB 81 ProAenGlyThAArgValProMetGluValIleuLeuLyseValSerSerGlyPne 100
QY 304 TGGGGGCTCATTAAGCTTTCGAGCTGGTGAAGAGCGGATGTTTCGTGCTGATCCG 363
DB 101 SerGlyValIleAArgLeuLeuAapTrpPheGluAArgProAapSerPheValIleu 120
QY 364 GAGAGGCCCAAGCCCGTCGAAGACCTTTCGACTTATCAACGAGGAGAGGCTTCAG 423
DB 121 GluAArgProGluProValGlnAerleuPheAapPheIleThrGluAArgIleAeuGln 140
QY 424 GAGAGAGTGGCCCGGAGCTTCTTGGCAGGTGCTGAGGCGGTGGGCACTTCCCAAC 483
DB 141 GluGluLeuAlaAArgSerPhePheTrpGlnValIleuGlnAlaValAArgIshCyshIleAaen 160
QY 484 TGGCGGGGTTTCCACCGCGACATCAAGAGAGAGAGACCTTATTCGACTGGAACCGCGG 543
DB 161 CyseGlyValIleuAlaAArgAapIleLyshAapGluAenIleuIleAapLeuAenAArgGly 180
QY 544 GAACTCAAACTCATCGACTTCGGGTCGGGGCGCTGCTCAAGAGACAGTCTTACAGGAC 603
DB 181 GluLeuLyseuIleAapPheGlySerGlyAlaIleuLeuLyshAapThrValTyThrAap 200
QY 604 TTTGAGAGGAACCCGAGTGTACAGTCTTCGAGAGTGGATTCGTAACATCGCTACAGGCG 663
DB 201 PheAapGlyThAArgValTySerProGluTrpIleAArgTyshAArgTyshIleGly 220
QY 664 AGGCGGCTGCTGTTGGTCCCTGGGGATCTGCTCATGACATGGCTGCGGAGATTT 723
DB 221 AArgSerAlaAlaValIlePheSerleuGlyIleuLeuLeuTyshAapPheValCyseGlyAapIle 240
QY 724 CCAATTTGAGACGACGAGAGATCTTCAGAGGCGCAAGTGTACTTAAAGCAAGGCTCTCT 783
DB 241 ProPheGluIleAapGluGluIleIleAArgGlyGlnValPhePheAArgGlnAArgValSer 260
QY 784 TCGAAGTGTCAACATCTTATTAAGTGTGCTCTCCCTGAGACCATTCGACCGGCGCTCC 843
DB 261 SerGlnCyseGlnIleAenIleAArgTrpCyseValIleuAArgProSerAapAArgProThr 280
QY 844 TTTGAAGAATTCAGAGACATCCGTCGAGTCAGAGAGTTCCTCGGCGCGGACGCGGCG 903
DB 281 PheGluGluIleGlnIleAenIleAArgProTrpMetGlnAapValIleuLeuProGlnIleuAla 300
QY 904 GAGATTCATCTGACAGGCTGTGACCATCAACCCAGCAAA 942
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DB 301 GluIleHleuHleuSerleuSerProGlyProSerLyS 313

RESULT 5

US-10-081-119-18

; Sequence 18, Application US/10081119

; Publication No. US20030045491A1

; GENERAL INFORMATION:

; APPLICANT: Reinhard, Christoph

; APPLICANT: Jefferson, Anne B.

; APPLICANT: Chan, Vivien W.

; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic

; FILE REFERENCE: 16932.002

; CURRENT APPLICATION NUMBER: US/10/081,119

; PRIOR FILING DATE: 2001-02-21

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 18

; LENGTH: 313

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-081-119-18

Alignment Scores:

Pred. No.:	4,25e-109	Length:	313
Score:	1636.00	Matches:	304
Percent Similarity:	99.04%	Conservative:	6
Best Local Similarity:	97.12%	Mismatches:	3
Query Match:	66.97%	Indels:	0
DB:	14	Gaps:	0

US-10-705-757-3 (1-1302) x US-10-081-119-18 (1-313)

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QY 4 ATGCTTTGTCCAAAGATCAACTCCCTGGCCCACTGGCGGCGAGCCCTTTCACGACCTG 63
DB 1 MetLeuLeuSerlyIleAenSerleuAlaHleuAArgAlaAlaProCyAaenAerleu 20
QY 64 CACGCCAACAGCTGGCGCGCGGCAAGAGAGAGCCCTGGAGTGGCACTGACGAGT 123
DB 21 HleAlaThrLyseuAlaProGlyLygLuLygLuProleuGlusSerGlnVal 40
QY 124 GGGCCGCTGTGGGAGCGGTGGCTTGGCTCGCTACTCGGGCAATCCGGCTGGCGGAC 183
DB 41 GlyProleuLeuGlySerGlyLygPneGlySerValTySerGlyIleAArgValSerAap 60
QY 184 AACTGCCGCTGGCCATCAAGACGTCGAGAGAGAGACCGGATTTCCGACTGGGGGAACTG 243
DB 61 AenLeuProValAlaIleLyshIleValGluLyshAArgIleSerAapTrpGlyIleu 80
QY 244 CCCAAGCGGACCCGAGTGGCCATGAGAGTGTCTCTGCAAGAGTGAAGTTCGGGCTTC 303
DB 81 ProAenGlyThAArgValProMetGluValIleuLeuLyseValSerSerGlyPne 100
QY 304 TGGGGGCTCATTAAGCTTTCGAGCTGGTGAAGAGCGGATGTTTCGTGCTGATCCG 363
DB 101 SerGlyValIleAArgLeuLeuAapTrpPheGluAArgProAapSerPheValIleu 120
QY 364 GAGAGGCCCAAGCCCGTCGAAGACCTTTCGACTTATCAACGAGGAGAGGCTTCAG 423
DB 121 GluAArgProGluProValGlnAerleuPheAapPheIleThrGluAArgIleAeuGln 140
QY 424 GAGAGAGTGGCCCGGAGCTTCTTGGCAGGTGCTGAGGCGGTGGGCACTTCCCAAC 483
DB 141 GluGluLeuAlaAArgSerPhePheTrpGlnValIleuGlnAlaValAArgIshCyshIleAaen 160
QY 484 TGGCGGGGTTTCCACCGCGACATCAAGAGAGAGAGACCTTATTCGACTGGAACCGCGG 543
DB 161 CyseGlyValIleuAlaAArgAapIleLyshAapGluAenIleuIleAapLeuAenAArgGly 180
QY 544 GAACTCAAACTCATCGACTTCGGGTCGGGGCGCTGCTCAAGAGACAGTCTTACAGGAC 603
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Db 181 GluLeuLysLeuIleAspPheGlyAlaLeuLeuLysAspThrValTyrThrAsp 200
 Qy 604 TTGGACCGAACCCGAGTGTACAGTCTCTCCAGAGTGGATTGGCTACCATCGCTACACGGC 663
 Db 201 PheAspGlyThrArgValTyrSerProGlyIleArgTyrHisArgTyrHisGly 220
 Qy 664 AGGCGGCTGCTGTTGGTGGTGGGAGTCTGCTGATGACATGGCTGGGAGATATT 723
 Db 221 ArgSerIleAlaValIlePheSerLeuGlyIleLeuLeuLysAspMetValCysGlyAspIle 240
 Qy 724 CCATTGAGACGACGAGAGATGTCAGAGGCGCAAGTGTACTTTAGCAAAAGGCTCTT 783
 Db 241 ProPheGlyIleHisArgIleGlyIleIleArgGlyIleValPhePheArgGlyIleValSer 260
 Qy 784 TCAGAAATGTCACATCTTATTAGTGGTGGCTGCTGCTGAGACCATGAGACCGGCTCC 843
 Db 261 SerGlyCysGlnHisLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProThr 280
 Qy 844 TTGAAGAATCCGACGACCATCCGATGATGAGATGTTCTCTGCGCCGACGACCGCC 903
 Db 281 PheGlyIleIleGlnAsnHisProTyrPheGlnAspValLeuLeuProGlnGlyIleAla 300
 Qy 904 GAGATTCATCTGCACAGCTGTGCACATCAACCCAGCAA 942
 Db 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313

RESULT 6

US-10-394-322A-52
 / Sequence 52, Application US/10394322A
 / Publication No. US20030232391A1
 / GENERAL INFORMATION:
 / APPLICANT: SUNEIS PHARMACEUTICALS, INC.
 / APPLICANT: Prescott, John C.
 / TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
 / FILE REFERENCE: 39750-0006 US
 / CURRENT APPLICATION NUMBER: US/10/394,322A
 / PRIOR FILING DATE: 2003-03-20
 / PRIOR APPLICATION NUMBER: US 60/366,892
 / NUMBER OF SEQ ID NOS: 70
 / SOFTWARE: PasteSeq for Windows Version 4.0
 / SEQ ID NO 52
 / LENGTH: 313
 / TYPE: PRF
 / ORGANISM: Homo sapiens
 US-10-394-322A-52

Alignment Scores:

Pred. No.: 4,25e-109 Length: 313
 Score: 1636.00 Matches: 304
 Percent Similarity: 99.04% Conservative: 6
 Best Local Similarity: 97.12% Mismatches: 3
 Query Match: 66.97% Indels: 0
 DB: 15 Gaps: 0

US-10-705-757-3 (1-1302) x US-10-394-322A-52 (1-313)

Qy 4 ATGCTCTGTGCAAGATCAATCCCTGGCCACCTGGGCGACGCCCTTGCACGACTG 63
 Db 1 MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgIleAlaProCysAsnAspLeu 20
 Qy 64 CAGGCCAAACAGCTGGCGCGCGGCAAGAGAGAGGCCCTTGAGTGCAGTACCAAGT 123
 Db 21 HisAlaThrLysLeuAlaProGlyLysGlyLysLeuProLeuGlnSerGlnTyrGlnVal 40
 Qy 124 GGCCTGCTGTGGGACAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
 Db 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
 Qy 184 AACTGCGGCTGGCCATCAACAGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
 Db 61 AsnLeuProValAlaIleLysHisValGlnLysAspArgIleSerAspTyrGlyLysLeu 80

Qy 244 CCGAACGGACCCGAGTGGCCATGAGATGCTGCTGTAAGAAAGGAGCTGGGCTTC 303
 Db 81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
 Qy 304 TCGGGGCTCATTTAGACTTCTGAGCTGATTCGAGAGGCCGAGTATGTTCTGCTGATCTG 363
 Db 101 SerGlyValIleArgLeuLeuAspTyrPheGlyIleArgProAspSerPheValLeuLeu 120
 Qy 364 GAGAGGCCGACACCCGTCGACAGACTCTTCTGACTTCAACGAGGAGAGAGCTTCAG 423
 Db 121 GluArgProGlyIleProValGlnAspLeuPheAspPheIleThrGlyIleArgGlyIleGln 140
 Qy 424 GAGAGCTGGCCGAGGCTCTCTGAGAGGCTGAGAGCGTGGGAGCTTGCACCAAC 483
 Db 141 GluGlnLeuAlaArgSerPhePheThrGlnValLeuGlnAlaValArgHisCysHisAsn 160
 Qy 484 TCGGGGATTCCTCCACCGCGACATCAAGACGAGAGACATCTTAACTGACCTGAACCGGCG 543
 Db 161 CysGlyValLeuHisArgAspIleLysAspGlyAsnIleLeuIleAspLeuAsnArgGly 180
 Qy 544 GAACCTCAACTCATCGACTTCGGGTCGGGGGCGCTGCTCAAGACACAGTCTTACAGGAC 603
 Db 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200
 Qy 604 TTGGACGGAACCCGAGTGTACAGTCTCTCCAGAGTGGATTGGCTACCATCGCTACACGGC 663
 Db 201 PheAspGlyThrArgValTyrSerProGlyIleArgTyrHisArgTyrHisGly 220
 Qy 664 AGGCGGCTGCTGTTGGTGGTGGGAGTCTGCTGATGACATGGCTGGGAGATATT 723
 Db 221 ArgSerIleAlaValIlePheSerLeuGlyIleLeuLeuLysAspMetValCysGlyAspIle 240
 Qy 724 CCATTGAGACGACGAGAGATGTCAGAGGCGCAAGTGTACTTTAGCAAAAGGCTCTT 783
 Db 241 ProPheGlyIleHisArgIleGlyIleIleArgGlyIleValPhePheArgGlyIleValSer 260
 Qy 784 TCAGAAATGTCACATCTTATTAGTGGTGGCTGCTGCTGAGACCATGAGACCGGCTCC 843
 Db 261 SerGlyCysGlnHisLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProThr 280
 Qy 844 TTGAAGAATCCGACGACCATCCGATGATGAGATGTTCTCTGCGCCGACGACCGCC 903
 Db 281 PheGlyIleIleGlnAsnHisProTyrPheGlnAspValLeuLeuProGlnGlyIleAla 300
 Qy 904 GAGATTCATCTGCACAGCTGTGCACATCAACCCAGCAA 942
 Db 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313

RESULT 7

US-10-348-081-13
 / Sequence 13, Application US/10348081
 / Publication No. US20040038246A1
 / GENERAL INFORMATION:
 / APPLICANT: KOEN, Marcue
 / APPLICANT: MOELLER, Guenter
 / APPLICANT: SCHNEIDER, Rudolf
 / APPLICANT: TSCHANZ, Georg
 / TITLE OF INVENTION: P1M-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
 / FILE REFERENCE: DE4V2002/0004 US NP
 / CURRENT APPLICATION NUMBER: US/10/348,081
 / PRIOR FILING DATE: 2003-01-21
 / NUMBER OF SEQ ID NOS: 14
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 13
 / LENGTH: 313
 / TYPE: PRF
 / ORGANISM: Homo sapiens
 US-10-348-081-13

Alignment Scores:
 Pred. No.: 4,25e-109 Length: 313
 Score: 1636.00 Matches: 304
 Percent Similarity: 99.04% Conservative: 6

Best Local Similarity: 97.12% Mismatches: 3
Query Match: 66.97% Indels: 0
DB: 15 Gaps: 0
US-10-705-757-3 (1-1302) x US-10-348-081-13 (1-313)
QY 4 ATGCTCTTCCAAAGATCAACTCCCTGGCCCACTGCGGCGAGCCCTTGCACGACCTG 63
DB 1 MetLeuLeuSerLySrlleahnsrleuAlahlsleuArghlaalaprocyasmbpLeu 20
QY 64 CACGCCAACAAGCTGGCGCGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
DB 21 HisAlaThrlyleuAlaproGlySglulysGluProleuLubserGlnlyrGlnVal 40
QY 124 GGGCCGCTGTGGGCGCGGTGCTTCGGCTCGGTCTACTCCGGGAGTCCGGCGCGAG 183
DB 41 GlyProleuLeuLyseryGlySglulysSerVallySerGlylleArghValSerAsp 60
QY 184 AACTTCCGGTGGCCATCAAGACAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
DB 61 AsnLeuProValAlahlsleuShlsvalGluLysAspArglleSerAspTrpGlyGluLeu 80
QY 244 CCCAAGCGGACCCGAGTCCCATGAGAGAGTGTCTCTGTAAGAGAGTGAAGCTCGGCTTC 303
DB 81 ProAsnGlyThrArghValProMetGluValleuLeuLysValSerSerGlyPhe 100
QY 304 TCGGGGCTGATTGACTTCTGGAAGTGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 363
DB 101 SerGlyValleuLyseryleuAspTrpPheGlnArghProAspSerPheValleuLeu 120
QY 364 GAGAGCCCGAAGCCGCTGCAAGACTCTTGAAGTTCATCAAGAGAGAGAGAGAGAGAG 423
DB 121 GluArghProGluProValGlnAspLeuPheAspPheillethrcGlnArghValleuGln 140
QY 424 GAGAGCTGGCGCGAGCTTCTTCTGAGAGTGTCTGAGAGCGCTGCGGACATTCGCAAC 483
DB 141 GluGluLeuAlaArghSerPhePheTrpGlnValleuGlnAlaValArghlsCyshlsAsn 160
QY 484 TGGGGGGTCTCAAGCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
DB 161 CySgllyValleuLyseryleuAspTrpPheGlnAsnilleuLeuLyseryleuAspTrp 180
QY 544 GAAGTCAAACTCATGCACTTGGGAGTGGGAGCGCTGCAAGAGACAGTCTACAGAGAG 603
DB 181 GluLeuLyseryleuLyseryleuGlyAlaLeuLeuLyseryleuVallyrThrAsp 200
QY 604 TTTGAGAGAGAGAGAGAGTGTCTCTGAGAGTGTGCTACAGTGTCTGCAAGAGAG 663
DB 201 PheAspGlyThrArghVallyrSerProProGluTrpilleArghlyrHisArghlyrHis 220
QY 664 AGGTGGGCTGTGTTGGTCCCTGGGAGAGTGTCTGATGAGAGAGTGTGGAGAGATTT 723
DB 221 ArghSerAlaAlaVallyrSerleuGlylleuLeuLyseryleuAspPheVallyrGlyAsp 240
QY 724 CCAATTGAGAGAGAGAGAGAGTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 783
DB 241 ProPheGlnLyseryleuLyseryleuLyseryleuLyseryleuLyseryleuLys 260
QY 784 TCGAAGTGTCAACATCTTATTAAGTGTGTCTCTGAGAGAGAGAGAGAGAGAGAGAG 843
DB 261 SerGlnCySgllyleuLyseryleuLyseryleuLyseryleuLyseryleuLysery 280
QY 844 TTTGAGAGAGAGAGAGAGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 903
DB 281 PheGlnGlnLyseryleuLyseryleuLyseryleuLyseryleuLyseryleuLys 300
QY 904 GAGATTCATCTGACAGCTGTGACAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 942
DB 301 GluLyseryleuLyseryleuLyseryleuLyseryleuLyseryleuLyseryleu 313
RESULT 8
US-10-664-421-1
; Sequence 1, Application US/10664421

/ Publication No. US2004014286A1
/ GENERAL INFORMATION:
/ APPLICANT: BREMER, RYAN
/ APPLICANT: IBRAHIM, PRABHA
/ APPLICANT: KUMAR, ABHINAV
/ APPLICANT: MANDIVAN, VALSAN
/ APPLICANT: MILEURN, MICHAEL V.
/ TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
/ FILE REFERENCE: 039363/0703
/ CURRENT APPLICATION NUMBER: US/10/664,421
/ PRIOR FILING DATE: 2003-09-16
/ PRIOR APPLICATION NUMBER: 60/412,341
/ PRIOR FILING DATE: 2002-09-20
/ PRIOR APPLICATION NUMBER: 60/411,398
/ PRIOR FILING DATE: 2002-09-16
/ NUMBER OF SEQ ID NOS: 169
/ SOFTWARE: Patentin Ver. 3.2
/ SEQ ID NO 1
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-664-421-1
Alignment Scores:
Pred. No.: 4,256-109 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 66.97% Indels: 0
DB: 16 Gaps: 0
US-10-705-757-3 (1-1302) x US-10-664-421-1 (1-313)
QY 4 ATGCTCTTCCAAAGATCAACTCCCTGGCCCACTGCGGCGAGCCCTTGCACGACCTG 63
DB 1 MetLeuLeuSerLySrlleahnsrleuAlahlsleuArghlaalaprocyasmbpLeu 20
QY 64 CACGCCAACAAGCTGGCGCGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
DB 21 HisAlaThrlyleuAlaproGlySglulysGluProleuLubserGlnlyrGlnVal 40
QY 124 GGGCCGCTGTGGGCGCGGTGCTTCGGCTCGGTCTACTCCGGGAGTCCGGCGCGAG 183
DB 41 GlyProleuLeuLyseryGlySglulysSerVallySerGlylleArghValSerAsp 60
QY 184 AACTTCCGGTGGCCATCAAGACAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
DB 61 AsnLeuProValAlahlsleuShlsvalGluLysAspArglleSerAspTrpGlyGluLeu 80
QY 244 CCCAAGCGGACCCGAGTCCCATGAGAGAGTGTCTCTGTAAGAGAGTGAAGCTCGGCTTC 303
DB 81 ProAsnGlyThrArghValProMetGluValleuLeuLysValSerSerGlyPhe 100
QY 304 TCGGGGCTGATTGACTTCTGGAAGTGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 363
DB 101 SerGlyValleuLyseryleuAspTrpPheGlnArghProAspSerPheValleuLeu 120
QY 364 GAGAGCCCGAAGCCGCTGCAAGACTCTTGAAGTTCATCAAGAGAGAGAGAGAGAGAG 423
DB 121 GluArghProGluProValGlnAspLeuPheAspPheillethrcGlnArghValleuGln 140
QY 424 GAGAGCTGGCGCGAGCTTCTTCTGAGAGTGTCTGAGAGCGCTGCGGACATTCGCAAC 483
DB 141 GluGluLeuAlaArghSerPhePheTrpGlnValleuGlnAlaValArghlsCyshlsAsn 160
QY 484 TGGGGGGTCTCAAGCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
DB 161 CySgllyValleuLyseryleuAspTrpPheGlnAsnilleuLeuLyseryleuAspTrp 180
QY 544 GAAGTCAAACTCATGCACTTGGGAGTGGGAGCGCTGCAAGAGACAGTCTACAGAGAG 603
DB 181 GluLeuLyseryleuLyseryleuGlyAlaLeuLeuLyseryleuVallyrThrAsp 200


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; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-377-268-9

Alignment Scores:
Pred. No.: 4,25e-109 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 66.97% Indels: 0
DB: 16 Gaps: 0

US-10-705-757-3 (1-1302) x US-10-377-268-9 (1-313)

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DB 1 MetLeuLeuSerLysIleAsnSerLeuLAlaIleuAArgAlaIleProCysAsnAspLeu 20
QY 64 CAGCCCAACAAAGCTGGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
DB 21 HisAlaThrIlySerLeuAlaProGlyLysGluLysGluProLeuGlnSerGlnIlyrGlnVal 40
QY 124 GGCCTGCTGTGGGCAAGCGGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
DB 41 GlyProLeuLeuGlySerGlyIlyPheGlySerValIlySerGlyIleArgValIleAsp 60
QY 184 AACTTGCGGCTGGCCATCAAGCAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
DB 61 AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyGluLeu 80
QY 244 CCCAAGCGGCAAGCGGCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
DB 81 ProAsnGlyThrArgValIleProMetGluValIleLeuLeuLysValIleSerSerGlyPhe 100
QY 304 TCGGCGCTGATTGACTTCTGAGCTGGTTCGAGAGCGCGAGATTCCTGCTGATCTTG 363
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGlyLysArgProAspSerPheValIleLeu 120
QY 364 GAGAGCGCCGAGACCCGTCGCAAGACCTTTCGACTTCATCAACGAGAGAGAGAGAGAG 423
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgValAlaLeuGln 140
QY 424 GAGAGCTGGCGGAGACTTCTTGAGAGCTGTCGAGAGCGCGGCGGCAATTCGCAAC 483
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValIleGlnAlaValIleArgHisCysHisAsn 160
QY 484 TCGCGGCTTCTCCACCGGCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
DB 161 CysGlyValIleuHisArgAspIleLysAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY 544 GAATCTCAATCAATCGACTTCGAGTGGGCGGCTGTCAGAGACAGACTTCACAGGAG 603
DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspTrpValIlyTrnAsp 200
QY 604 TTGAGCGGAACCGGAGTGTACAGCTCTCAGAGTGTATTCGTAACCTGCTGCAAGCG 663
DB 201 PheAspGlyThrArgValIlyrSerProProGluTrpIleArgTrpHisAspGlyrHisGly 220
QY 664 AGGTGGCTGCTGTTGGTCCCTGAGGAGCTTCGCTATGACATGCTTCGAGAGATTT 723
DB 221 ArgSerAlaIleValIleTrpSerLeuGlyIleLeuLeuLysAspMetValCysGlyAspIle 240
QY 724 CATTGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 783
DB 241 ProPheGlnHisAspGluGluIleIleArgGlyGlnValIlePheAspArgGlnArgValSer 260
QY 784 TCAGATGTCAACATCTTATTAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
DB 261 SerGluCysGlnHisLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280
QY 844 TTGAGAGAAATCCAGAACATCCGTGAGTCAAGAGATTTCTCTGCGCCAGGCGCACCGCC 903
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DB 281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValIleLeuProGlnGluThrAla 300
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DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313

RESULT 11
US-10-951-389-18
/ Sequence 18, Application US/10951389
/ Publication No. US20050058627A1
/ GENERAL INFORMATION:
/ APPLICANT: Reinhard, Christoph
/ APPLICANT: Jefferson, Anne B.
/ APPLICANT: Chan, Vivien W.
/ TITLE OF INVENTION: TTK in diagnosis and as a Therapeutic
/ TITLE OF INVENTION: Target in Cancer
/ FILE REFERENCE: 16932.002
/ CURRENT APPLICATION NUMBER: US/10/951,389
/ PRIOR FILING DATE: 2004-09-27
/ PRIOR APPLICATION NUMBER: US/10/081,119
/ PRIOR FILING DATE: 2002-02-21
/ PRIOR APPLICATION NUMBER: 60/289,813
/ PRIOR FILING DATE: 2001-02-21
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-951-389-18

Alignment Scores:
Pred. No.: 4,25e-109 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 66.97% Indels: 0
DB: 17 Gaps: 0

US-10-705-757-3 (1-1302) x US-10-951-389-18 (1-313)

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DB 1 MetLeuLeuSerLysIleAsnSerLeuLAlaIleuAArgAlaIleProCysAsnAspLeu 20
QY 64 CAGCCCAACAAAGCTGGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
DB 21 HisAlaThrIlySerLeuAlaProGlyLysGluLysGluProLeuGlnSerGlnIlyrGlnVal 40
QY 124 GGCCTGCTGTGGGCAAGCGGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
DB 41 GlyProLeuLeuGlySerGlyIlyPheGlySerValIlySerGlyIleArgValIleAsp 60
QY 184 AACTTGCGGCTGGCCATCAAGCAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
DB 61 AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyGluLeu 80
QY 244 CCCAAGCGGCAAGCGGCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
DB 81 ProAsnGlyThrArgValIleProMetGluValIleLeuLeuLysValIleSerSerGlyPhe 100
QY 304 TCGGCGCTGATTGACTTCTGAGAGCTGTCGAGAGCGCGGCAATTCGCTGATCTTG 363
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGlyLysArgProAspSerPheValIleLeu 120
QY 364 GAGAGCGCCGAAACCGGTCGCAAGACCTTTCGACTTCATCAACGAGCGAGAGAGAGAG 423
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgValAlaLeuGln 140
QY 424 GAGAGCTGGCGGAGACTTCTTGAGAGCTGTCGAGAGCGCGGCGGCAATTCGCAAC 483
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValIleGlnAlaValIleArgHisCysHisAsn 160
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Db      21 HislaLthrlyseuLaIaProgllylysgluLysleuProleuGusertGlnTyrglnVal 40
Qy      124 GGGCCGCTGTGGGCGACGGTGGCTTCGGCTCGGCTTACTCGGCGACCCGCGTCCGAC 183
Db      41 GlyProleuLeuGlyserGlygLyPheGlySerValTyserGlylleargValSerAsp 60
Qy      184 AACTGCGGGTGGCCATCAAGCAAGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
Db      61 AsnuLeuProValAlaIlelyshIsvaGluLysAspArgIleSerAspTrpGlyGluLeu 80
Qy      244 CCCAAGCGGCAACCGAGTGCCTCAAGAGTGGTCTCGTCAAGAGAGTGAAGTGAAGTGGCTTC 303
Db      81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
Qy      304 TCGGGCGCTCAATTAAGTCTTGAGTGGTTCAGAGGCGCCAGATGTTTCGTGTCGATCTTG 363
Db      101 SerGlyValIleArgLeuLeuAspTrpPheGlyLysArgProAspSerPheValLeuLeu 120
Qy      364 GAGAGCGCCGAGACCCGCGCAAGACCTTCGAGCTTCATCAACGAGAGAGAGAGAGAGAGAGAG 423
Db      121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGlyLysArgGlyAlaLeuGln 140
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Qy      484 TCGGGGGTTCCTCCACCGCGCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
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Qy      784 TCAGAAATGTCAGATCTTATTAGATGGTGGCTGGCTGGAGAGAGAGAGAGAGAGAGAGAGAG 843
Db      261 SerGluCyserGlnIleLeuLysArgTrpCyserLeuAlaLeuArgProSerAspArgProThr 280
Qy      844 TTGAGAGAAATCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 903
Db      281 PheGluGluIleGlnIleAsnIleAspTrpMetGlnAspValLeuLeuProGlnIleuTrAla 300
Qy      904 GAGATTCATTCGACAGAGCTTCATCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 942
Db      301 GluIleLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeu 313

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RESULT 15 US-10-705-757-2

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/ Sequence 2, Application US/10705757
/ Publication No. US20040146942A1
/ GENERAL INFORMATION:
/ APPLICANT: GRUBENTHAL GMBH
/ TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
/ FILE REFERENCE: 029310.52818US
/ CURRENT APPLICATION NUMBER: US/10/705.757
/ PRIOR FILING DATE: 2003-11-12
/ PRIOR APPLICATION NUMBER: PCT/EP02/05234
/ PRIOR FILING DATE: 2002-05-13
/ PRIOR APPLICATION NUMBER: DE 101 23 055.9
/ PRIOR FILING DATE: 2001-05-11

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-757-2

Alignment Scores:
Pred. No.: 4.25e-109 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 66.97% Indels: 0
DB: 18 Gaps: 0

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Db      21 HislaLthrlyseuLaIaProgllylysgluLysleuProleuGusertGlnTyrglnVal 40
Qy      124 GGGCCGCTGTGGGCGACGGTGGCTTCGGCTCGGCTTACTCGGCGACCCGCGTCCGAC 183
Db      41 GlyProleuLeuGlyserGlygLyPheGlySerValTyserGlylleargValSerAsp 60
Qy      184 AACTGCGGGTGGCCATCAAGCAAGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
Db      61 AsnuLeuProValAlaIlelyshIsvaGluLysAspArgIleSerAspTrpGlyGluLeu 80
Qy      244 CCCAAGCGGCAACCGAGTGCCTCAAGAGTGGTCTCGTCAAGAGAGTGAAGTGAAGTGGCTTC 303
Db      81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
Qy      304 TCGGGCGCTCAATTAAGTCTTGAGTGGTTCAGAGGCGCCAGATGTTTCGTGTCGATCTTG 363
Db      101 SerGlyValIleArgLeuLeuAspTrpPheGlyLysArgProAspSerPheValLeuLeu 120
Qy      364 GAGAGCGCCGAGACCCGCGCAAGACCTTCGAGCTTCATCAACGAGAGAGAGAGAGAGAGAGAG 423
Db      121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGlyLysArgGlyAlaLeuGln 140
Qy      424 GAGAGCTGGCCCGGAGCTTCTTCGAGAGTGGTGGAGGCGCGTGGCGAGTGGCGAGCAAC 483
Db      141 GluGluLeuLysArgSerPhePheTrpGlnValLeuGlnAlaValArgIleScyShIAsn 160
Qy      484 TCGGGGGTTCCTCCACCGCGCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
Db      161 CygGlyValLeuLysArgAspIleLysAspGlyLysLeuLysLeuLysLeuLysLeuLysLeu 180
Qy      544 GAATCTGAATCATTCGACTTCGGGTGGGGGGCGCTGCTCAAGAGAGAGTCTACAGAGAG 603
Db      181 GluLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeu 200
Qy      604 TTGACGGAACCGGAGTGCCTTCGAGTGGTTCAGAGGCGCCAGATGTTTCGTGTCGATCTTG 663
Db      201 PheAspGlyThrArgValTyserProGluTrpIleArgGlyThrIleArgGlyThrIleArg 220
Qy      664 AGGTGGCTGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 723
Db      221 ArgSerAlaIleValIleTrpSerLeuGlyIleLeuLeuLysLeuLysLeuLysLeuLysLeu 240
Qy      724 CCATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 783
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Qy      784 TCAGAAATGTCAGATCTTATTAGATGGTGGCTGGCTGGAGAGAGAGAGAGAGAGAGAGAGAG 843
Db      261 SerGluCyserGlnIleLeuLysArgTrpCyserLeuAlaLeuArgProSerAspArgProThr 280

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 15:59:25 ; Search time 214.949 Seconds
(without alignments)
6203.583 Million cell updates/sec

Title: US-10-705-757-3

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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-DB=uniprot -OPMT=faasta -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPT=0 -LOOPEXT=0
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-OUTPM=pco -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MAMP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot 03:.*
1: uniprot.sprot:.*
2: uniprot.trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1638	67.0	313	1 PIM1_HUMAN	095110 felis
3	1636	67.0	313	1 PIM1_HUMAN	P11309 homo
4	1630	66.7	313	1 PIM1_BOVIN	Q9N099 bos
5	1589	65.0	313	2 Q8CFN8	Q8CFN8 mus
6	1584	64.8	313	1 PIM1_MOUSE	P06803 mus
7	1140	46.7	323	1 PIM3_CORYA	Q9P855 colum
8	1136.5	46.4	326	1 PIM3_HUMAN	Q86V86 homo
9	1132.5	46.5	326	1 PIM3_MOUSE	P58750 mus
10	1131.5	46.3	326	1 PIM3_RAT	Q70444 ratu
11	1119	45.8	325	2 Q811X8	Q811X8 mus
12	1110.5	45.5	318	2 Q611I1	Q611I1 xenop
13	1104	45.2	323	1 PIM3_XENLA	Q91822 xenop
14	878	35.9	311	2 Q8R2B0	Q8R2B0 mus
15	878	35.9	370	1 PIM2_MOUSE	Q62070 mus
16	866.5	35.5	311	1 PIM2_HUMAN	Q9P149 homo

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18	858	35.1	310	2 Q8JFW9	Q8JFW9 brachy
19	853	34.9	310	1 PIM1_BPAR	Q9Y1N5 brachy
20	851	34.8	310	2 Q6DI52	Q6DI52 brachy
21	716.5	29.3	221	2 Q8R1Z0	Q8R1Z0 mus
22	626	25.6	441	2 Q20443	Q20443 caenor
23	485	20.3	378	2 Q8T3F1	Q8T3F1 caenor
24	455	20.3	366	2 Q17737	Q17737 caenor
25	421	17.2	134	2 Q6P2J9	Q6P2J9 homo
26	406	16.6	1283	1 PASK_MOUSE	Q8CE66 mus
27	403	16.5	125	2 Q6Q2K5	Q6Q2K5 canis
28	396	16.2	658	2 Q64IK5	Q64IK5 mus
29	394	16.1	794	1 K111_HUMAN	Q8IC63 homo
30	387.5	15.9	514	2 Q9XFZ5	Q9XFZ5 glycine
31	385	15.8	688	2 Q95UP4	Q95UP4 ancylo
32	385	15.8	776	2 Q699J6	Q699J6 mus
33	384	15.7	1107	2 Q6C310	Q6C310 yarrowia
34	381.5	15.6	504	2 P93113	P93113 cucumis
35	381.5	15.6	661	1 ARK5_HUMAN	Q60285 homo
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37	380	15.6	535	1 K110_ARATH	Q38997 arabid
38	380	15.6	1398	2 Q7Z268	Q7Z268 drosoph
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40	379.5	15.5	432	2 Q70XR8	Q70XR8 giardia
41	379	15.5	1206	2 Q6FTU1	Q6FTU1 candida
42	379	15.5	1336	2 Q6FRS7	Q6FRS7 candida
43	378.5	15.5	698	2 Q61298	Q61298 halocynth
44	377.5	15.5	1229	2 Q6CKM4	Q6CKM4 kluyveromyc
45	374.5	15.3	643	2 Q7R0B9	Q7R0B9 giardia

ALIGNMENTS

RESULT 1
PIM1_RAT STANDARD; PRT; 313 AA.
ID P26794;
AC P26794;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB Protoc-oncogene serine/threonine-protein kinase Pim-1 (BC 2.7.1.37).
GN Name=Pim1; Synonyms=Pim-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=92319652; PubMed=1620615;
RA Wingate D., Reeves R., Magnuson N.S.;
RT "Characterization of the testes-specific pim-1 transcript in rat.";
RL Nucleic Acids Res. 20:3183-3189(1992).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Binds to R99 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -!- PTM: Autophosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM subfamily.
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CC EMBL; X63675; CAA45214.1; -
CC PIR; S26298; S26298.
CC RGD; 3330; Pim1.
CC InterPro; IPR011009; Kinase_like.
CC InterPro; IPR00719; Prot_Kinase.

US-10-705-757-3 (1-1302) x PIM1_FELCA (1-313)

```

QY 4 ATGCTCTTTCGAAGATCAACTCCCTGGCCCACTGGCCGACGCCCTTGCAAGACTCTG 63
DB 1 MetleuSeuSerlyIleAenSerleuAlaHleuAlaGThraAlaProCyAsnAspLeu 20
QY 64 CAGCGCAACAAGCGGGGGGGGCAAGAGAGAGAGCGCCCTGGAGTACCAAGTCAAGT 123
DB 21 HleAlaThraLyseAlaAProGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 40
QY 124 GGGCCGCTGTGGGACGCGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 183
DB 41 GlyProleuSeuGlySerGlyGlyPheGlySerAlaYleSerGlyIleAlaGlyAlaAsp 60
QY 184 AACTTGGCCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 243
DB 61 AsnleuProValAlaIleYleVhLeValGlyLysAspArgIleSerAspArgGlyLysLeu 80
QY 244 CCCAAGGCGACCCGAGGCGCATGGAAGTGGTCTCGTGAAGAGAGAGTGGAGTGGCTTC 303
DB 81 ProAsnGlyThraArgValProMetGlyValValLeuLeuYlyValSerSerGlyPhe 100
QY 304 TCGGCGCTCATTAAGTCTGCACTGGTTCGAGAGCGCCGATAGTTCGAGTCTGATCTCT 363
DB 101 SerGlyValIleAlaGlyLeuLeuAspTrpPheGlyLysArgProAspSerPheValLeuLeu 120
QY 364 GAGAGGCGCGAACCCTGCAAGACTCTTGGACTTCATCAACGAGGAGAGAGCCCTTCAG 423
DB 121 GlyLysArgProGlyLysProValGlyLysAspPhePheIleThraGlyAlaLeuGly 140
QY 424 GAGAGGCTGGCCGCGAGCTCTTCTGGCAGTCTGGAGGCGCGGCGCGCATTTGGCAAC 483
DB 141 GlyGlyLeuAlaAspSerPhePheTrpGlyAlaLeuAlaValAlaGlyAspGlyAsn 160
QY 484 TGGCGGCTTCCACCGCGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
DB 161 CysGlyValLeuHleuHleuAspArgIleYleYAspGlyLysLeuIleLeuIleAspLeuAsnArgGly 180
QY 544 GAACTCAACTCATGCACTTGGGCTGGGCGCGCTGCTCAAGAGACAGTCTTACAGGAG 603
DB 181 GlyLeuYleuLeuIleAspPheGlySerGlyValLeuLeuYleuYAspTrpValYTrpThraAsp 200
QY 604 TTTGACGGAACCGGAGTGCACAGTCTCCAGAGTGGATTCGATCCCTACCTACAGGCG 663
DB 201 PheAspGlyThraArgValYTrpSerProGlyLysTrpIleArgYTrpAspGlyYTrpGly 220
QY 664 AGGTCGCTGCTGTTGGTCCCTGGGAGCTCGTCTATGACATGCTGCGAGATATT 723
DB 221 ArgSerAlaAlaValAlaTrpSerLeuGlyIleLeuLeuYTrpAspPheValCysGlyAspIle 240
QY 724 CCATTGAGACGACGAGAGAGATGTCAGAGGCGCAAGTGTACTTTAGCAAAAGGCTCT 783
DB 241 ProPheGlyLysHleuAspArgGlyLysIleAlaArgGlyValAlaPhePheAspGlyAlaValSer 260
QY 784 TCAGATGTCACACTTTATTAAGTGGTGGCTGCTCCCTGAGACGATGAGCCGCGCTCC 843
DB 261 SerGlyCysGlyHleuIleAlaArgTrpCysLeuAlaLeuArgProSerAspArgProSer 280
QY 844 TTTGAAGAATTCGACGACATCCGTCGATGATGAGAGATTTCTCCGCGCGAGCGACCGCC 903
DB 281 PheGlyLysIleGlyAlaHleuHleuAspArgTrpMetGlyAlaHleuLeuProGlyLysAla 300
QY 904 GAGATTGATGTCAGACGCTGTCACATCAACCCAGCAAA 942
DB 301 GlyIleHleuHleuHleuSerLeuSerProGlyProSerLys 313

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RESULT 3

PIM1_HUMAN STANDARD; PRT; 313 AA.
AC P1309; Q96RG3;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Proto-oncogene serine/threonine-protein kinase pim-1 (BC 2.7.1.37).
OS Name=Pim1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90382681; PubMed=2205533; DOI=10.1016/0378-1119(90)90195-W;
RA Reeves R., Spies G.A., Klefer M., Barr P.J., Power M.;
RT "Primary structure of the putative human oncogene, pim-1.";
RL Gene 90:303-307(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
RA Zakut-Houri R., Hazum S., Givol D., Telexman A.;
RT "The cDNA sequence and gene analysis of the human pim oncogene.";
RL Gene 54:105-111(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88217305; PubMed=3329709;
RA Domen J., von Lindern M., Hermans A., Breuer M., Grosveld G.,
RA Berns A.;
RT "Comparison of the human and mouse PIM-1 cDNAs: nucleotide sequence and immunological identification of the in vitro synthesized PIM-1 protein.";
RL Oncogene Res. 1:103-112(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=88115604; PubMed=3429489;
RA Meeker T.C., Nagarajan L., Ar-Rushdi A., Croce C.M.;
RT "Cloning and characterization of the human PIM-1 gene: a putative oncogene related to the protein kinases.";
RL J. Cell. Biochem. 35:105-112(1987).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Datchenko L., Matrasova K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tomiyuki S., Carninci P., Prange C.,
RA Bha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
RA Rosh S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hylk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skaleka U., Smalms D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 1-302 FROM N.A.
RX MEDLINE=21354098; PubMed=11460166; DOI=10.1038/35085588;
RA Pasqualucci L., Neumeister P., Goossens T., Nannjand G.,
RA Chaganti R.S.K., Kupperts R., Dalla-Favera R.;
RT "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-cell lymphomas.";
RL Nature 412:341-346(2001).
RN [7]
RP CHARACTERIZATION.
RX MEDLINE=88246418; PubMed=2837645;
RA Telexman A., Amson R., Zakut-Houri R., Givol D.;
RT "Identification of the human pim-1 gene product as a 33-kilodalton cytoplasmic protein with tyrosine kinase activity.";
RL Mol. Cell. Biol. 8:1498-1503(1988).

RN [8]
 RP FUNCTION
 RA MEDLINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4;
 RA Koike N., Maiba H., Taira T., Ariga H., Iguchi-Ariga S.M.M.;
 RT "Identification of heterochromatin protein 1 (HP1) as a
 RT phosphorylation target by Pim-1 kinase and the effect of
 RT phosphorylation on the transcriptional repression function of
 RT HP1(1)."
 RL FEBS Lett. 467:17-21(2000).
 RN
 RP SUBCELLULAR LOCATION.
 RA MEDLINE=22567470; PubMed=12680209;
 RA Ionov Y., Le X., Tungstet B.J., Sweetenham J., Sachs T., Ryder J.,
 RA Johnson T., Lilly M.B., Kraft A.S.;
 RT "Pim-1 protein kinase is nuclear in Burkitt's lymphoma: nuclear
 RT localization is necessary for its biologic effects.";
 RL Anticancer Res. 23:167-178(2003).
 CC -1- FUNCTION: Thought to play a role in signal transduction in blood
 CC cells. May affect the structure or silencing of chromatin by
 CC phosphorylating HP1 gamma/CBX3.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBUNIT: Binds to Rps (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
 CC -1- TISSUE SPECIFICITY: Expressed primarily in cells of the
 CC hematopoietic and germ line lineages.
 CC -1- PTM: Autophosphorylated on tyrosine residues.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
 CC subfamily.
 CC -1- DATABASES: NAMB=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW=http://www.infobiosgen.fr/services/chromocancer/Genes/PIM1ID261.html".
 CC
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 CC
 DR EMBL; M27903; AAA60090.1; -;
 DR EMBL; M16750; AAA60089.1; -;
 DR EMBL; M54915; AAA36447.1; -;
 DR EMBL; M24779; AAA81553.1; -;
 DR EMBL; BC020224; AAH20224.1; -;
 DR EMBL; AF386792; AAK70871.1; -;
 DR PIR; J00327; TYHUP1.
 DR Genew; HGNC:8986; PIM1.
 DR H-InvDB; HIX005835; -;
 DR MIM; 164960; -;
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser Thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
 KM ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
 KM Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 38 290 Protein kinase.
 FT NP BIND 44 52 ATP (By similarity).
 FT BINDING 67 67 ATP (By similarity).
 FT ACT SITE 167 167 Proton acceptor (By similarity).
 FT CONFLICT 15 16 AP -> RA (in Ref. 2).
 SQ SEQUENCE 313 AA; 35685 MM; 35BA76D3668B69A3 CRC64;
 Alignment Scores: 1.9e-97 Length: 313
 Pred. No.: 1636.00 Matches: 304
 Score:

Percent Similarity: 99.04% Conservative: 6
 Best Local Similarity: 97.12% Mismatches: 3
 Query Match: 66.97% Indels: 0
 DB: 1 Gaps: 0
 US-10-705-757-3 (1-1302) x PIM1_HUMAN (1-313)
 QY 4 ATGGCTTGTCCAGATGATCCCTGGCCGACCTGCGGCGAGCCCTTGACAGCAGCTG 63
 DB 1 MetLeuSerLysAlaIleHisSerLeuAlaHisLeuArgAlaHisProCysHisMetLeu 20
 QY 64 CAGCCCAACAGCTGGCGCGGCGCAAGAGAGAGCCCTGAGTCCGAGTACCAAGTGT 123
 DB 21 HisAlaThrIleLeuAlaProGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 40
 QY 124 GCGCGCGCTGTGGGCGCGGTGGCTTGGCTGGCTTACTCGGGGACCTCGCGTCCGCG 183
 DB 41 GlyProLeuLeuGlySerGlyGlyLysSerValTyrSerGlyIleArgValSerMet 60
 QY 184 AACTTGGCGGTGGCGCATCAAGCAGTGGAGAGAGCCGAGTTCGACTGGGAGGAACTG 243
 DB 61 AsnLeuProValAlaIleIleValHisValGlyLysMetArgLysSerMetProGlyLysLeu 80
 QY 244 CCCAAGCGGACCCGAGTGGCCATGAGAGTGTCTGCTGAGAGAGGTAGCTCGGCTTC 303
 DB 81 ProMetGlyThrArgValProMetGlyValValLeuLeuLysValSerSerGlyPhe 100
 QY 304 TGGGCGCTGATTAAGCTTGTGAGCTGTTCGAGAGCCCGAGATGTTGCTGTCATCTCG 363
 DB 101 SerGlyValIleArgLeuLeuMetProPheGlyLysGlyLysGlyLysGlyLysGlyLysLeu 120
 QY 364 GAGAGCGCGGACCCGAGTGGAGAGCTTGTGACTTCATCAGCAGGAGAGAGCCCTCG 423
 DB 121 GlyArgProGlyProValGlnHisMetProMetPheMetIleThrGlyArgGlyLysGln 140
 QY 424 GAGAGCTGGCCCGGAGCTTCTTGGAGGTGTGAGAGCCGCTGGGAGTTCGACAAAC 483
 DB 141 GluGlyLeuAlaArgSerPheMetProGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 160
 QY 484 TGGCGGCTTCCACCGGACATCAAGAGCAGAGCACTTTAATGACCTGAACCGCGGC 543
 DB 161 CysGlyValLeuHisArgMetLeuLysMetGlyLysGlyLysGlyLysGlyLysGlyLysGly 180
 QY 544 GAATCAATCATGAGCTTGGGCTCGGAGGCGGCTGAGAGAGCAGTTCATCAGCAG 603
 DB 181 GluLeuLysLeuIleAspPheIleSerGlyLysAlaLeuLeuLysMetThrValTyrThrMet 200
 QY 604 TTGAAGGAAACCGAGTGAAGCTCTCCAGAGTGAATTCGTTACATGCTTACACGCG 663
 DB 201 PheMetGlyThrArgValTyrSerProGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 220
 QY 664 AGCTGGCTGCTGTTGGCTTGGCTTGGGAGATCCGCTTGAAGATGCTGCGGAGTATT 723
 DB 221 ArgSerAlaAlaValTyrSerLeuGlyIleLeuLeuTyrAspMetValCysGlyMetPhe 240
 QY 724 CCATTGAGCAGCAGCAGAGATGCTCAAGGCGCAAGTACTTTAGGCAAGGAGTCTCT 783
 DB 241 ProPheGlyLysHisMetGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 260
 QY 784 TGAAGATGCAATCTTATTAAGATGCTGCTGCTGCTGAGACCATGAGCCGCGCTTC 843
 DB 261 SerGlyCysGlyHisIleLeuIleArgTyrCysLeuAlaLeuArgProSerMetArgProThr 280
 QY 844 TTGAAGAAATTCAGAACCATCCGAGAGCAGAGATGTTCTCTGCGCAGGCGACGCG 903
 DB 281 PheGlyLysIleGlyLysHisMetProMetGlyLysGlyLysGlyLysGlyLysGlyLysGly 300
 QY 904 GAGATTCATGTCAGAGCTGTCACCATCAGCAGCAGCAAA 942
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313
 RESULT 4
 PIM1_BOVIN

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ID PIM1_BOVIN STANDARD; PRT; 313 AA.
AC Q9N0P9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN Name=PIM1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21109090; PubMed=11182156; DOI=10.1016/S0165-2427(00)00259-2;
RA Wang Z., Petersen K., Weaver M.S., Magnuson N.S.;
RT "cDNA cloning, sequencing and characterization of bovine pim-1."
RL Vet. Immunol. Immunopathol. 78:177-195(2001).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Binds to Rps (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -1- PTM: Autophosphorylated (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC -----
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CC or send an email to license@ebi.ebi.ch).
CC -----
DR EMBL; AF259078; AAF67200.1; -.
DR HSP; Q63450; 1A06.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 38 290 Protein kinase.
FT NP BIND 44 52 ATP (By similarity).
FT BINDING 67 67 ATP (By similarity).
FT ACT_SITE 167 167 Proton acceptor (By similarity).
SQ SEQUENCE 313 AA; 35629 MW; 9EF40229A847AD47 CRC64;

Alignment Scores:
Pred. No.: 4,64e-97 Length: 313
Score: 1630.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 66.72% Indels: 0
DB: Gaps: 0

US-10-705-757-3 (1-1302) x PIM1_BOVIN (1-313)
OY 4 ATGCTCTTTCAGATCACTCCCTGGCCCACTGGCGGAGCCCTTGCACGACCTG 63
DB 1 Metleuenseerlylleasnsertleuhaltsleuarglaalaprocysserapleu 20
OY 64 CAGCCCAACAGCTGGGGCGGGGCAAGAGAGAGCCCTGGAGTGGGAGTACAGATG 123
DB 21 HislaThrlyslleuAlaProGlylyseGluylsleuProleuGluSerGlnlyrGlnVal 40
OY 124 GGCCCGCTGTGGCAGGCGGTGGCTGGCTGACTACGCGGATCCGCGTCCGCGAC 183
DB 41 GlytroleuenglyserGlyGlyPheGlyserValtyrserGlylleargValAlaasp 60

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OY 184 AACTTCGGGTGGCCATCAAGCAGTGGAGAACCCGATTTCCGACTGGGGGAACTG 243
DB 61 AsnleuProValAlaIlelyshlsvalGluylsAspArglliseraptrpGlyGluLeu 80
OY 244 CCCAAGCGCACCCGAGTGGCCATGAGATGGTCTCTGTAAGAAAGGTGAGCTGGCTTC 303
DB 81 ProAsnGlyThrargValProMetGluValIleleuLeuIleuValylserSerGlyPhe 100
OY 304 TCGGGGCTCATTTGACTCTTGACCTGGCTTGGAGAGCCCGCATAGTTTTCGTCGATCTCG 363
DB 101 SerGlyValIleargleuLeuAspTrpPheGluArgProAspserPheValIleuIleu 120
OY 364 GAGAGGCGCGAACCCGNGAAGACTCTTCCACTTCATCAGCAGGAGGAGCCCTCCAG 423
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
OY 424 GAGAGCTGGCCCGGAGCTTCTTCTGGCAGTGTGAGAGCCCGTGGCGCATTTGCCAAC 483
DB 141 GluGluLeuAlaArgserPhePheTrpGlnValIleuGluAlaValArgHisGlySerAsp 160
OY 484 TCGGGGTTCTCCACCGCCGACATCAAGACAGAACATCTTAATGACCTGAAACCGCGCG 543
DB 161 CyGlyValleuHisArgAspIlelyAspGluAsnIleleuIleAspLeuAsnArgGly 180
OY 544 GAACCTAACTCATGACTTCGGGTGGGGGCGCTGCTCAAGGACAGTCTACAGGAC 603
DB 181 GluLeuIleuLeuIleAspPheGlyserGlyAlaLeuLeuIleuAspThrVallyrTrnAsp 200
OY 604 TTTCAGCGAACCCGAGTGTACAGTCTCCAGAGTGTGATTCGATACCATGCTACCAAGCG 663
DB 201 PheAspGlyThrargValtyrserProProGluTrpIleArglyrHisArglyrHisGly 220
OY 664 AGGTGGCTGCTGTGTTGTCCTGGGAGTCTGCTCTAAGACATGGTCTGGCGAGATATT 723
DB 221 ArgSerAlaAlaValIlePserLeuGlyIleLeuLeuTyraAspMetValCyseGlyAspIle 240
OY 724 CCATTTGAGACGACGACGAGATGTCGACGGGCGAGTGTACTTGGCAAGAGGTCTCT 783
DB 241 ProPheGluHisAspGluGluIleValArgGlyGlnValaPhePheArgGlnArgValSer 260
OY 784 TCAGAAATGTCACATCTTATTAGATGATGCTGCTGCTGAGACCATCGAGCCGCTCC 843
DB 261 SerGluGlyserGlnHisleuIleArgTrpCybleuAlaLeuArgProserAspArgProThr 280
OY 844 TTTCAGAAATGTCACATCTTATTAGATGATGCTGCTGCTGAGACCATCGAGCCGCTCC 903
DB 281 PheGluGluIleGlnAsnHisPserTrpMetGlnAspValleuLeuProGlnGlnTrnAla 300
OY 904 GAGATTCATCTGACGAGCCCTGTCACATCAACCCAGCAA 942
DB 301 GluIleHisleuHisSerleuSerProGlyProSerLys 313

RESULT 5
O8CFN8 PRELIMINARY; PRT; 313 AA.
AC O8CFN8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Provitral integration site 1.
GN Name=Pim1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C7BL/6; TISSUE=Brain, and Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaller G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

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RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,
 RA Brownstein M.J., Uedon T.B., Tohyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzyzanski M.I., Skalka U., Smalls D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL, BC042885; AAH42885.1; -.
 DR EMBL, BC053019; AAH53019.1; -.
 DR EMBL, MGI:97584; Piml.
 DR MGI:97584; Piml.
 DR GO: GO:0005524; P:ATP binding; IEA.
 DR GO: GO:0016740; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011009; Kinase_Like.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR InterPro: IPR008271; Ser_Thr_pkinase.
 DR Pfam: PF00069; Pkinase: I.
 DR Pfam: PF00069; Pkinase: I.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KM ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 313 AA; 35451 MW; 1294716A03B7CD7 CRC64;

Alignment Scores:
 Pred. No.: 2,07e-94 Length: 313
 Score: 1589.00 Matches: 296
 Percent Similarity: 97.12% Conservative: 8
 Best Local Similarity: 94.57% Mismatches: 9
 Query Match: 65.04% Indels: 0
 DB: 2 Gaps: 0

US-10-705-757-3 (1-1302) x Q8CFN8 (1-313)

QY 4 ATGCTCTTCCAGATCACTCCCTGCGCCACCTGCGCGAGCCCTTGCACAGACTG 63
 DB 1 MetLeuLeuSerIysIleAsnSerLeuAlaHisLeuAlaIaIaProCyAsnAspLeu 20
 QY 64 CAGCCCAAGAGCTGGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
 DB 21 HIAIAIAIhrySLeuAlaIaProGlyIySgIuIySgIuProLeuGluSerGlnIyrgIuVal 40
 QY 124 GGGCCGCTGTGGGAGCGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 183

DB 41 GIyProLeuLeuGIySerGIyGIyPheGlySerValIyTyrSerGIyIleArgValAlaIaAsp 60
 QY 184 AACCTTGGCGGTCGATCAAGACGATGGAGAGACCGGATTTCCGACTGGGGAGAACTG 243
 DB 61 AAnLeuProValAlaIleIyehIeValGIuIyAspArgIleSerAspTrpGIyGIuIleu 80
 QY 244 CCCAAGCGGACCCGAGTCGCCATGGAAGTGTCTCTGTCGAAGAGAGTGAAGTCTGGAGCTTC 303
 DB 81 ProAnGlyIyThrArgValProMetGIuValIleuLeuIyGIyValSerSerAspPhe 100
 QY 304 TGGGCGCTATTAGACTTCTGAGCTGTTCCAGAGAGCCCGATGATTTGCTGCTGATCTCG 363
 DB 101 SerGIyValIleArgIleuLeuAspTrpPheGIuArgProAspSerPheValIleuIleu 120
 QY 364 GAGAGCCCGGACCCGTCGAAGACCTTCCATTCATCAGAGAGAGAGAGCCCTCCAG 423
 DB 121 GIuArgProGIuProValGIuAspLeuPheAspPheIleThrGIuArgGIyAlaLeuGIu 140
 QY 424 GAGAGCTGGCCGAGCTTCTTGGCAGTGTGTGAGGCCGTCGCGCATTCGACAAAC 483
 DB 141 GIuAspLeuAlaIaArgGIyPhePheTrpGIuValIleuGIuAlaValAlaArgHisCyHisAsn 160
 QY 484 TCGGAGGCTTCTCCACCGGACATCAAGACGAAACATTTATGACTGACCGCGGC 543
 DB 161 CySgIyValIleuIleArgAspIleIyAspGIuAsnIleuIleAspLeuSerArgGIy 180
 QY 544 GAAGTCGAACATGATGAGCTTGGGTCGGGGCGGCTGTCGAAGACAGCTTACACGAGC 603
 DB 181 GIuIleIyLeuIleAspPheGIySerGIyAlaLeuIyIyAspTrpValIyTrpAsp 200
 QY 604 TTTGACGGAACCCGAGTATGACATGCTCCGAGAGTGGATTCGATTCGATTCGATTCGACGAGC 663
 DB 201 PheAspGIyThrArgValIySerProProGIuTrpIleArgTrpHisArgTrpHisGIy 220
 QY 664 AGTGCGCTGCTGTTTGGTCTGCTGGGAGATCTGCTCTATGACATGCTCTGGAGATATT 723
 DB 221 ArgSerAlaIaIaValIyTrpSerIleuGIyIleuLeuIyIyAspMetValCySgIyAspIle 240
 QY 724 CCATTGAGCAGCAGGAGAGATCGTCGAAGGCGCAAGTACTTTAGGCAAGGCTCT 783
 DB 241 ProPheGIuIleAspGIuIleIleIySgIyGIuValPhePheArgGIuIleIyAsp 260
 QY 784 TCAGATGTCACATCTTATAGATGTCCTGTCCTGAGACATTCGAGCCGCGCTTC 843
 DB 261 SerGIuCySgIuIleuIleuIleuIleuIyTrpCyLeuSerLeuArgProSerAspArgProSer 280
 QY 844 TTTGAAGAAATCCAGAACCATCCGTCGATGTCAGATGTTCTCTGCGCCAGCGCCAGCGC 903
 DB 281 PheGIuGIuIleArgAsnIleProTrpMetGIuIyAspLeuProGIuAlaIaSer 300
 QY 904 GAGATTGATCTGACAGCGCTGTCACCATCAGCCAGCAAA 942
 DB 301 GIuIleHisLeuHisSerLeuSerProGIySerSerIyS 313

RESULT 6
 PIM1 MOUSE STANDARD; PRT; 313 AA.
 ID PIM1 MOUSE
 AC P06803;
 DT 01-JAN-1988 (rel. 06, Created)
 DT 01-JAN-1988 (rel. 06, Last sequence update)
 DT 05-JUL-2004 (rel. 44, Last annotation update)
 DE Proto-oncogene serine/threonine-protein kinase Pim-1 (BC 2.7.1.37).
 GN Name=Pim1; Synonyms=Pim-1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
 RA Seiten G., Guybers H.T., Boelens W., Robanus-Maandag E., Versteek J.,
 RA Domen J., van Beveren C., Berns A.;
 RT "The primary structure of the putative oncogene pim-1 shows extensive


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RT  homology with protein kinases."
RL  Cell 46:603-611(1986).
RN  [2]
RP  INTERACTION WITH RP9.
RX  MEDLINE=20389540; Pubmed=10931201;
RA  Maita H., Harada Y., Nagakubo D., Kikaura H., Ikeda M., Tamai K.,
RA  Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
RT  "RAP-1, a novel target protein of phosphorylation by P1m-1 kinase.";
RL  Eur. J. Biochem. 267:5168-5178(2000).
CC  -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC  -1- SUBUNIT: Binds to RP9.
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC  -1- PTM: Autophosphorylated (By similarity).
CC  -1- DISEASE: Frequently activated by provirus insertion in murine
CC  leukemia virus-induced T-cell lymphomas.
CC  -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. P1M
CC  subfamily.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb.ch/announce/
CC  or send an email to license@isb-rib.ch).
CC  -----
DR  EMBL, M13945; AAA39930.1; -.
DR  PIR, A24169; TVMSPL.
DR  HSSP, Q63450; 1A06.
DR  MGD, MG1:97584; P1m1.
DR  InterPro, IPR011009; Kinase like.
DR  InterPro, IPR000719; Prot. kinase.
DR  InterPro, IPR008271; Ser_Ehr_pkin_AS.
DR  Pfam, PF00069; Pkinase; 1.
DR  ProDom, PD000001; Prot. kinase; 1.
DR  PROSITE, PS00107; PROTEIN KINASE ATP; 1.
DR  PROSITE, PS50011; PROTEIN KINASE DOM; 1.
DR  PROSITE, PS00108; PROTEIN KINASE-ST; 1.
KW  ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
KW  Serine/threonine-protein kinase; transferase.
FT  DOMAIN 38 290
FT  NP BIND 44 52
FT  BINDING 67 67
FT  ACT SITE 167 167
FT  ACT SITE 167 167
SQ  SEQUENCE 313 AA; 35536 MW; 79F4779B9DCBDC16 CRC64;

Alignment Scores:
Pred. No.: 4,36e-94
Score: 1584.00
Percent Similarity: 96.81%
Best Local Similarity: 94.25%
Query Match: 64.84%
DB: 1
Length: 313
Matches: 295
Conservative: 8
Mismatch: 10
Indels: 0
Gaps: 0

US-10-705-757-3 (1-1302) x P1M_MOUSE (1-313)
QY 4 ATGCTCTTGTCAAGATCAACTCCCTGCGCCAGCCCTTGCACCACTG 63
DB 1 MetLeuLeuSerLeuYsIleAenSerLeuAlaIleLeuYgIlaIrgProCyAaAaAerLeu 20
QY 64 CAGGCAACAAAGTGGGCGCGGCAAGAGAGAGCGCTGAGTCCGATCCAGAGT 123
DB 21 HlaAlaThrIleuLeuAaProGlyIleGlyIleuLeuIleuSerGlnIleuVal 40
QY 124 GGGCGGCTGTGGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
DB 41 GlyProLeuLeuGlySerGlyIleuPheGlySerValIleSerGlyIleAaGValAlaAaP 60
QY 184 AACTGCGGCTGCGCATCAAGCAAGTGAAGAGAGAGCGGATTTCCGACTGGGGGAACTG 243
DB 61 AaIleuProValAlaIleuYsIleuValGlyIleuAaAaPrgIleSerAerTrpGlyIleu 80
QY 244 CCAAGCGGCAACCGAGTGGCCCATGAAGTGTCTGTGAAGAAAGTGAAGCTGCGGCTTC 303

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DB 81 ProAaGlyThrAaIleuProMetGluValIleuLeuYsIleuValSerSerAaPhe 100
QY 304 TCGGCGCTGATTTGACTTGTGAGCTGTTGAGAGCGCCGAGATGTTTGTGCTGATCTG 363
DB 101 SerGlyValIleIleAaGlyLeuAaPrgTrpPheGluAaPrgProAaSerPheValIleuLeu 120
QY 364 GAGAGCGGCAACCGCTGCAAGACCTCTTGCATTCATCAACGAGAGAGAGCGCTCCG 423
DB 121 GluAaPrgIleuProValGlnAaPheLeuPheAaPheIleThrGluAaGlyAlaLeuGln 140
QY 424 GAGAGCTGCGCGGAGCTTCTTCTGCGAGTCTGAGAGCGCTGCGGCTGCGCAAC 483
DB 141 GluAaPheLeuAaIleAaGlyIlePheTrpGlnValIleuGlnAlaValAaIleuValSer 160
QY 484 TCGGCGGCTTCTGCAACCGCAATCAAGAGAGAGAGAGATTTAATGACCTGAACCGGCG 543
DB 161 CysGlyValIleuIleAaPrgIleuYsAaPrgIleuAaIleuIleuAaPheSerAaGly 180
QY 544 GAGCTCAACCTGATCGACTTGGGCTGGGCGCTGCTGCAAGAGAGAGAGAGAGAGAGAG 603
DB 181 GluIleuYsIleuIleAaPheGlySerGlyAlaLeuLeuYsAaPrgValIleuValAaP 200
QY 604 TTTGAGCAACCGGAGTGAAGTCTTCCAGAGTGAATTCGATCAACCTGCTCAAGCG 663
DB 201 PheAaPrgIleuAaIleuYsAaPrgIleuIleuIleuYsAaPrgIleuIleuYsAaPrg 220
QY 664 AGGTCGCTGCTGTTGCTGCTGCGGAGTCTGCTGATGACATGCTGCGGAGATTT 723
DB 221 ArgSerAlaIleuValIleuPheLeuGlyIleuLeuYsAaPheValCysGlyAaPhe 240
QY 724 CCAATTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 783
DB 241 ProPheGlyIleuAaPrgIleuIleuIleuYsGlyIleuAaPheAaPrgIleuValSer 260
QY 784 TCAGATGTCACATCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
DB 261 SerGluCysGlnIleuIleuIleuIleuYsTrpCysLeuSerLeuAaPrgProSerAaPrg 280
QY 844 TTTGAGCAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 903
DB 281 PheGluGluIleuIleuYsAaPrgIleuIleuIleuYsAaPrgIleuIleuIleuAaSer 300
QY 904 GAGATTCATCTGCAAGCTGCTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCT 942
DB 301 GluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 313

RESULT 7
P1M3_COTUA STANDARD; PRT; 323 AA.
AC Q9P085;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
GN Serine/threonine-protein kinase P1m-3 (Ec 2.7.1.37) (p1m).
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OC NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20180111; Pubmed=10713710; DOI=10.1038/sj.onc.1203355;
RA Bichmann A., Yuan L., Breant C., Alitalo K., Koskinnen P.J.;
RT "Developmental expression of P1m kinases suggests functions also
RT outside of the hematopoietic system.";
RL Oncogene 19:1215-1224(2000).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- PTM: Autophosphorylated.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. P1M
CC subfamily.

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CC or send an email to license@sb-sib.ch).

DR EMBL; AJ130845; CAB62386.1; -
DR HSSP; Q63450; 1A06
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferrase.
FT DOMAIN 40 291 Protein kinase.
FT NP_BIND 46 54 ATP (By similarity).
FT BINDING 69 69 ATP (By similarity).
FT ACT_SITE 168 168 Proton acceptor (By similarity).
SQ SEQUENCE 323 AA; 36597 MW; E2A4FA20B6F6396C CRC64;

Alignment Scores:
Pred. No.: 2,18e-65 Length: 323
Score: 1140.00 Matches: 216
Percent Similarity: 78.48% Conservative: 43
Best local Similarity: 65.45% Mismatches: 61
Query Match: 46.66% Indels: 10
DB: 1 Gaps: 5

US-10-705-757-3 (1-1302) x PIM3_COTUA (1-323)

QY 4 ATGCTCTGTGCAAGATCACTCCCTGGCCACCTG---CGCGACGCCCTTGACAGAC 60
DB 1 MetLeuLeuSerYsbhegLySerLeuAlaHisIleCySerProAlaSerMetAcPHis 20
QY 61 CTGACAGCCCAACGATGCGCGGCAAA---GAGAAAGAGCCCTGTGAGTCAGTAC 117
DB 21 LeuProValylrIleuProProValylValGluIleuIleuProheaspLyValTyr 40
QY 118 CAGGTGGCCCGCTGTGGGACAGCGGTGCTGTGCTGCTACTCGGACATCCGCGTC 177
DB 41 GlnValGlySerValIleuGlySerGlyGlyPheGlyThrValTyrIleGlySerArgThr 60
QY 178 GCGCAACAATTGCGCGGTGCGATCAAGACGTGAGAAAGACCGGATTCGCACTG 237
DB 61 AlaAspGlyLeuProValAlaValAlaValValValValValValValValValValVal 80
QY 238 GAATGCCCAACGACCGGACCGGATGCGGATGCTGTGCTGTGAGAAAGTGAAGCTG 297
DB 81 ThrIle---GlyGlyValMetValProIleuGluIleValIleuLeuLysValGlySer 99
QY 298 GGGTCTTCGGGCGCTATTAGACTTGTGACTGTGTGAGAGGCCGATAGTTTCGTCG 357
DB 100 GlyPheArgGlyValIleIleLysLeuLeuAspTrpIleuArgProAspGlyPheLeuIle 119
QY 358 ATCTGTGAGAGGCGCGCAACCGTGCAAGACTCTTGCACTTCAACCGGACGAGAGCC 417
DB 120 ValMetGluArgProGluLeuValLysAspLeuPheAspPheIleThrGluLysGlyAla 139
QY 418 CTCAGAGAGAGCTGCGCGAGACTTCTTGTGACAGGTGTGAGAGCGCGTGCAGATTGC 477
DB 140 LeuAspGluAspGlnAlaArgGlyPhePheArgGlnValLeuGluAlaValAlaGlnIle 159
QY 478 CACAACTGCGGGGTTCTCCACCGGACATCAAGAGCAAGAACTTTAATGACTGAAC 537
DB 160 TyrGlyCyseGlyValValHisArgAspIleLysAspIleuAsnLeuValAspLeuArg 179

QY 538 CGCGGCAACTCAACTATCATGACTTGGGGTGGGGCGCTGCTCAAGACACAGTCTAC 597
DB 180 ThrGlyIleuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyr 199
QY 598 ACGAATTGACGGAACCGGACGTGACATGCTCCAGAGTGGATTGCTTACATCGCTAC 657
DB 200 ThrAspPheAspGlyThrArgValTyrSerProProGluTrpIleArgTrHisArgTyr 219
QY 658 CACGACAGGTGGCGCTGTTGTGCTGGGGGATCGCTGATGACATGCTGCGGCA 717
DB 220 HisGlyArgSerAlaThrValTyrSerLeuGlyValLeuLysTyrAspMetValCyseGly 239
QY 718 GATATTCATTTGACACGACGACGAGAGATTCGTCAAGGGCGGACGTACTTATGAGCAAG 777
DB 240 AspIleProPheGluGlnIleAspGluIleLeuArgGlyArgLeuTyrPheArgArgArg 259
QY 778 GTCTCTTCAAGATGTCACATTTATAGATGTCCTGTGCTGACACCATCGACCGG 837
DB 260 IleSerProGluCyseGlnGlnIleuLysTrpCyseLysSerLeuArgProSerArgArg 279
QY 838 CCTCCTTTGAGAAATCCAGAACATCGCTGGATG---CAGGATGTTCTCGTGGCCGAC 894
DB 280 ProThrLeuGluGlnIlePheAspHisGlnTrpMetHisLysSerGluValValLysSer 299
QY 895 GCGACCGCGGACATTCATGTGCAAGCGCTGTGACCATCACCCAGAAATAGACGCAATTC 954
DB 300 GluAspCyseAspIleArgLeuArgThrLeuAspThrAspValSer----- 314
QY 955 TGTCAAGACCTTCAGGAGAGAGAGACTTG 984
DB 315 ---SerThrSerSerArgAsnIleuSer 323

RESULT 8
PIM3_HUMAN STRAND; PRT; 326 AA.
ID PIM3_HUMAN STANDARD; PRT; 326 AA.
AC Q86V86;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN Name=PIM3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schlier G.D.,
Altekar S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Caavaant T.L., Scheetz T.E.,
Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Villarion D.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
Richardson D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
Rachner A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP IDENTIFICATION FROM ESTS.
RX MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6;

RA Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.;
 "Consistency checks for characterizing protein forms";
 RL Comput. Biol. Chem. 27:29-35(2003).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
 subfamily.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL: BC052339; AHS2239.1; ALT_INIT.
 DR InterPro: IPR011009; Kinase like.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_A5.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
 KW Transferrase.
 KM DOMAIN 40 293 Protein kinase.
 FT NP_BIND 46 54 ATP (By similarity).
 FT BINDING 69 69 ATP (By similarity).
 FT ACT_SITE 170 170 Proton acceptor (By similarity).
 SQ SEQUENCE 326 AA; 35863 MW; 41FDF9DD2467A162 CRC64;

Alignment Scores:
 Pred. No.: 3,67e-65 Length: 326
 Score: 1136.50 Matches: 224
 Percent Similarity: 77.25% Conservative: 34
 Best Local Similarity: 67.07% Mismatches: 61
 Query Match: 46.52% Indels: 15
 DB: 1 Gaps: 8

US-10-705-757-3 (1-1302) x PIM3_HUMAN (1-326)

QY 4 ATGCTCTTTCGAAGTCAACTCCCTGGCCGCGAGCCCT-----TGCAAC 57
 |||||
 DB 1 MetLeuLeuSerIysPheGlySerIleAlaHisLeu---CysGlyProGlyGlyValAsp 19
 |||||
 QY 58 GACCTGCACCGCAACAAGCTGGCGCGCGGCAAA---GAGAAGAGCCCTCGAGTCGCG 114
 |||||
 DB 20 HisLeuProValIysIleLeuGlnProAlaIleAlaAspIysSerIleValAla 39
 |||||
 QY 115 TACCAAGTGGGCGCGCTTGGGAGGCGTGGCTTGGCTTACTCGGCGATCCGC 174
 |||||
 DB 40 TyGlnValAlaGlyAlaValLeuGlySerGlyGlyPheGlyThrValTyralaGlySerArg 59
 |||||
 QY 175 GTGCGCAACAATTGCGCGTGCATCAACAGCTGGAGAAGAGCCGATTCGACATG 234
 |||||
 DB 60 IleAlaAspGlyLeuProValAlaValIysHisValValIysGluValIleGluTyr 79
 |||||
 QY 235 GGGGAAGTGGCAACGCGACCCGATGCCATGAGTGTCTCTGTGAAGAAGTGT--- 291
 |||||
 DB 80 GlySerLeu---GlyGlyAlaThrValProLeuGlnValValLeuLeuArgIysValGly 98
 |||||
 QY 292 ---AGTCGGGGCTTCTCGGCGCTTACATTAAGCTTGTGACGTGTTCGAGAGCCGATG 348
 |||||
 DB 99 AlaAlaGlyGlyAlaValIleArgIysValIleArgLeuLeuAspIlePheGluArgProAspGly 118
 |||||
 QY 349 TTCGTGCTGCTCCGAGAGAGCCGCAACCGCTGCAAGAGCTCTTCGACTTCATCAACGAG 408
 |||||
 DB 119 PheLeuLeuValIleGluIleArgProGluProAlaGlnAspLeuPheIleTyrGln 138
 |||||
 QY 409 CGAAGAGCCCTCGAGAGAGAGTGGCCGCGAGCTTCTTCGAGAGGTGTGAGAGCCG 468
 |||||
 DB 139 ArgGlyAlaLeuLeuAspGluProLeuAlaArgIlePhePheAlaGlnValLeuAlaVal 158

QY 469 CGGATTCGCAACAATCGCGGGTTCCTCCACCGGACATCAAGAGCAGAACTTTATC 528
 |||||
 DB 159 ArgHisCysHisSerCysGlyValValHisAspIleIysAspGluAlaLeuVal 178
 |||||
 QY 529 GACCTGAACCGCGCGCAACTCAAACTCATGACTTCGCGTGGCGCGCTCAAGAC 588
 |||||
 DB 179 AspLeuArgSerGlyGlyIleuLeuIleAspPheGlySerGlyAlaLeuLeuAsp 198
 |||||
 QY 589 ACGTGTACACGGAATTTAGACGAAACCCGAGGTATACGTCTTCAGAGTGGATTCG 648
 |||||
 DB 199 ThrValTyThrAspPheAspGlyThrArgValTySerProGluTyr 218
 |||||
 QY 649 CATCGTACACGAGCGAGTGGTGGCTGCTTCCTCGGAGTCCGCTTATGACATG 708
 |||||
 DB 219 HisArgTyHisIleGlyIleAspSerAlaThrValTyrSerLeuIleValLeuLeuTyAspMet 238
 |||||
 QY 709 GTCTGCGAGATATTCATTTAGACAGCAGAAAGATGTCGAAGGCGCAAGTACTTT 768
 |||||
 DB 239 ValCysGlyIAspIleProPheGluGlnAspGluGlnIleuArgGlyArgLeuLeuPhe 258
 |||||
 QY 769 AGCGAAAGGTCCTTCAGAAATGTCACATTTATTAAGATGTGCTGCTCGAGACCA 828
 |||||
 DB 259 ArgArgArgValSerProGluCysGlnGlnLeuIleArgTyrCysLeuSerLeuArgPro 278
 |||||
 QY 829 TCGGACCGCGCTTCCTTGAAGAAATCCAGAACATCCCGGATG-----CAGATGTT 882
 |||||
 DB 279 SerGluArgProSerLeuLeuGlnIleAlaHisProTyrPheLeuGlyAlaAspGly 298
 |||||
 QY 883 CTCCTGCCCCAGGCGCACCGCGGATTCATCTGCACAGCCTGCATCAACCCAGCAAA 942
 |||||
 DB 299 GlyAlaProGlu---SerCysAspLeuArgLeuCysThrLeuAspPro----- 313
 |||||

QY 943 TAGCAGCCATTTCTGTCAACCTTCAGGGAAGAGAGACTTG 984
 |||||
 DB 314 ---AspAspValAlaSerThrThrSerSerSerGluSerLeu 326
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RESULT 9
 PIM3_MOUSE
 ID PIM3_MOUSE STANDARD; PRT; 326 AA.
 AC P58750;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
 GN Name=Pim3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon, and Salivary gland;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marcusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Umed T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S., Schen J.E., Krzywinski M.I., Skalska U., Smalios D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.1sb-sib.ch/announce/
CC or send an email to license@1sb-sib.ch).
CC -----
DR EMBL; BC017621; AAH17621.1; -.
DR EMBL; BC026639; AAH26639.1; -.
DR HSSP; Q03656; 1HOW.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferrase.
FT DOMAIN 40 293 Protein kinase.
FT NE_BIND 46 54 ATP (By similarity).
FT BINDING 69 69 ATP (By similarity).
FT ACT_SITE 170 170 Proton acceptor (By similarity).
SQ SEQUENCE 326 AA; 35970 MW; DD68CBF6354851B CRC64;

Alignment Scores:
Pred. No.: 6.66e-65 Length: 326
Score: 1132.50 Matches: 214
Percent Similarity: 82.71% Conservative: 30
Best Local Similarity: 72.54% Mismatch: 44
Query Match: 46.36% Indels: 7
DB: 1 Gaps: 5

US-10-705-757-3 (1-1302) x PIM3_MOUSE (1-326)
QY 4 ATGCTCTTTCGAAGTCAACTCCCTGGCCCACTGGCGCAGCCCT-----TGCAC 57
DB 1 MetLeuSerSerIysPheGlySerLeuAlaHisLeu---CysGlyProGlyIyValaIap 19
QY 58 GACCTGCACCGCAACAAGCTGCGCGCGGCAAA---GAGAAGAGCCCTTGAGTGCAG 114
DB 20 HisLeuProValIySerIleLeuGlnProAlaIyAlaIapIySgluSerPheGlyIyVal 39
QY 115 TACCAAGTGGGCGCGCTGTTGGGCAAGGCTTGGCTCGGCTCTAATCGGGCATCCGC 174
DB 40 TyGlnValIyGlyAlaValIeugIySerGlyIyPheGlyThrValIyTalaGlySerAgy 59
QY 175 GTGCGCAACAAGTTCGGCGGCGCATCAACAAGCTGGAAGAAGACCGGATTCGACATG 234
DB 60 IleAlaIapIyLeuProValIaIaValIyHisIleValIyValIyGluIyValIyTrnGluTrp 79
QY 235 GGGGAAGTGGCCCAAGCCGACCCAGTGCATGAGTGGTCTGCTGTAAGAAGATG--- 291
DB 80 GlySerLeu---GlyGlyValIaIaValIyProLeuGlnValIyLeuAlaGlyIyValGly 98
QY 292 ---AGCTGGGCTTCTTCGGCGCTGATTGAATTTCTGACTGTGTTGAGAGCCCGATAGT 348
DB 99 AlaAlaGlyIyGlyAlaIyValIyIleArgLeuLeuSerPheGlyIyValIyProAgyIy 118
QY 349 TTGCTGTGATCTCTGGAAGAGCCCGAACCCTGGAAGAAGCTTTCGACTTCAATCAGAG 408
DB 119 PheLeuLeuValIeugIyValIyGlyProGluProAlaGlnAapIyPheAapPheIleTrnGln 138
QY 409 CGAGAGCCCTCCAGAGAGAGTGGCCCGGAGCTTCTTTCGAGAGGTGCTGAGAGCCGNTG 468

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DB 139 ArgGlyAlaLeuAapIyIyProLeuAlaIyArgAapPheAlaGlnValIeulAlaIaVal 158
QY 469 CGGCAATTCGCAACAATGGGGGTTCCTCCACCGCGCATCAAGAGAGCAATCTTAATC 528
DB 159 ArgHisCyHisAapIySerIyValIyAlaIyAapIyIyLeuAapIyIyIyIyIyIyIyIy 178
QY 529 GACCTGAACCGCGGCAACTCAACTCATGCACTTCGAGTGGCGGCGCTGCTCAAGAC 588
DB 179 AapIyAapIySerGlyIyGlnIyLeuIyLeuIyAapPheGlySerGlyAlaIyValIyIyAap 198
QY 589 AAGCTTCAACGCAATTTGACGGAACCGGATGTACAGTCTTCAGAGTGAATTCGCTAC 648
DB 199 ThrValIyThrAapPheAapIyIyThrArgValIyIySerProGluTrpIleArgIy 218
QY 649 CATTCGCTACCAAGGAGGCTGCTGCTGTTGCTCCCTGGGAGTCCGCTCATATGACAG 708
DB 219 HisArgIyIyHisGlyIyArgSerAlaThrValIyIyIyIyIyIyIyIyIyIyIyIyIy 238
QY 709 GTCTCGAGATATTCATTTGAGACAGACGAAGAAGATGCTCAAGGCGCAAGTACTTT 768
DB 239 ValIyGlyIyAapIyIyProPheGlnIyAapIyIyGlnIyIyLeuArgIyIyArgLeuPhe 258
QY 769 AGGCAAGGGTCTTTCAGATGCAATCTTAATGATGTCCTGCTGACAGCA 828
DB 259 ArgArgValIySerProGluIyGlnIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 278
QY 829 TCGACCGGCGCTCTTGAAGAATCCAGAACCATCGTGATG 873
DB 279 SerGluArgProSerLeuAapIyIyIyAlaIyAapIyIyIyIyIyIyIyIyIyIyIyIy 293

RESULT 10
PIM3 RAT STANDARD; PRT; 326 AA.
ID PIM3 RAT
AC 070464;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Protein kinase
DE Kld-1) (Kinase induced by depolarization).
GN Name=Pim3; Synonyms=Kld1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Konietzko U., Kuhl D.;
RT "Pim-3 is a member of the pim kinase family.";
RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=98298176; PubMed=9632723; DOI=10.1074/jbc.273.26.16535;
RA Feldman J.D., Vician L., Crispino M., Tocco G., Marcheselli V.L.,
RA Bazan N.G., Baudry M., Herschman H.R.;
RT "Kld-1, a protein kinase induced by depolarization in brain.";
RL J. Biol. Chem. 273:16535-16543(1998).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- TISSUE SPECIFICITY: Present in a number of unstimulated tissues,
CC including brain.
CC -1- INDUCTION: By membrane depolarization or forskolin.
CC -1- PTM: Autophosphorylated.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@1sb-sib.ch).

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CC -----
DR EMBL; AF086624; AAC68900.1; ALT_INIT.
DR EMBL; AF087026; AAC66065.1; -.
DR HSP; Q03656; HKM.
DR RGD; 620462; Pim3.
DR InterPro; IPR011009; Kinase_1like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferrase.
FT DOMAIN 40 293 Protein kinase.
FT NE_BIND 46 54 ATP (By similarity).
FT BINDING 69 69 ATP (By similarity).
FT ACT_SITE 170 170 Proton acceptor (By similarity).
SQ SEQUENCE 326 AA; 36002 MW; DD6C9BF4635F851E CRC64;

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Alignment Scores:
Pred. No.: 7,73e-65 Length: 326
Score: 1131.50 Matches: 214
Percent Similarity: 82.71% Conservative: 30
Best Local Similarity: 72.54% Mismatches: 44
Query Match: 46.32% Indels: 7
DB: Gaps: 5

US-10-705-757-3 (1-1302) x PIM3_RAT (1-326)

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QY 4 ATGCTCTTGTCCAAAGTCAATCCCTGCGCCAGCCCT-----TGCAC 57
DB 1 MetLeuLeuSerIySerPheGlySerLeuAlaHisLeu---CyGdlProGlyGlyValAsp 19
QY 58 GACCTGCACGCGCAACAAAGCTGGCGCGGCGAA---GAGAAGAGCCCTGGAGTGGCAG 114
DB 20 HisLeuProValIyIleLeuGlnProAlaLysValAspIySerPheGlyVal 39
QY 115 TACAGAGTGGCGCCGCTGTGTGGCAGCGGTGGCTTGGCTGCTGATCCGATCCGC 174
DB 40 TyGlnValGlyValLeuGlySerGlyGlyPheGlyThrValIyTralAsgIySerHis 59
QY 175 GTCCGCGCAACTTGGCGGTGGCTGATCAAGACAGTGGAGAAGACCGGATTTCCGATGG 224
DB 60 IleAlaAspGlyLeuProValAlaValIyHisValIyValIyGlyValIyThrGlyTyr 79
QY 235 GGGGAAGTCCGCAACGCGCCAGTCCATGGAAGTGTCTGCTGAAAGAGTG--- 291
DB 80 GlySerLeu---GlyIyMetAlaValProLeuGlnValIyValLeuIyAsgIyValGly 98
QY 292 ---AGCTCGGAGCTTCTCGGCGTCAATTAAGCTTGTGAGTGTGGTTCGAGAGCCGATAGT 348
DB 99 AlaAlaGlyGlyAlaArgIyValIleAsgIyValIleAsgIyLeuAspIyTrpPheGlyIyAspIy 118
QY 349 TTCGTCTGATCTCTGAGAGAGCCGCAACCCGTCGAAGACTTCTGATTCATCAGCAG 408
DB 119 PheLeuLeuValIleuGlnArgProGlnProAlaGlnAspLeuPheAspIleThrGln 138
QY 409 CGAGAGAGCCCTCCAGAGAGAGCTGGCCCGGAGCTTCTTCTGCGAGGTGCGAGGCCGCG 468
DB 139 ArgGlyAlaLeuAspIyProLeuAlaAsgIyPheAspIyAspIyValIleValIleAlaVal 158
QY 469 CGGCAATTCGCAACAGTGGGGTCTTCACCGGAGATCAAGAGAGCAATCATTTAATC 528
DB 159 ArgHisGlyHisIleAspIySerGlyValIleHisArgAspIyIleAspIyAspIyValIle 178
QY 529 GACCTGCACGCGCAACAAAGCTGATCAATGACTTGGGCTGGGGCGCTGCTCAAGAC 588
DB 179 AspLeuAspIySerGlyIyLeuIyValIleAspIySerGlyIyAlaValIleValIyAsp 198

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QY 589 ACAGTCAACGAGCTTTGACGAGACCCGAGTGTATGATGCTCCAGAGTGTATCGCTAC 648
DB 199 ThrValIyThrAspPheAspIyThrArgValIySerProGlnIyTrpIleAsgIyTr 218
QY 649 CATCGCTACCAACGAGAGTCTGGCTGTGGTTCCTGGGAGATCTGCTATGACATG 708
DB 219 HisArgTyHisIleGlyIyArgSerAlaThrValIyTrpSerLeuGlyValLeuIyTralAsp 238
QY 709 GTCTGGGAGATATTCATTTTGACACAGCAAGAGATGTCACAGGCCCAAGTACTTT 768
DB 239 ValCyGlyAspIyIleProPheGlnIyAspIyGlnIyIleValIyGlyIyAspIyPhe 258
QY 769 AGGCAAGGCTCTTCCAGATGTCAACATCTTATTAAGATGAGTGGCTGCTGAGACCA 828
DB 259 ArgArgArgValSerProGlnIyGlnIyGlnIyIleValIyGlnIyTrpCyLeuSerLeuAsp 278
QY 829 TCGAGCGGCGCTCTTGAAGAAATCCAGAACATCCGTGATG 873
DB 279 SerGlnArgProSerLeuAspIyGlnIleAlaHisProIyTrpMet 293

RESULT 11
ID 0811X8 PRELIMINARY; PRT; 325 AA.
AC 0811X8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KID1.
GN Name=Pim3; Synonyms=Kidl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu L.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY026239; AKL1606.1; -.
DR HSP; Q03656; IQ99.
DR MGD; MGI:1355297; Pim3.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:transferrase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_1like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferrase.
SQ SEQUENCE 325 AA; 35931 MW; 77DBF8B20F41B3F4 CRC64;

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Alignment Scores:
Pred. No.: 4.96e-64 Length: 325
Score: 1119.00 Matches: 213
Percent Similarity: 82.71% Conservative: 31
Best Local Similarity: 72.20% Mismatches: 43
Query Match: 45.80% Indels: 8
DB: Gaps: 6

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US-10-705-757-3 (1-1302) x 0811X8 (1-325)
QY 4 ATGCTCTTGTCCAAAGTCAATCCCTGCGCCAGCCCT-----TGCAC 57
DB 1 MetLeuLeuSerIySerPheGlySerLeuAlaHisLeu---CyGdlProGlyGlyValAsp 19
QY 58 GACCTGCACGCGCAACAAAGCTGGCGCGGCGAA---GAGAAGAGCCCTGGAGTGGCAG 114
DB 20 HisLeuProValIyIleLeuGlnProAlaLysValAspIySerPheGlyVal 39

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Qy	113	TACAGGTGGGGCCCGGCTTTGGGACGGGTGGCTTCGGTGGCTACTCGGAGATCGC	174
Db	40	TTyElmaIdIyAlaValLeuGIySerGIyGIyPheGIyThnValYAlaGIySerGIy	59
Qy	175	GTGGCCGCAACATTGGCCGGTGGCCCAACAGCATGTGGAGAAAGACCGGATTTCCGACTGG	234
Db	60	IlleIlaSerpIyLeuPProValAlaValGhIleValValValyGIuArGIyValThnGIuTrp	79
Qy	235	GGGGAATTGGCCCAACGGCACCCGAGTGGCCCATGGAAGTGTCTCTGTGAAGAAGTG---	231
Db	80	GIySerIeu---GIyGIyValAlaValProIeuGIuValValIleuIleaArGIyValGIy	98
Qy	292	---AGCTCGGGCTTTCTCGGGCGTCAATTGAACTTTCGACTGGTTGAGAGGCCCGGATAGT	348
Db	99	AlAlaIdIyGIyAlaArGIyValIleIhIyGleuIleaSerTrpPheGIuArGIyProIaSerGIy	118
Qy	349	TTTCGTCTGATCTCTGGAGAAGCCCGGACCCGTGCAAGACTTCTTGACTTCATGACCGAG	408
Db	119	PheIleuValIleuGIuArGIyProGIuProAlaGIuArPheArPheIleThnGIu	138
Qy	409	CGAGGAGCCCTCCAGAGGAGCTGGCCCGGAGCTTCTTGGCAGGTCTGGAAGCCGTG	468
Db	139	ArGIyAlaIleuIleaSerGIuProIleuAlaAGyArPhePheAlaGIuValIleuAlaIaVal	158
Qy	469	CGGCAATTGGCCCAACCTGGGGGTTCTCCACCGGCAATCAAGAGACGAACAACTTATATC	528
Db	159	ArGIhIeCyhIaSerhIeArGIyValIaIhIaGIhArPheIleIyIaSerGIuArhIeIuVal	178
Qy	529	GACCTGAAACCGCGCGGAATCAAACTCATGACTTCGGGTGGGGCGCTCTCAAGAC	588
Db	179	ArpIeuArGIerGIyGIuIleuIyIleuIleArPheGIySerGIyAlaValIleuIyArp	198
Qy	589	ACAGTCTACACCGCACTTTGACCGGAACCGGAGTGTACAGTCTCCGAGATGGATTCGCTAC	648
Db	199	ThrValIyThrIaSerPheArPheGIyThrArGIyValIySerProGIuTrpIleArGIyTr	218
Qy	649	CATGCTACACACGAGAGTGGGTGGTGGTGGTCCCTGGGGATCTCTCATGACATG	708
Db	219	HIaArGIyThrIaSerGIyArGIySerAlaIaThrValITrpSerIleuGIyValIleuIyThrArp	238
Qy	709	GTCTGCGAGATATTCATTTTGAGCAGCAGAAAGATGTGCMAAGCGGACGAGTACTTT	768
Db	239	ValGIySerGIyArPheIleProPheGIuGIuArGIuIleuArGIyGIyArGIyIleuPhe	258
Qy	769	AGGGAAGGGTCTCTTCAGAATGTCAACATCTTATTAAGTGTGGCTCTCCCTGAGACA	828
Db	259	ArGIyArGIyArGIyIleArPheProGIuCyGIuGIuIleuIleGIuTrpCyIleuSerIleuArGIyPro	278
Qy	829	TCCGACCGGCGCTCTTTTGAAGAAATCCAGAAACCAATCCGATGATG 873	
Db	279	SerGIuArGIyProSerIleuArGIyIleu---CyGIhArPheTrpIleArp 252	
RESULT 12			
ID	066111	PRELIMINARY;	PRT; 318 AA.
AC	066111;		
DT	25-OCT-2004 (TREMBLrel. 28, Created)		
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)		
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)		
DE	Hypothenical protein.		
OS	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoes; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8364;		
RA	NCBI (1)		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Embryo;		
EX	PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow R.H., Scheffer C.F., Bat N.K.,		

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marinova K., Farmer A.A., Rubin G.M., Hong L.,
RA Stagleben M., Soares M.B., Bonaldi M.F., Casavante T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rahn S.S., Lougalan N.A., Peters G.J., Abramson R.D., Mallaby S.J.,
RA Boase S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahley J., Helton E., Kettelman M., Madan A.C., Rodtchenko Y., Boufield G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISUB=Embryo;
RA Klein S., Gerhard D.S.,
RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC081340; AAH81340.1;
DR InterPro: IPR011009; Kinase_1ike.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR Prodom: PD000001; Prot_Kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein.
SQ SEQUENCE 318 AA; 36547 MW; 48CFCF12797F01FDC CRC64;

Alignment Scores:
Pred. No.: 1.75e-63 Length: 318
Score: 1110.50 Matches: 205
Percent Similarity: 82.21% Conservative: 40
Best Local Similarity: 68.75% Mismatches: 44
Query Match: 45.46% Indels: 9
DB: 2 Gaps: 4

US-10-705-757-3 (1-1302) x Q66111 (1-318)

QY 10 TTGTTCAGAGATCAACTCCCTGCGCCACCTCGCGCGAGCCCTTGCAACAGCACTGCAGCGC 69
DB 1 MetSerSerValGlnValIleTyrThrGlnIys-----IleHisAntyThrIleu 17
QY 70 AACCAAGCTGGCGCGCGGCAAGAG-----AAGAGAGCCCTGGAGTGGCACTAC 117
DB 18 AenSerValIlePheProLysAphSerPheProAlaValLysGlnProPheIleuencyTyr 37
QY 118 CAGGTGGCGCGCGCTTTGGTGGCGCGCGCTTGGCTTGGCTTACTCGGAGCACTCGCGCT 177
DB 38 GlnValGlyProValIleGlyThrGlyGlyPheGlyThrValTyrSerGlyValAlaGile 57
QY 178 GCCGCAAACTGGCGCGTGGCCATCAAGCACTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 237
DB 58 SerAapLysLeuProValAlaIleLysHisValSerAArgAAspArgIleGlyIleuetyls 77
QY 238 GAACAGCCCAACCGGAGCCGAGTGGCCATGAGAGAGTGCCTCTGAGAGAGAGAGAGAGAGCTG 297
DB 78 HisMet-----AsnGlyThrLeuValProLeuGlnIleTyrLeuLeuLysValSerAen 96
QY 298 GAGCTTCGCGCGCGCATTAAGACTTGTGAGCTGGTTCGAGAGAGCCGATAGTTCGTCGT 357
DB 97 GlyCysArgGlyValIleArgIleuLeuAspTyrGlyIuArgProAspGlyPheIleIle 116
QY 358 ATCCGAGAGAGCGCCGAAACCGGTGCAAGACTCTTGCATTCATCAACGAGCAGAGAGCC 417

Db 117 ILeMeGcLuhgrProgluProValGlnaBrleuPhearsPheIlethrtGluArgGlyAla 1366
|||:::|||||
Qy 418 CTCGAGAGAGAGCTGGCCCGGACCTTTCTTGCGAGGTGTGGAGGCCGTGGCATTCG 4777
|||:::|||||
Db 137 LeuGlGluGluLeuAlaThrAnaPheArgGlnValAlaGluAlaValArgHisCys 1566
|||:::|||||
Qy 478 CAACTGGGGGGTTCTCCACCCCGGACATCAAGAGACGAAACATCTTAATTCAGCTAAC 5377
|||:::|||||
Db 157 HisSerCysaBrAlaValHisArgaBrIleLysaBrIleuAnIleuValaAerleuArg 1766
|||:::|||||
Qy 538 CGCGGCGAACTCAATCATCATGCACTTCGGGTCGGGGCGCTGTGCAGAGACAGCTTAC 5977
|||:::|||||
Db 177 ThrAlaGluLeuLysLeuIleAspPheGlySerCylAlaLeuLeuArgaBrAlaValIlyr 1966
|||:::|||||
Qy 598 ACGGACTTTGACGGAAACCGGAGTGTAAGTCTTCAGAGTGAGATTGGTACCATCGCTAC 6577
|||:::|||||
Db 197 ThrAspPheAspIlyThrArgValIlySerProProGluIlyrIleArgPheHisLysIyr 2166
|||:::|||||
Qy 658 CACGGGAGGTCCGGCTGCTGTGTGGTCCCGGGGATCCTGTCTATGACATGAGTCTGGGA 7177
|||:::|||||
Db 217 HisGlyArgSerAlaThrValIlyrSerLeuGlyIleLeuLeuLysaPheMetValCysGly 2366
|||:::|||||
Qy 718 GATATTCGATTTGAGCAGCAGCAAGAGATGCTCAAGGGCCAAAGTGATCTTTAGGCAAAAG 7777
|||:::|||||
Db 237 AspIleProPheGluHisAspAspGluIleLeuLysGlyLysIleGlnIlyrArgCysArg 2566
|||:::|||||
Qy 778 GTCTCTTCAGAAATGCACACATCTTAATTAAGATGGTCCCTGTCCGTGAGACCATGGACCCGG 8377
|||:::|||||
Db 257 ValSerArgIlyCysGlnHisLysLeuIleGluIlyrCysLeuSerLysArgProSerAspArg 2766
|||:::|||||
Qy 838 CCCTCTTTAGAAATCCGAAACCATCGGTGATG---CAGAGTGTTCCTCG 888
|||:::|||||
Db 277 ProSerLeuGluGlnIleLeuAlaHisProIlyrPheSerGlnAspAnPheLeu 294
|||:::|||||

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DR  EMBL, L29495; AAA85389.1; .
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CC  the European Bioinformatics Institute.
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  -----
CC  -1- CAUTION: Was originally (Ref.1) called Pim-1 but seems to
CC      represent the pim-3 isoform.
CC
CC  -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC      subfamily.
CC
CC  -1- PIM: Autophosphorylated.
CC
CC  -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC
CC  J. Biol. Chem. 272:10514-10521(1997) .
CC  Pim-1 proto-oncogene-encoded protein kinase." ;
CC  RA  Aeberhold R., Pelech S.L.;
CC  RA  Palaty G.K., Kalmat G., Tai G., Oh S., Amakawa L., Atfoltter M.,
CC  RX  MEDLINE=97256766; PubMed=9099665; DOI=10.1074/jbc.272.16.10514;
CC  OX  NCBI_TaxId=83355;
CC  OX  (1)
CC  SEQUENCE FROM N.A., AND PHOSPHORYLATION SITES.
CC  RP  MEDLINE=97256766; PubMed=9099665; DOI=10.1074/jbc.272.16.10514;
CC  RA  Palaty G.K., Kalmat G., Tai G., Oh S., Amakawa L., Atfoltter M.,
CC  RT  "Identification of the autophosphorylation sites of the Xenopus laevis
CC  RL  Pim-1 proto-oncogene-encoded protein kinase." ;
CC
CC  J. Biol. Chem. 272:10514-10521(1997) .
CC
CC  -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC
CC  -1- PIM: Autophosphorylated.
CC
CC  -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC      subfamily.
CC
CC  -1- CAUTION: Was originally (Ref.1) called Pim-1 but seems to
CC      represent the pim-3 isoform.
CC
CC  -----
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CC  or send an email to license@lsb-sb.ch .
CC
CC
CC  EMBL, L29495; AAA85389.1; .

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DR		InterPro: IPR01009; Kinase-like.
DR	InterPro: IPR00719; Prot_Kinase.	
DR	InterPro: IPR008271; Ser_cmr_pkin_AS.	
DR	Pfam: PF00069; Pkinase; 1.	
DR	ProDom: PD000001; Prot_kinase; 1.	
DR	PROSITE: PS00107; PROTEIN_KINASE_APP; FALSE_NEG.	
DR	PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.	
KW	ATP-binding; Phosphorylation; Serine/threonine-protein kinase; Transferase.	
FT	DOMAIN 40 291	Protein kinase.
FT	NP_BIND 46 54	APP (By similarity).
FT	BINDING 69 69	APP (By similarity).
FT	ACT_SITE 168 168	Proton acceptor (By similarity).
FT	MOD_RES 4 4	Phosphoserine (by autocatalysis) (partial).
FT	MOD_RES 190 190	Phosphoserine (by autocatalysis).
FT	MOD_RES 205 205	Phosphothreonine (by autocatalysis) (partial).
SQ	SEQUENCE 323 AA; 36964 MW; AB4DD61E7A99A38F CRC64;	
Alignment Scores:		
Pred. No.:	4_62e-63	Length: 323
Percent Similarity:	1104.00	Matches: 210
Best Local Similarity:	76.65%	Conservative: 46
Query Match:	62.87%	Mismatches: 60
DB:	45.19%	Indels: 18
	Gaps: 6	
US-10-705-757-3 (L-1302) x PLM3_XENIA (1-323)		
OY	4 ATGCTCTTGTGCCAGATCAACTCCCTGGGCCCATCGGCGCAGCCCTTGCAAC-----	57
Db	1 MetLeuLeuSerLyPheGlySerIleuAlaHisIle-----CysAsnProSer 16	
OY	58 -----GACCTGCAGCCCAACAGCTGGCGCGGGGAAA---GAGAAGAGCCCTTG	105
Db	17 AsnMetGliuHisLeuProValLySrlLeuGlnProValLyValAspLySrlProPhe 36	
OY	106 GAGTCGACGATACCAAGTAGGCGCGCGCTGGGACGCGGTGGCTTCGCTCGCTCTCG	165
Db	37 GliuLySrlValTyrglInValIgLyserValValAlaSerGlyGlyPheGlyThrValTySer 56	
OY	166 GGCAATCGCGCTGCCGACAACTTGGCCGCTGACCATCAACACGTTGAGGAAGACCGGATT	229
Db	57 AspSerArgIleAlaAspGlyglnProValAlaValIleValHisIleValAlaLySrlAlaGlyVal 76	
OY	226 TCCGACTGGGGGAACTGCCCAAGGGCACCCGATGCCATGGAAGTGGTCTCTGTGAAG	285
Db	77 ThrGlutTrpGlyThrLeu---AsnGlyValMetValProLeuGluInIleValIleuLeuLyS 95	
OY	286 AAGGAGACCTGGGGCTTCGCGGCGCTTAACITTCGACCTGGCTTCGAGAGGCCCGAT	345
Db	96 LySrlValProThrAlaPheArgGlyValIleAsnLeuLeuAspTrpTyrgluArgProAsp 115	
OY	346 AGTTTCGCTGCATCTCTCGAGAGAGGCCCGAACCCGTCGACAAGACTCTTCGACTCATCAC	405
Db	116 AlaPheLeuIleValMetGluArgProgluInProValLyAspLeuPheAspTryIleThr 135	
OY	406 GAGCGAGAGCCCTTCAGAGGAGGAGCTGGCCCGGAGCTTCTTTCGACGAGTGTGAGGCC	465
Db	136 GluLySrlGlyProLeuAspGlyuAspThrAlaArgGlyPhePheArgGluInValIleuGluAla 155	
OY	466 GTGGCGCAATTCGCAACATCGCGGGGCTTCGCAACCGCGACATGAAGAAGAAACATCTTA	525
Db	156 ValAlaGhiIsCytyrAsnCySrlValValAlaHisAspAspIleLyAspGlyuInIleuLeu 175	
OY	526 ATCGACCTGAAACCGCGGCGAATCAATCAATCGACTTCGAGTTCGGGCGCGCTGCTCAAG	585
Db	176 ValAspThrArgAsnGlyGluLeuLySrlIleAspPheGlySerGlyAlaIleuLeuLyS 195	
OY	586 GACACAGTCTACACGCACTTTGACGGAACCGAGTGTAACAGTCTTCGACAGTGAATTGCC	645


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Db      196 AspThrValIytrAspAhpheAegIythrArgValIySerProProglutPrValArg 215
Qy      646 TACCATCGTACACAGCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 705
Db      216 TyHIAArgIytrHIAArgIySerSerIAlmHValItrSerIeuIyValIeuIytrAbp 235
Qy      706 ATGTCGCGAGATATTCATTGTGAGACGACGACGACGACGACGACGACGACGACGACGACGAC 765
Db      236 MeValIyrcIyAspIleProPheGluGlnIlePheAspIleProIyMetCysIyAsp 255
Qy      766 TTATGCGAAGGGCTCTTCATGAAATGTCAACATCTTATGATGGTGGTGGTGGTGGTGGTGA 825
Db      256 PheArgArgArgIleSerThrGluCysGlnGlnIleuIleYerIytrCysIeuSerIeuArg 275
Qy      826 CCATTCGACCGCGGCTCTTCATGAAAGAAATCCAGAACCATCCGCGATG---CAGGATGT 882
Db      276 ProSerAspArgProThrIeuGluGlnIlePheAspIleProIyMetCysIyAsp 295
Qy      883 CTCCTGCGCCGACGCGACCGCGGACGATTCATCTGCACACCTGTACCATCACCACGACGAC 942
Db      296 LeuValIySerIeuIyAspCysAspIeuArgIeuArgIyThrIleAspIeuAspSerSer 314
Qy      943 TACGACGACATTCGTGACACCTTCACGAGGAAAGAGAGCTTG 984
Db      315 -----SerThrSerSerSerAsnGluSerIeu 323

RESULT 14
QBR2P0 PRELIMINARY; PRT; 311 AA.
ID      QBR2P0;
AC      QBR2P0;
DT      01-JUN-2002 (TREMBLrel. 21, Created)
DT      01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      P1m2 protein.
OS      Mus musculus (mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;

SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA      Diatchenko L., Marulita K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Udell T.B., Toshtyuk S., Carninci P., Prange C.,
RA      Raha S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA      Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Viallaon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzyzanski M.I., Skalska U., Smalins D.B., Schermer A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]
RN      SEQUENCE FROM N.A.
RP      STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RC      Strausberg R.;
RL      Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
CC      1-1 SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR      EMBL, BC027376; AAH27376.1;
DR      GO: GO:0005524; F:ATP binding; IEA.
DR      GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR      GO: GO:0016740; F:transferase activity; IEA.
DR      GO: GO:0006468; F:protein amino acid phosphorylation; IEA.

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DR      InterPro; IPR011009; Kinase like.
DR      InterPro; IPR000719; Prot kinase.
DR      InterPro; IPR002290; Ser Thr kinase.
DR      InterPro; IPR008271; Ser_thr_kin_AS.
DR      Pfam; PF00069; Kinase; 1.
DR      ProDom; PD000001; Prot. kinase; 1.
DR      SMART; SM00220; S_TKC; 1.
DR      PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR      PROSITE; PS50011; PROTEIN KINASE DM; 1.
DR      PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW      ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ      SEQUENCE 311 AA; 34486 MW; F7B770908D23A710 CRC64;

Alignment Scores:
Pred. No.: 1,85e-48 Length: 311
Score: 878.00 Matches: 173
Percent Similarity: 69.93% Conservative: 41
Best Local Similarity: 56.54% Mismatches: 79
Query Match: 35.94% Indels: 13
DB: Gaps: 4

US-10-705-757-3 (1-1302) x QBR2P0 (1-311)
Qy      27 CCTGGCCACCTGCGCGACGCCCTTGCAACGACTGCAGCCCAAGCTGGCGCGG 86
Db      10 ProSerProProVal---ThrProThrGlnProPro-----Gly-Gl 22
Qy      87 CAAAGAGAGAGAGCCCGCTGAGTCCGACGATACGAGTGGCGCGCGCTGGTGGAGCGGTGG 146
Db      22 IyAspArgAlaAlaPheGluAlaGluIytrArgIeuGlyProIeuIeuGlyIyAspI 42
Qy      147 CTCGCGCTGCTCTACTCGGAGCATCCGCTGCGCGGACCACTTGCCGCGTGGCATCAGCA 206
Db      42 IyPheGlyThrValPheAlaGlyHIAArgValIthrAspArgGlnValAlaIleYerVa 62
Qy      207 CGTGAGAGAGAGCCGAGATTCGAGCTGGGGGAGACTGCCCAAGCGACCGGAGTCCCAT 266
Db      62 IlySerArgAsnArgValIeuGlyIyPheSerThrValSerAspSerValIthrCysPro 82
Qy      267 GGAAGTGTCTCTGCAAGAGAGTG-----AGCTGGGCTCTCGCGGCTCATTTGACT 320
Db      82 uGluValAlaIeuIeuIytrIyValAlaGlyGluIyAsnGlyHIAProGlyValIleArgIe 102
Qy      321 TCTGAGCTGTTGAGAGGCGCGATAGTTCTGCTGATCTGAGAGGCGCGGACCGGT 380
Db      102 uIeuAspIytrPheGluIythrProGluIyPheIeuIeuValIeuGluIyArgProIeuProAl 122
Qy      381 GCAAGACTCTTGACTCATCAACGAGCGAGAGGCTTCAGAGAGAGCTGGCCGAG 440
Db      122 eGlnAspIeuPheAspIytrIleThrGluIyGlyProIeuGlyIySerCysSerArgSe 142
Qy      441 CTCTCTCTGCGAGTGTGAGGCGCGGCGGATTCGCAACCTGGGGGTTCTCCACGG 500
Db      142 rPhePheThrGlnValValAlaIaValAlaValAlaIyAsnIyCysHIAIyArgIyValAlaI 162
Qy      501 CGACATCAAGAGAGGAGACATCTTAATCGACTGAAACCGCGGAGACTCAAACTCATCA 560
Db      162 gAspIleIyAspGluAsnIleIeuIleAspIeuCysArgGlySerIleIyAspIleIeAs 182
Qy      561 CTTCGGGTGGGGCGCTGCTCAAGAGACAGTTCACAGGACTTTCAGCGAAACCGAGT 620
Db      182 pPheGlySerGlyAlaIeuIeuIleIyAspGluProIytrIthrAspPheAspGlyIytrArgVa 202
Qy      621 GTACACTCTCTCGAAGATGATTCGACATCGCTACCGAGCTGCGAGGCTCGCTGCTTGG 680
Db      202 IyYserProProGluIytrIyIleSerArgIyGlnIytrHIAIeuProAlaIytrValIytr 222
Qy      681 GTCCCTGGGAGATCTGCTATGACATGCTGCGAGATATTCATTTGAGACGACGAG 740
Db      222 pSerIeuGlyValIeuIeuIytrAspMetValCysGlyAspIleProPheGluIyArgAspI 242
Qy      741 AGAGATGTCAAGGCGCAAGTACTTTAAGGCAAGGCTCTTCAAGATGTCAACATCT 800

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Db 242 ngllleleuGlulagluLeuHlsPheProAlaHlsValSerProAspCysCysAlaLe 262
 QY 801 TATTAGATGGTGGCTGTCCCTGAGACCATGACCGGCTCTTGAAGAAATCCAGAA 860
 Db 262 uilleaGArxCysleuAlaProLysProCysSerArgProSerLeuGlulLeuLe 282
 QY 861 CCATCCGATGATGAGATGTTCTCCGCGGACGACCGGAGATTGATCTGCACAG 920
 Db 282 uaaPProLysPheGlnSer-----ProAlaGlulLysProLysSerSerLys 299
 QY 921 CCTGTACCATCACCC 936
 Db 299 eglYserProThrPro 304

RESULT 15
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 ID PIM2_MOUSE STANDARD; PRT; 370 AA.
 AC 062070; 062071; 062072;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Serine/threonine-protein kinase Pim-2 (EC 2.7.1.37).
 GN Name=Pim2; Synonym=Plm-2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN 11)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95300786; Pubmed=1781606;
 RA van der Lugt N.M., Domen J., Verhoeven E., Linders K.,
 RT "Proviral tagging in B mu-myc transgenic mice lacking the Pim-1 proto-
 oncogene leads to compensatory activation of Pim-2.";
 RL EMBO J. 14:2536-2544(1995).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative initiation;
 CC Comment=3 isoforms, 1 (shown here), 2 and 3, are produced by
 CC alternative initiation. Isoform 1 and isoform 2 initiate from
 CC CTG codons;
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
 subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@1sb-sib.ch).
 CC -----
 CC EMBL; LA1495; AAA98922.1; -
 CC EMBL; LA1495; AAA98923.1; -
 CC EMBL; LA1495; AAA98924.1; -
 CC PIR; S55333; S55333.
 CC HSSP; Q63450; 1A06.
 CC MGD; MG1:97587; Pim2.
 CC GO; GO:0005515; P:protein binding; IPI.
 CC GO; GO:0004674; P:protein serine/threonine kinase activity; IDA.
 CC GO; GO:0006916; P:anti-apoptosis; IDA.
 CC GO; GO:0006373; P:apoptotic mitochondrial changes; IDA.
 CC InterPro; IPR011009; Kinase-like.
 CC InterPro; IPR000719; Kinase.
 CC InterPro; IPR008271; Ser_Thr_kinase.
 CC InterPro; IPR002290; Ser_Thr_kinase.
 CC Pfam; PF00069; Pkinase; 1.
 CC ProDom; PD000001; Proc_kinase; 1.
 CC SMART; SM00220; S_TKc; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC Alternative initiation; ATP-binding; Phosphorylation;

KW Serine/threonine-protein kinase; Transferase.
 FT CHAIN 1 370 Serine/threonine-protein kinase Pim-2,
 FT CHAIN 1 Isoform 1.
 FT CHAIN 26 370 Serine/threonine-protein kinase Pim-2,
 FT CHAIN 2 Isoform 2.
 FT CHAIN 60 370 Serine/threonine-protein kinase Pim-2,
 FT CHAIN 3 Isoform 3.
 FT INIT_MET 26 26 For isoform 2.
 FT INIT_MET 60 60 For isoform 3.
 FT DOMAIN 91 345 Protein kinase.
 FT NP_BIND 97 105 ATP (By similarity).
 FT BINDING 120 120 ATP (By similarity).
 FT ACT_SITE 222 222 Proton acceptor (By similarity).
 SQ SEQUENCE 370 AA; 40059 MW; 12BB70BF04DBE8A CRC64;

Alignment Scores:
 Pred. No.: 1,91e-48 Length: 370
 Score: 878.00 Matches: 173
 Percent Similarity: 69.93% Conservative: 41
 Best Local Similarity: 56.54% Mismatches: 79
 Query Match: 35.94% Indels: 13
 DB: 1 Gaps: 4

US-10-705-757-3 (1-1302) x PIM2_MOUSE (1-370)

QY 27 CCTGGCCCACTGGCGCGACGCCCTTGCAACGACTGCACGCCCAAGCTGGCGCGG 86
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 QY 87 CAAAGAGAGAGAGCCCTGGAGTGCAGTACGAGGCGCGCTGTGGGAGCGGTGG 146
 Db 81 ylyaaPaPaGAlaAlaPheGlnAlaGluTyrArgLeuGlyProLeuGluGlyGly 101
 QY 147 CTTGGCTGGCTGCTACTCGGCGCATCCGCTGCCGCAACTTGGCGGCTCAAGCA 206
 Db 101 yPheGlyThrValPheAlaGlyHlsArgValThrSerArgGlnValAlaLeuVal 121
 QY 207 CGTGAGAGAGACCGGATTTCCGACTGGGGGAGAACTGCCAAGCGACCCGAGTCCAT 266
 Db 121 lIleSerArgAaArgValLeuGlyTyrSerThrValSerAaSerValThrCysProLe 141
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 Db 141 uGlnValAlaLeuLeuTyrLysValGlyGluGlyLysGlyHlsProGlyValAlaLeuArg 161
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 Db 161 uLeuAaPTrPheGlnThrProGluGlyPheMetLeuValLeuGluArgProMetProAl 181
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Search completed: September 22, 2005, 17:14:48
 Job time : 223.949 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus.n2p model

Run on: September 22, 2005, 16:20:36 ; Search time 34.242 Seconds

(Without alignments)
5676.828 Million cell updates/sec

Title: US-10-705-757-3

Perfect score: 2443
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Xgapop 10.0 , Xgapext 0.5

Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues 1027090

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1668	68.3	313	3	US-09-237-543-8	Sequence 8, Appl1
2	1668	68.3	313	3	US-09-644-450-8	Sequence 8, Appl1
3	1636	67.0	313	3	US-09-237-543-9	Sequence 9, Appl1
4	1636	67.0	313	3	US-09-644-450-9	Sequence 9, Appl1
5	1623	66.4	313	2	US-08-463-081B-26	Sequence 26, Appl1
6	1623	66.4	313	2	US-08-461-379A-26	Sequence 26, Appl1
7	1623	66.4	313	2	US-08-462-390B-26	Sequence 26, Appl1
8	1623	66.4	313	3	US-08-463-074B-26	Sequence 26, Appl1
9	1623	66.4	313	3	US-08-465-585C-26	Sequence 26, Appl1
10	1623	66.4	313	3	US-08-652-446-26	Sequence 26, Appl1
11	1584	64.8	313	3	US-09-237-543-7	Sequence 7, Appl1
12	1584	64.8	313	3	US-09-644-450-7	Sequence 7, Appl1

13	1304.5	53.4	257	2	US-07-857-224B-41	Sequence 41, Appl1
14	1136.5	46.5	326	3	US-09-237-543-2	Sequence 2, Appl1
15	1136.5	46.5	326	3	US-09-644-450-2	Sequence 2, Appl1
16	1131.5	46.3	355	3	US-09-237-543-5	Sequence 5, Appl1
17	1131.5	46.3	355	3	US-09-644-450-5	Sequence 5, Appl1
18	1104	45.2	323	3	US-09-237-543-6	Sequence 6, Appl1
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20	1083.5	44.4	254	3	US-09-237-543-4	Sequence 4, Appl1
21	1083.5	44.4	254	3	US-09-644-450-4	Sequence 4, Appl1
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28	370.5	15.2	630	4	US-10-355-975A-38	Sequence 38, Appl1
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37	353	14.4	779	4	US-08-817-832B-31	Sequence 31, Appl1
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44	343	14.0	722	4	US-10-274-194-4	Sequence 4, Appl1
45	342.5	14.0	724	4	US-09-984-890-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-237-543-8
; Sequence 8, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-237-543-8

Alignment Scores:

Pred. No.: 4.27e-131
Score: 1668.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 68.28%
DB: 3
Gaps: 0

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DB 21 HieAlahshlySleuAlaProGlyIySgluIySgluProIeuIuSerIntyIyIrnAl 40

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Db      61 AenLeuProValAlaIleLeuSerValGluLeuYAspArgIleSerAspTrpGlyLeu 80
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Db      81 ProAsnGlyThrArgValProMetGluValIleLeuLeuLeuValSerSerGlyPhe 100
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QY      424 GAGAGCTGGCCCGGAGCTTCTTCTGGCAGGTGCTGAGGCGCTGGCGCATTTGCCAAGC 483
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Db      161 CysGlyValLeuHisArgAspIleLeuYAspGluAsnIleLeuIleAspLeuAsnArgGly 180
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; Sequence 8, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HK1D-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT

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; ORGANISM: Rattus norvegicus
US-09-644-450-8
Alignment Scores:
Pred. No.: 4,27e-131
Score: 1668.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 68.28%
DB: 3 Gaps: 0

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RESULT 3

US-09-237-543-9
Sequence 9, Application US/09237543A
Patent No. 6143540
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237, 543A
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-09-237-543-9

Alignment Scores:

Pred. No.:	2,02e-128	Length:	313
Score:	1636.00	Matches:	304
Percent Similarity:	99.04%	Conservative:	6
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Query Match:	66.97%	Indels:	0
DB:	3	Gaps:	0

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QY 184 AACTTCCGCTGGCCATCAAGCACTGGAGAGAGACCGGATTTCCGACTGGGGGAACTG 243
DB 61 AeuLeuProValAlaIleLySHISValGluLyAaPArgIleSerAepTrpGlyGluLeu 80
QY 244 CCGAAGCGCAACCGGAGTGCCTGAGAGTGTCTGTGAAAGAGTGAAGTCCGGCTTC 303
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QY 304 TCGGCGCTCATTAAGTCTTGAAGTGGTTCGAGAGGCGGATGTTTCGCTGATCTG 363
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DB 301 GUILIEHISLEUHSERLEUSERPROGlyProSerLyS 313

RESULT 4

US-09-644-450-9
Sequence 9, Application US/09644450
Patent No. 6383791
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644, 450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-09-644-450-9

Alignment Scores:

Pred. No.:	2,02e-128	Length:	313
Score:	1636.00 <td>Matches:</td> <td>304</td>	Matches:	304
Percent Similarity:	99.04% <td>Conservative:</td> <td>6</td>	Conservative:	6
Best Local Similarity:	97.12% <td>Mismatches:</td> <td>3</td>	Mismatches:	3
Query Match:	66.97% <td>Indels:</td> <td>0</td>	Indels:	0
DB:	3	Gaps:	0

US-10-705-757-3 (1-1302) x US-09-644-450-9 (1-313)

QY 4 ATGCTCTTGTCCAGATCAACTCCCTGGCCACCTGGCGCGAGCCCTTGCAAGCACTG 63
DB 1 MetLeuLeuSerLySILeAaNSerLeuAlaHISLeuKrgAlaAlaProCySaNaApleu 20
QY 64 CAGGCCAACAAGCTGGCGCGCGCAAGAAGAAGAGCCCTGGAGTGCAGTCCAGAGT 123
DB 21 HIsAlaThrLyLeuAlaProGlyLyGluLyGluProLeuLuserGlnTyrgInVal 40
QY 124 GGCCTGCTGTTGGGCAAGCGGTGCTTGGCTCGGTCTACTCGGAGCATCCGCTCGCGCAG 183
DB 41 GlyProLeuLeuGlySerGlyLyGlyPheGlySerValTySerGlyLyLeaGlyValSerAep 60
QY 184 AACTTCCGCTGGCCATCAAGCACTGGAGAGAGACCGGATTTCCGACTGGGGGAACTG 243
DB 61 AeuLeuProValAlaIleLySHISValGluLyAaPArgIleSerAaPTrpGlyGluLeu 80
QY 244 CCGAAGCGCAACCGGAGTGCCTGAGAGTGTCTGTGAAAGAGTGAAGTCCGGCTTC 303
DB 81 ProAaNGlyThrArgValProMetGluValValLeuLeuLySValSerSerGlyPhe 100


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/ TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
/ TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Ratner & Prestia
/ CITY: Valley Forge
/ STATE: Pennsylvania
/ COUNTRY: USA
/ ZIP: 19482
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/462,390B
/ FILING DATE: 5-JUNE-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US9N 08/330,108
/ FILING DATE: 27-OCT-1994
/ APPLICATION NUMBER: US9N 08/104,736
/ FILING DATE: 10-AUG-1993
/ APPLICATION NUMBER: US9N 07/796,066
/ FILING DATE: 20-NOV-91
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Viviana Amzel, Ph. D.
/ REGISTRATION NUMBER: 30,930
/ REFERENCE/DOCKET NUMBER: DART-040
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (610)407-0700
/ TELEFAX: (610)407-0701
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 313 amino acids
/ TYPE: peptide
/ STRANDEDNESS: n.a.
/ TOPOLOGY: n.a.
/ MOLECULE TYPE: peptide
/ US-08-462-390B-26

Alignment Scores:
Pred. No.: 2,46e-127 Length: 313
Score: 1623.00 Matches: 302
Percent Similarity: 98.40% Conservative: 6
Beet Local Similarity: 96.40% Mismatches: 5
Query Match: 66.43% Indels: 0
Gaps: 0

US-10-705-757-3 (1-1302) x US-08-462-390B-26 (1-313)
QY 4 ATGCTGTTCGAAGTCAACTCCCTGGCCACCTGGCGGAGCCCTTGCAGACGCTG 63
Db 1 MetLeuLeuSerLyIleAsnSerLeuAlaHisLeuAlaArgAlaCyAsnAspLeu 20
QY 64 CAGCCCAACAAGCTGGCGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
Db 21 HisAlaThrLyIleuAlaProGlyLyIleuGluProLeuGluSerGlnTyrGlnVal 40
QY 124 GGGCCGCTGTGGGAGCGGCTGCTTGGCTCGCTACTCGGAGCATCCGCTGCCGAC 183
Db 41 GlyProLeuLeuGlySerGlyGlyIleuGlySerValTyrSerGlyIleArgValSerAsp 60
QY 184 AACTTGGCGGTGGCCATCAAGCAGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
Db 61 AsnLeuProValAlaIleuYHisValGluLyAspArgTgIleSerAspTyrGlyGluLeu 80
QY 244 CCGAAGCGGACCGAGTGGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
Db 81 ProAsnGlyThrArgValIleProMetGluValValLeuLeuLyIleValSerSerGlyPhe 100
QY 304 TCGGGCGCTCAATTGACTTTCGACTGGTTGAGAGAGCCGAGATGTTTGGTGAATCTTG 363

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Db 101 SerGlyValIleArgLeuLeuAspTyrPheGluArgProAspSerPheValIleuLeu 120
QY 364 GAGAGCCCGAAGCCCGTGAAGACCTTTCGACTTCATCAGGAGGAGAGCCCTCGAG 423
Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 424 GAGAGCTGGCCGAGAGCTTCTTTCGAGAGTGTGTGAGAGCCGTCGCGGATTCGCAAC 483
Db 141 GluGluLeuAlaArgSerPheThrProGlnValIleGluAlaValArgHisCyHisAsn 160
QY 484 TCGGGGCTTTCACCCGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
Db 161 CyGlyValLeuHisArgAspIleLeuYAspArgIleuAsnIleLeuIleAspLeuAsnArgGly 180
QY 544 GAAGTCAAGTATGAGCTTGGGTCGGGGGCGGTCGTCAGAGACAGAGTATCAGAGGAC 603
Db 181 GluLeuLyIleuIleAspPheGlySerGlyAlaLeuLeuLyAspArgTyrValTyrThrAsp 200
QY 604 TTTGACGAAACCGAGTGAAGTCCCTCCAGAGTGAATTGCTACCATGCTACAGAGGAC 663
Db 201 PheAspGlyThrArgValTyrSerProProGluTyrIleArgTyrHisArgTyrHisGly 220
QY 664 AGCTGGCTGCTGTTTGGTCCCTGGGAGTCTGCTCTATGACATGCTTGGGAGATATT 723
Db 221 ArgSerAlaAlaValTyrSerLeuGlyIleuLeuTyrAspMetValCySerIleAspIle 240
QY 724 CATTGAGCAGCAGAGAGAGATCGCAAGGCGCAAGTACTTTAGCGAAAGGCTCTCT 783
Db 241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnTyrValSer 260
QY 784 TCAGATGTCAACATCTTATTAGATGTGCTGTGCTCCCTGAGACATCGAGCCGCGCTTC 843
Db 261 SerGluCyGlnHisLeuIleArgTyrCyIleuAlaLeuArgProSerAspArgProThr 280
QY 844 TTTGAAGAAATCAAGAACATCTCGGAGATGCGAGATGTTCTCTGCGCCAGGACCGCC 903
Db 281 PheGluGluIleGlnAsnHisProTyrMetGlnAspValLeuLeuProGlnIleThrAla 300
QY 904 GAGATTCATCTGACAGCCTGTCAACATCAGCAGCAGCAA 942
Db 301 GluIleHisLeuHisSerLeuSerProGlyProSerLyAs 313

RESULT 8
US-08-463-074B-26
/ Sequence 26, Application US/08463074B
/ Patent No. 6020155
/ GENERAL INFORMATION:
/ APPLICANT: Smith, Kendall A. & Beadling, Carol
/ TITLE OF INVENTION: Nucleic Acids Encoding CRI Fusion Protein, Vector an
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: PRETTY, SCHROEDER & POPLAWSKI
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: USA
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0,
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/463,074B
/ FILING DATE: 5-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/104,736
/ FILING DATE: 10-AUG-1993
/ APPLICATION NUMBER: US 07/796,066
/ FILING DATE: 20-NOV-91
/ ATTORNEY/AGENT INFORMATION:

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Db      1 MetLeuLeuSerIyLeaSenSerLeuAlaHleuNrgAlaArgAlaCySaanaPLeu 20
Qy      64 CAGGCCAACAAGCTGGGGCCGGGCAAGAGAAGAGCCCTGGAGTGCAGTACAGAGTG 123
Db      21 HlaAlaThrIySvleuAlaProGlyLySgIuLySgIuProLeuGIsuSerGIntYrGlnVal 40
Qy      124 GGGCCGCTGTGGGACGGGTGGCTTGGGCTCGGCTACTCGGGCAATCGGGCTCGGAC 183
Db      41 GlyProLeuLeuGIsuSerGlyLyPheGlySerValYrSerGlyIleArgValSerAsp 60
Qy      184 AACTTGGCGGTGGCCATCAAGACAGTGGAGAGAGCCGGAATTTCCGACTGGGGGAACTG 243
Db      61 AsnLeuProValAlaIleYrSvleuAlaGluLyAspArgIleSerAspTrpGlyGluLeu 80
Qy      244 CCCAAGCGGACCCGAGTGGCCATGAAAGTGCTCTGCTGAAGAAAGTGAGCTGGGCTTC 303
Db      81 ProAsnGlyThrArgValProMetGluValIleuLeuYrSvleuValSerSerGlyPhe 100
Qy      304 TGGGGGCTCATTTAGACTTCTGAGCTGGTTGAGAGGCGCGATGTTTCGTGCTGATCTTG 363
Db      101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleuLeu 120
Qy      364 GAGAGCCCGAACCCGTGCAAGACCTTCTGACTTCATCAACGAGCGAGAGGCGCTTCAG 423
Db      121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
Qy      424 GAGAGCTGGCCCGAGACTTCTTCTGGCAGCTGTCGAGGCGCGTGGCGCATTCGCAAC 483
Db      141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnIleValArgHisCySHAsn 160
Qy      484 TGGGGGTTCTCCACCGCGCATCAAGAGAGAGAACTTTAATCCACTGGAACCGCGGC 543
Db      161 CysGlyValLeuAlaArgAspIleYrAspGlnAsnIleuLeuIleAspLeuAsnArgGly 180
Qy      544 GAACTCAAACTCATCGACTTCGGGTCGGGGCGCTGCTCAAGGACACAGTCTACACGAG 603
Db      181 GluLeuYrSvleuIleAspPheGlySerGlyAlaIleuLeuYrAspPheTrValYrThrAsp 200
Qy      604 TTGACGGAACCCGAGTGTACAGTCTCCAGAGTGATTCGTAACCATCGCTACCAAGGC 663
Db      201 PheAspGlyThrArgValYrSerProGluTrpIleArgTyHisArgTyHisGly 220
Qy      664 AGGTGGCTGCTGTGGTTCCTGGGGATGCTGCTCATGACATGGCTTCGGAGATATT 723
Db      221 ArgSerAlaAlaValIleTrpSerLeuGlyIleLeuLeuYrAspMetValCysGlyAspIle 240
Qy      724 CCATTGAGCAGCAGAGAGATCGTCAAGAGGCGCAAGTACTTTAGGCAAAAGGTCTCT 783
Db      241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
Qy      784 TCAGAAATGTCACATCTTATTAGATGGTGCCTGCTCCCTGAGACATCGACCGGCTTC 843
Db      261 SerGluCysGlnHisIleuLeuIleArgTrpCysLeuAlaIleuArgProSerAspArgProThr 280
Qy      844 TTGGAAGAATCCAGAAACCATCCGTGATGACAGAGTGTCTCTGCCCCAGGCGCACCGCC 903
Db      281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGlnGluThrAla 300
Qy      904 GAGATTCATCTGCACAGCCTGTCAACCATCAACCCAGCAAA 942
Db      301 GluIleHisIleuHisSerLeuSerProGlyProSerIleYr 313
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; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-237-543-7

Alignment Scores:
Pred. No.:      4,48e-124      Length:      313
Score:          1584.00      Matches:      295
Percent Similarity: 96.81%      Conservative: 8
Best Local Similarity: 94.25%      Mismatches: 10
Query Match:    64,84%      Indels:      0
DB:              3          Gaps:      0

US-10-705-757-3 (1-1302) x US-09-237-543-7 (1-313)

Qy      4 AATGCTTTGTCCAAATCAATTCCTCGGCCCACTCGGGCGAGCCCTTGCAACGACTTG 63
Db      1 MetLeuLeuSerIyLeaSenSerLeuAlaHleuNrgAlaArgProCySaanaPLeu 20
Qy      64 CAGGCCAACAAGCTGGGGCCGGGCAAGAGAAGAGCCCTGGAGTGCAGTACAGAGTG 123
Db      21 HlaAlaThrIySvleuAlaProGlyLySgIuLySgIuProLeuGIsuSerGIntYrGlnVal 40
Qy      124 GGGCCGCTGTGGGACGGGTGGCTTGGGCTCGGCTACTCGGGCAATCGGGCTCGGAC 183
Db      41 GlyProLeuLeuGIsuSerGlyLyPheGlySerValYrSerGlyIleArgValIleAsp 60
Qy      184 AACTTGGCGGTGGCCATCAAGACAGTGGAGAGAGCCGGAATTTCCGACTGGGGGAACTG 243
Db      61 AsnLeuProValAlaIleYrSvleuAlaGluLyAspArgIleSerAspTrpGlyGluLeu 80
Qy      244 CCCAAGCGGACCCGAGTGGCCATGAAAGTGCTCTGCTGAAGAAAGTGAGCTGGGCTTC 303
Db      81 ProAsnGlyThrArgValProMetGluValIleuLeuYrSvleuValSerSerGlyPhe 100
Qy      304 TGGGGGCTCATTTAGACTTCTGAGCTGGTTGAGAGGCGCGATGTTTCGTGCTGATCTTG 363
Db      101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleuLeu 120
Qy      364 GAGAGCCCGGAACCCGTGCAAGACCTTCTGACTTCATCAACGAGCGAGAGGCGCTTCAG 423
Db      121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
Qy      424 GAGAGCTGGCCCGAGACTTCTTCTGGCAGTGTGAGAGGCGCGTGGCGCATTCGCAAC 483
Db      141 GluAspLeuAlaArgGlyPhePheTrpGlnValIleuGlnIleValArgHisCySHAsn 160
Qy      484 TGGGGGTTCTCCACCGCGCATCAAGAGAGAGAACTTTAATCCACTGGAACCGCGGC 543
Db      161 CysGlyValLeuAlaArgAspIleYrAspGlnAsnIleuLeuIleAspLeuAsnArgGly 180
Qy      544 GAACTCAAACTCATCGACTTCGGGTCGGGGCGCTGCTCAAGGACACAGTCTACACGAG 603
Db      181 GluIleYrSvleuIleAspPheGlySerGlyAlaIleuLeuYrAspPheTrValYrThrAsp 200
Qy      604 TTGGAAGAAACCGAGTGTACAGTCTCCAGAGTGATTCGCTACCATGCTGACCAAGGC 663
Db      201 PheAspGlyThrArgValYrSerProGluTrpIleArgTyHisArgTyHisGly 220
Qy      664 AGGTGGCTGCTGTGGTTCCTGGGGATGCTGCTCATGACATGGCTTCGGAGATATT 723
Db      221 ArgSerAlaAlaValIleTrpSerLeuGlyIleLeuLeuYrAspMetValCysGlyAspIle 240
Qy      724 CCATTGAGCAGCAGAGAGATCGTCAAGAGGCGCAAGTACTTTAGGCAAAAGGTCTCT 783
Db      241 ProPheGluHisAspGluGluIleIleYrSgIuGlnValPhePheArgGlnThrValSer 260
Qy      784 TCAGAAATGTCACATCTTATTAGATGGTGCCTGCTCCCTGAGACATCGACCGGCTTC 843
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Db      261 SerGIuCybGlnHlsleuilelystrCybLeuSerleuAArgProSerAspArgProSer 280
QY      844 TTTGAAGAAATCCAGAACCATCCGTGGATGACAGAGATTCTCTGCGCCAGGACCGCCG 903
Db      281 PheGIuGlnIleArgAsnHlsProTrpMetGlnGlyAspLeuLeuProGlnIleAlaSer 300
QY      904 GAGATTCAATCTGCACAGCCTGTGCACCATCACCAGCAAA 942
Db      301 GIuIleHlsleuHlsSerleuSerProGlySerSerIys 313

RESULT 12
US-09-644-450-7
; Sequence 7, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-644-450-7

Alignment Scores:
Pred. No.:      4,48e-124      Length:      313
Score:          1584.00      Matches:      295
Percent Similarity: 96.81%      Conservative: 8
Best Local Similarity: 94.25%      Mismatches: 10
Query Match:     64.84%      Indels:      0
DB:              3          Gaps:      0

US-10-705-757-3 (1-1302) x US-09-644-450-7 (1-313)
QY      4 ATGCTCTTTCGAAGATCAACTCCCTGGCCCACTGGGCGGACCCCTTGCAACGACCTG 63
Db      1 MetLeuLeuSerIysIleAsnSerLeuAlaHlsleuArgIleArgProCysAsnAspLeu 20
QY      64 CAGCCCAACAGCTGGGCGCGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
Db      21 HlsIleHlsIysleuAlaProGlyIysGlnIysGlnProleuGlnSerGlnIysArgIleVal 40
QY      124 GGGCCGCTGTGGGACAGCGGTGCTTGGCTCGGCTTACTCGGACATCGCGTCCGCGAC 183
Db      41 GlyProleuLeuGlySerGlyIysPheGlySerValIysSerGlyIleArgValAlaAsp 60
QY      184 AACTGCGCGGTGGCCATCAAGCAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
Db      61 AsnLeuProValAlaIleIysHlsValGlnIysAspArgIleSerAspTrpGlyGlnLeu 80
QY      244 CCAAGAGGACCGGAGTGGCCATGAGAGAGTGTCTGCTGTAAGAAGTGAAGTGAAGTGAAG 303
Db      81 ProHsnGlyHlsArgValIlePrometGlnValValleuLeuIysValIleSerSerAspPhe 100
QY      304 TCGGGCGCTCATTAAGTCTTGAGTGTGAGAGGCCGATATGTTTCTGTCGATCTTG 363
Db      101 SerGIyValIleArgleuLeuAspTrpPheGlnArgProAspSerPheValleuIleLeu 120
QY      364 GAGAGGCGCCGAGACCCGTGCAAGACCTTTGACTTTCATCAACGAGCGAGAGAGAGAGAG 423
Db      121 GluArgProGlnProValGlnAspLeuPheAspPheIleHlsArgGlyAlaLeuGln 140
QY      424 GAGAGGTGGCCCGGAGACTTCTTGGCAGGTGCTGAGAGCGGCGGCGGATGGCAAC 483
Db      141 GluAspLeuAlaArgGlyPhePheTrpGlnValIleuGlnIleValAlaArgHlsCysHlsAsn 160
QY      484 TGGCGGGTCTCCACCGCGCATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543

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Db      161 CysGlyValleuHlsArgAspIleIysAspGlnIleuIleAspLeuSerArgGly 180
QY      544 GAATCAAAATCATGACTTCGAGGTCCGGGCGGCTGTCAAGACAGACAGTCTACACGAGAC 603
Db      181 GIuIleIysleuIleAspPheGlySerGlyAlaIleuLeuIysAspThrValIysThrAsp 200
QY      604 TTTGACGGAACCCGAGGTGTACAGTCTCCAGAGTGGATTCGCTACCAATCGCTACCAAGCC 663
Db      201 PheAspGlyThrArgValIysSerProProGlnIleArgTyrHlsArgTyrHlsGly 220
QY      664 AGTGGCTGCTGTGTTTGTCTCCCTGGGAGTCCGCTCTATGACATGCTCGGAGATAT 723
Db      221 ArgSerIleAlaValAlaTrpSerleuGlyIleuLeuTyrAspMetValCysGlyAspIle 240
QY      724 CCATTGAGCAGCAGACGAGATCGTCAAGGCGCAAGGTACTTTAGGCAAGGCTCTCT 783
Db      241 ProPheGlnHlsAspGlnIleIleIysGlyGlnValPhePheArgGlnThrValSer 260
QY      784 TCAGATGTCAACATCTTATTAAGATGTGCTGTCTGCTGAGACCATCGGACCGGCTTC 843
Db      261 SerGIuCybGlnHlsleuilelystrCybLeuSerleuAArgProSerAspArgProSer 280
QY      844 TTTGAAGAAATCCAGAACCATCCGTGGATGACAGATTTCTCTGCGCCAGGACCGCCG 903
Db      281 PheGIuGlnIleArgAsnHlsProTrpMetGlnGlyAspLeuLeuProGlnIleAlaSer 300
QY      904 GAGATTCAATCTGCACAGCCTGTGCACCATCACCAGCAAA 942
Db      301 GIuIleHlsleuHlsSerleuSerProGlySerSerIys 313

RESULT 13
US-07-857-224B-41
; Sequence 41, Application US/07857224B
; Patent No. 5958764
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION:
; ORIGINAL SOURCE:
; ORGANISM: rat
; FEATURE: Protein kinase; Table 8 Column 46
; PUBLICATION INFORMATION:
; AUTHORS:
; AUTHORS: Hanks, S. K.
; AUTHORS: Quinn, A. M.

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AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
PAGES: 42-52
DATE: 1988
US-07-857-224B-41

Alignment Scores:

Pred. No.:	9,476-101	Length:	257
Score:	1304.50	Matches:	244
Percent Similarity:	97.67%	Conservative:	7
Best Local Similarity:	94.94%	Mismatches:	3
Query Match:	53.40%	Indels:	3
DB:	2	Gaps:	2

US-10-705-757-3 (1-1302) x US-07-857-224B-41 (1-257)

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QY 109 TCGCAGTACGAGTGGGCGGCTGTTGGGAGCGGCTTGGGCTGCTGCTACTCGGAGC 168
    |||
DB 1 SerGlnTyrGlnValGlyProLeuLeuGlySerGlyValPheGlySerValTyrSerGly 20
    |||
QY 169 ATCCGCGTCCGCGCAACTTGCCTGCGTCCATCAAGCAGTGAAGAACCGGATTTCC 228
    |||
DB 21 IleArgValAlaAphAenLeuProValAlaIleValHisValGlnValSerPargIleSer 40
    |||
QY 229 GACTGGGGGGAATGCCCCAACGGCAGCCGAGTCCCATGGAAGTGGTCTGCTGAAGAG 288
    |||
DB 41 AspTrpGlyGlu-----AenGlyThrArgValProMetGluValValLeuLeuValLeu 58
    |||
QY 289 GTAGAGCTGGGCTTCTCGGGGCTCATTAAGCTTGTGAGCTGTGTCGAGAGCCCGATAGT 348
    |||
DB 59 ValSerSerAphSerGlyValIleArgLeuLeuAphTrpPheGlnValArgProAphSer 78
    |||
QY 349 TTCGTCTGATCTTGGAGAGCGCCGAAACCGTGCAGAGCTTCTGCACTTCAATCAGCAG 408
    |||
DB 79 PheValLeuLeuLeuGlnArgProGlnProValGlnAphLeuPheAphIleTrnGlu 98
    |||
QY 409 CGAGAGAGCTTCCAGAGAGAGCTGGCCCGAGCTTCTTGGGAGGCTGCTGAAGCCGCTG 468
    |||
DB 99 ArgGlyAlaLeuGlnGlnAphLeuAlaArgGlyPheSerTrpGlnValLeuGlnAlaVal 118
    |||
QY 469 CGGATTTGCCAACAAGTGGGGTTCTCCACCGGCACTCAAGAGCGAATCATCTTAATC 528
    |||
DB 119 ArgHisCysHisAphCysGlyValLeuHisAphSerIleLeuAphGlnAphIleLeuIle 138
    |||
QY 529 GACCTGAACCGCGCGCAACTCAATCATGACTTCGGGTCGGGCGGCTGCTCAAGGAC 588
    |||
DB 139 AapLeuSerArgGlyGlnIleValLeuIleAphPheGlySerGlyAlaLeuLeuValAph 158
    |||
QY 589 ACAAGTACACGGAATTGACGGAACCGGAGTGAAGTCTTCAAGAGTGGATTCCGTAC 648
    |||
DB 159 ThrValTyrThrAphPheAphSerGlyThrArgValTyrSerProGlnTrpIleArgTyr 178
    |||
QY 649 CATCGGTACCAACGAGGAGTGGGCTGTTGGTCCCTGGGAGTCCGCTTGAACAG 708
    |||
DB 179 HisAphTyrHisValArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyrAphMet 198
    |||
QY 709 GTCTGCGAGATATTCATT---GAGCAGCAGAGAGAGTCTCAAGCGCAGGTGATC 765
    |||
DB 199 ValCysGlyAphSerIleProPheAphGlnHisAphGlnIleIleValSerGlyGlnValPhe 218
    |||
QY 766 TTTAGGCAAGGGTCTTTCAGAAATGTCACATCTTAATTAAGATGGTGGCTGCTGAGAG 825
    |||
DB 219 PheArgGlnThrValSerSerGlnCysGlnHisLeuIleValTrpCysLeuSerLeuArg 238
    |||
QY 826 CGATCGGACCGGCGCTTCTTGAAGAAATCAAGACATCCGAGTGAAGCAG 876
    |||
DB 239 ProSerAphArgProSerPheGlnGlnIleArgHisHisProTrpMetGln 255
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RESULT 14
US-09-237-543-2
Sequence 2, Application US/09237543A

Patent No. 6143540
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
US-09-237-543-2

Alignment Scores:

Pred. No.:	1,146-86	Length:	326
Score:	1136.50	Matches:	224
Percent Similarity:	77.25%	Conservative:	34
Best Local Similarity:	67.07%	Mismatches:	61
Query Match:	46.52%	Indels:	15
DB:	3	Gaps:	8

US-10-705-757-3 (1-1302) x US-09-237-543-2 (1-326)

```
QY 4 ATGCTTTGTCCAAATCAATCTCCCTGGCCACCTGCGGAGCCCT-----TGCAAC 57
    |||
DB 1 MetLeuLeuSerLeuAphSerPheGlySerLeuAlaHisLeu---CysGlyProGlyGlyValAph 19
    |||
QY 58 GACCTCCACGCCCAACAAGCTGGGCGCGCGCAAA---GAGAAGAGCCCTGAGTGGCAG 114
    |||
DB 20 HisLeuProValIleValLeuGlnProAlaValAphValAphValLeuValArgValTrnGlu 39
    |||
QY 115 TACAGATGGGCGCGCTGTGGAGAGCGGAGTGGCTGCGCTGCTGCTACTGAGCATCCG 174
    |||
DB 40 TyrGlnValGlyAlaValLeuGlnGlySerGlyPheGlyThrValTyrAlaGlySerArg 59
    |||
QY 175 GTGCGCGCAACAATTGCGCGGCTGCATCAAGCAGTGAAGAGAGCGGATTTCCGACTGG 234
    |||
DB 60 IleAlaAphGlyLeuProValAlaValIleValHisValValLeuGlnValArgValTrnGlu 79
    |||
QY 235 GGGGAATGCGCCCAACGGGCAACCGGAGTGAAGTGGTCTGCTGAAGAGG--- 291
    |||
DB 80 GlySerLeu---GlyValAlaThrValProLeuGlnValValLeuLeuArgValGly 98
    |||
QY 292 ---AGCTCGGCGCTTCTCGGCGCTCATTAAGCTTGTGAGTGGTTCGAGAGCCCGATAGT 348
    |||
DB 99 AlaAlaGlyGlyAlaArgGlyValIleArgLeuLeuAphTrpPheGlnTrpProAphGly 118
    |||
QY 349 TTCGTCTGATCTTGGAGAGCGCCGAAACCGTGCAGAGCTTCTGCACTTCAATCAGCAG 408
    |||
DB 119 PheLeuLeuValLeuGlnArgProGlnProValGlnAphLeuPheAphIleTrnGlu 138
    |||
QY 409 CGAGAGAGCTTCCAGAGAGAGCTGGCCCGAGCTTCTTGGGAGGCTGCTGAAGCCGCTG 468
    |||
DB 139 ArgGlyAlaLeuAphSerIleProLeuAlaArgAphPheAlaGlnAlaValLeuAlaAlaVal 158
    |||
QY 469 CGGATTTGCCAACAAGTGGGGTTCTCCACCGGCACTCAAGAGCGAATCATCTTAATC 528
    |||
DB 159 ArgHisCysHisAphSerGlyGlnValValHisAphSerIleValAphGlnAphIleVal 178
    |||
QY 529 GACCTGAACCGGCGCAACTCAATCATGACTTCGGGTCGGGCGGCTGCTCAAGGAC 588
    |||
DB 179 AapLeuArgSerGlyIleLeuLeuValLeuIleAphPheGlySerGlyAlaLeuLeuValAph 198
    |||
QY 589 ACAAGTACACGGAATTGACGGAACCGGAGTGAAGTCTTCAAGAGTGGATTCCGTAC 648
    |||
DB 199 ThrValTyrThrAphPheAphSerGlyThrArgValTyrSerProGlnTrpIleArgTyr 218
    |||
QY 649 CATCGGTACCAACGAGGAGTGGGCTGTTGGTCCCTGGGAGTCCGCTTGAACAG 708
    |||
DB 219 HisArgTyrHisValArgSerAlaThrValTrpSerLeuGlyValLeuLeuTyrAphMet 238
    |||
```

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QY 709 GTCTGGAGATATTCATTGTGAGCAGCAAGAGATGTCAGAGGCGCAAGTACTTT 768
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 239 ValCyBgIyAspIleProPhegluInAspGluInIleuAspGlyYArgLeuAsp 258
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 769 AGCAAAAGGCTCTTCAGAAATGTCAAATCTTATTAGATGTCCTGCTGAGACCA 828
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 259 ArgAspArgValSerProgluInleuIleAlaArgTrpCysLeuSerIleuAspPro 278
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 829 TCGAGACCGGCTCTTGAAGAAATCCAGAACCATCCGTGATG-----CAGATGTT 882
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 279 SerGluArgProSerIleuAspGlnIleAlaAlaAspProTrpMetLeuGlyAlaAspGly 298
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 883 CTCCTGCCCCAGGCGCGCCGAGATTTCATCTGCACAGCTGTCACCATCACCCAGCAAA 942
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 299 GlyAlaProGlu---SerCysAspLeuAlaGlyCysThrIleuAspPro----- 313
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 943 TAGCAGCCATTCTGTCAAGCCCTCCAGGAGAGAGAGAGCTTG 984
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 314 ---AspAspValAlaSerThrTrpSerSerSerGluSerIleu 326
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
US-09-644-450-2
; Sequence 2, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HK1D-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 326
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-644-450-2

Alignment Scores:
Pred. No.: 1,14e-86 Length: 326
Score: 1136.50 Matches: 224
Percent Similarity: 77.25% Conservative: 34
Best Local Similarity: 67.07% Mismatches: 61
Query Match: 46.52% Indels: 15
DB: 3 Gaps: 8

US-10-705-757-3 (1-1302) x US-09-644-450-2 (1-326)
QY 4 ATGCTCTTGTCCAAAGATCAACTCCCTGGCCCACTGCGGAGCCCT-----TGCAC 57
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MetLeuLeuSerIleuAspGlySerLeuAlaIleLeu---CysGlyProGlyGlyValAsp 19
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 58 GACCTGCAGCCCAACAAGCTGGCGCGCGGCAAA---GAGAGAGAGCCCTGAGTGCAG 114
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20 HisLeuProValIleuArgIleuGlnProAlaIleValAlaAspIleuSerPheGluValAla 39
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 115 TACCAAGTGGGCGGCTGTGGGAGCGGTGGCTTGGCTCGGTCTACTGAGGATCCGC 174
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 40 TyrGlnValGlyAlaValIleuGlySerGlyPheGlyThrValTyrAlaGlySerArg 59
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 175 GTGCGGAGCAAACTTGGCGGTGATCAAGCAGTGAAGAGAGAGAGGAGATTTCGAGCTG 234
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 IleAlaAspGlyLeuProValAlaValAlaValAlaValAlaValAlaValAlaValAlaVal 79
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 235 GGGGAATGCGCCCAACCGGACCCGAGTGCAGGAAAGTGTCTGCTGAAGAGGTG--- 291
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 GlySerLeu---GlyGlyAlaThrValProLeuGluValValLeuLeuAspGlyValGly 98
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 292 ---AGCTCGGGCTTCTCGGGCGTCAATTGACTTGTGAGCTGGTTCAGAGAGCCCGATAGT 348
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 99 AlaAlaGlyGlyAlaArgGlyValIleArgLeuLeuAspTrpPheGluArgProAspGly 118
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 349 TTGCTGATATCTTGGAGAGGCGCCGAACCCGNGCAAGACTTCTGACTTCAACCGAG 408
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 PheLeuLeuValIleuGluInArgProGluProAlaGlnAspLeuPheAspPheIleThrGlu 138
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 409 CGAGAGGCTCTTCAGAGAGAGCTGGCCCGAGCTTCTTCTGCGAGCTGTGAGGCGCTG 468
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 139 ArgGlyAlaLeuAspGluProLeuAlaArgArgPhePheAlaGlnValLeuAlaValAla 158
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 469 CGGCTTTCGCAACTGTGGGGGTCTCCAGCGCGCATCAAGAGAGAGAACTTAATC 528
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 159 ArgHisCysHisSerCysGlyValAlaHisArgAspIleLysAspGluAsnLeuVal 178
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 529 GACCTGAACCGCGGCGAAGCTCAAACTCATTCGACTTCGGGTCGGGCGCTGCTCAAGAC 588
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 AspLeuAspSerGlyGluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAsp 198
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 589 ACAGTCTACAGGACTTGTGACGGAACCCGAGTGTACAGTCTCCAGAGTGTGATTCGCTAC 648
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 199 ThrValTyrThrAspPheAspGlyThrArgValTyrSerProProGluTrpIleArgTyr 218
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 649 CATGCTACACCGGAGCTGGCTGTGTTGTCTGCTGGGAGATCCTGTATGACATG 708
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 219 HisArgTyrHisArgLysSerAlaThrValTrpSerLeuGlyValLeuLeuTyrAspMet 238
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 709 GTCTCGGAGATATTCATTGTGAGCAGCAAGAGATGTCAGAGGCGCAAGTACTT 768
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 239 ValCyBgIyAspIleProPhegluInAspGluInIleuAspGlyYArgLeuAsp 258
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 769 AGCAAAAGGCTCTTCAGAAATGTCAAATCTTATTAGATGTCCTGCTGAGACCA 828
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 259 ArgAspArgValSerProgluInleuIleAlaArgTrpCysLeuSerIleuAspPro 278
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 829 TCGAGCGGCGCTCTTGAAGAAATCCAGAACCATCCGTGATG-----CAGATGTT 882
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 279 SerGluArgProSerIleuAspGlnIleAlaAlaAspProTrpMetLeuGlyAlaAspGly 298
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 883 CTCCTGCCCCAGGCGCGCCGAGATTTCATCTGCACAGCTGTCACCATCACCCAGCAAA 942
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 299 GlyAlaProGlu---SerCysAspLeuArgLeuCysThrIleuAspPro----- 313
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 943 TAGCAGCCATTCTGTCAAGCCCTCCAGGAGAGAGAGAGCTTG 984
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 314 ---AspAspValAlaSerThrTrpSerSerSerGluSerIleu 326
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Search completed: September 22, 2005, 17:24:35
 Job time : 42.242 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus.n2p model

Run on: September 22, 2005, 15:57:45 ; Search time 170.006 Seconds
(without alignments)
5924.037 Million cell updates/sec

Title: US-10-705-757-3

Perfect score: 2443

Sequence: 1 gggatgctctgtcccaagat.....ggatctaaactagacacat 1302

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+np.model -DEV=xlp
-O=/cgn21/USPTO.spool.p/US10705757/runat.22092005.115014.22122/app.query.fasta_1.5333
-DB=A.GeneSeq -QFMT=fastcan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pcpt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcpt -NORHEXC -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US10705757 @CGN_1_1_753 @runat.22092005.115014.22122 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A_GeneSeq_16Dec04: +
1: geneseqp1980s: +
2: geneseqp1990s: +
3: geneseqp2000s: +
4: geneseqp2001s: +
5: geneseqp2002s: +
6: geneseqp2003as: +
7: geneseqp2003bs: +
8: geneseqp2004s: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1668	68.3	313	5	ABG33016
2	1668	68.3	313	7	AAO19789
3	1668	68.3	313	6	ABR62938
4	1636	67.0	313	5	ABP54943
5	1636	67.0	313	5	ABG33017
6	1636	67.0	313	6	AAO19788
7	1636	67.0	313	7	ABU61613
8	1636	67.0	313	7	ABR62939
9	1636	67.0	313	7	AD55368
10	1636	67.0	313	7	ADF45083

11	1636	67.0	313	8	ADO19690	Ado19690 Human PRO
12	1636	67.0	313	8	ADR88370	Adr88370 Human PIM
13	1636	67.0	313	8	ADP24227	Adp24227 PRO polyp
14	1623	66.4	313	2	AAW08139	Aaw08139 Human CRT
15	1623	66.4	313	3	AAH87959	Aah87959 Human CR7
16	1623	66.4	313	8	AD157202	Ad157202 Human PIM
17	1623	66.4	313	8	ADN03170	Adn03170 Human PIM
18	1584	64.8	313	5	ABG33015	Abg33015 Mouse pro
19	1584	64.8	313	6	AAO19790	Aao19790 Murine PI
20	1584	64.8	313	7	ABR62940	Abrc62940 Mouse ser
21	1584	64.8	313	8	ADN97347	Adn97347 Murine PI
22	1584	64.8	313	8	ADR88371	Adr88371 Mus muscu
23	1345	55.1	253	8	AD157241	Ad157241 PIM1 dom1
24	1304.5	53.4	257	2	AAV43942	Aav43942 Rat prote
25	1267.5	51.9	254	8	ADK71853	Adk71853 Human kin
26	1140	46.7	323	8	ADR88376	Adr88376 Colutrinix
27	1138.5	46.6	326	2	AAV06886	Aav06886 HWHH20 P
28	1136.5	46.5	326	4	AAAB29788	Aab29788 Human ser
29	1136.5	46.5	326	5	AAE23834	Aae23834 Human HKI
30	1136.5	46.5	326	5	ABG33011	Abg33011 Human ser
31	1136.5	46.5	326	7	ABR62932	Abrc62932 Human pro
32	1136.5	46.5	326	8	ADU96625	Adu96625 Human cal
33	1136.5	46.5	326	8	ADL97960	Adl97960 Human PIM
34	1136.5	46.5	382	8	ADQ20314	Ado20314 Human PRO
35	1136.5	46.5	382	8	ADP55593	Adp55593 Human PRO
36	1132.5	46.4	326	6	AAO19792	Aao19792 Murine PI
37	1132.5	46.4	326	7	ABR62933	Abrc62933 Mouse pro
38	1132.5	46.4	326	8	ADO60032	Ado60032 CRH bigna
39	1132.5	46.4	326	8	ADR88375	Adr88375 Mus muscu
40	1131.5	46.3	326	5	AAO20524	Aao20524 Protein s
41	1131.5	46.3	326	6	AAO19791	Aao19791 Rat PIM3
42	1131.5	46.3	326	7	ABR62936	Abrc62936 Rat prote
43	1131.5	46.3	455	5	AAE23836	Aae23836 Rat KTD-1
44	1131.5	46.3	455	5	ABG33013	Abg33013 Rat prote
45	1131.5	46.3	455	7	AD55366	Ad55366 Rat Prote

ALIGNMENTS

RESULT 1	ABG33016	standard; protein; 313 AA.
ID	ABG33016	
XX	ABG33016;	
AC		
XX		
DT	20-DEC-2002 (first entry)	
XX		
DE	Rat protein kinase phosphorylation site #2.	
XX		
KW	HKID-1; serine/threonine kinase; cellular proliferative disorder;	
KW	differentiative disorder; cancer; hematopoietic neoplastic disorder;	
KW	acute promyeloid leukemia; APLM; Chronic myelogenous leukaemia; CML;	
KW	Waldenstrom's macroglobulinemia; WM; rat.	
XX		
OS	Rattus norvegicus.	
XX		
FN	US2002115120-A1.	
XX		
PD	22-AUG-2002.	
XX		
PF	04-OCT-2001; 2001US-00971791.	
XX		
PR	26-JAN-1999; 99US-00237543.	
XX		
PR	23-AUG-2000; 2000US-00644450.	
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
XX		
PI	Kapeller-Libermann R, Rudolph-Owen LA, Machbeth K;	
XX		
DR	WPI; 2002-712471/77.	
XX		
PT	Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting	

PT cell expressing the polypeptide with a modulator of the polypeptide.
 XX
 PS Example 3; Page 39-40; 48pp; English.

CC The invention describes a method of modulating the level or activity of
 CC human HKID-1 polypeptide, a member of serine/threonine kinase
 CC superfamily. The method involves contacting a cell expressing the
 CC polypeptide or nucleic acid with an agent to modulate the level or
 CC activity of polypeptide, or level of nucleic acid molecule. The method is
 CC useful for modulating the level or activity of HKID-1 polypeptide or
 CC polynucleotide in a subject having or predisposed to having a disorder
 CC involving cancer. Modulating HKID-1 expression or activity is useful for
 CC therapeutic purposes, for treating cellular proliferative and/or
 CC differentiative disorders including cancer or haematopoietic neoplastic
 CC disorders e.g. Acute promyeloid leukaemia (APML). Chronic myelogenous
 CC leukemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
 CC amino acid sequence of a rat protein kinase phosphorylation site

XX Sequence 313 AA:

Alignment Scores:

Pred. No.:	1,09e-128	Length:	313
Score:	1668.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	68.28%	Indels:	0
DB:	5	Gaps:	0

US-10-705-757-3 (1-1302) x ABG33016 (1-313)

QY	4	ATGCTCTTTCAGAGATCACTCCCTGGCCACCTGGCGGAGCCCTTTCAGACCTTG	63
DB	1	MetLeuLeuSerIyrlaLeuSerLeuAlaHisLeuArgLalaIaProCySaNaAspLeu	20
QY	64	CAGGCCCAACAGCTGGCGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	123
DB	21	HisAlaAsnIySLeuAlaProGlyLysGluLysGluProLeuIuSerGlnTyrglnVal	40
QY	124	GAGCCGCTGTGGGAGCGGCTGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCG	183
DB	41	GlyProLeuLeuSerIySLeuSerGlyLysGlySerValIySLeuSerIySLeuSerIyS	60
QY	184	AACCTTGGCGTGGCCATCAAGACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	243
DB	61	AsnLeuProValAlaIleIySHisValGluLysAspArgLysSerAspTrpGlyIuLeu	80
QY	244	CCCAAGGCGACCCGAGTGGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	303
DB	81	ProAsnGlyThrArgValProMetGluValIleuLeuIySValSerSerGlyPhe	100
QY	304	TGCGGCGCTATTGACTTTCGAGCTGGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	363
DB	101	SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleuLeu	120
QY	364	GAGAGGCGCCGAGACCCGTCAGACCTTTCGACTTATCAACGAGAGAGAGAGAGAGAG	423
DB	121	GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln	140
QY	424	GAGAGAGTGGCGCGGAGCTTCTTGGCAGAGTCTGAGAGAGAGAGAGAGAGAGAGAG	483
DB	141	GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn	160
QY	484	TGGGAGGTTCTCCAGCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	543
DB	161	CysGlyValIleuLeuHisArgAspIleIySAspGluAsnIleLeuIleAspLeuAsnArgGly	180
QY	544	GAACTCAAACTCATTCGCTTGGGCTGGGCGCGCTGTCAGAGACAGCTTACAGAGAC	603
DB	181	GluLeuIySLeuIleAspPheGlySerGlyAlaLeuLeuIySAspThrValTyThrAsp	200
QY	604	TTTGAGAGGAAACCGAGGTACAGTCTCCGAGAGTGGATTGCTACCATCGTACACGCG	663
DB	201	PheAspGlyThrArgValTySerProGluTrpIleArgTyHisArgTyHisArgGly	220

QY	664	AGTGGCGCTGCTGTGGTCCCTGGGAGTCTGTCTATGACATGAGTCTGGGAGATATT	723
DB	221	ArgSerAlaHisValTrpSerLeuGlyIleLeuLeuTyArgPheMetValCysGlyAspIle	240
QY	724	CCATTGAGCAGCAGAGAGAGAGTCTCAAGGCGCAAGTACTTTCAGGAAAGGCTCTT	783
DB	241	ProPheGluHisAspGluGluIleValIySValIySValIySValIySValIySValIyS	260
QY	784	TGAGATGTCACATCTTATTGATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	843
DB	261	SerGluCysGlnHisLeuLeuIleArgTyPheLeuSerLeuArgProSerAspArgProSer	280
QY	844	TTTGAAGAAATCCAGAACCATCCGTGAGATGAGATGTTCTCTGCGCCAGGCGCACCGC	903
DB	281	PheGluGluIleGlnHisHisProTrpMetGlnAspValLeuLeuProGlnIleThrAla	300
QY	904	GAGATTTCATTCGACAGCCCTGTCACCATCACCAGCAAA	942
DB	301	GluIleHisLeuHisSerLeuSerProSerProSerLys	313

RESULT 2

AA019789 standard, protein, 313 AA.

AA019789;

11-AUG-2003 (first entry)

Rat PIM1 kinase.

Rat, PIM1 kinase, PIM3 kinase, pain; analgesic.

Rattus sp.

W0200293173-A2.

21-NOV-2002.

13-MAY-2002; 2002MO-BP005234.

11-MAY-2001; 2001DE-01023055.

(CHEF) GRUENENTHAL GMBH.

Weine E, Schaefer MK;

WPI; 2003-120715/11.

N-PSDB; ABZ69187.

Method for identifying analgesics, useful particularly for treating chronic pain, by screening compounds for interaction with PIM-1 or -3 kinase, or related compounds.

Claim 1; Fig 1D; 97pp; German.

The present invention relates to a method of identifying pain-regulating compounds, involving screening candidate compounds for interaction with PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are useful for treating chronic pain, particularly of neuropathic or inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or neurodegenerative diseases). The present sequence is rat PIM1 kinase

Sequence 313 AA;

Alignment Scores:

Pred. No.:	1,09e-128	Length:	313
Score:	1668.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	68.28%	Indels:	0
DB:	6	Gaps:	0

US-10-705-757-3 (1-1302) x AAO19789 (1-313)

```

QY 4 ATGCTCTTGTCCAAAGATCAACTCCCTGGCCCACTGGCGGAGCCCTTGCAAGACCTG 63
DB 1 MetIeuLeuSerIysIleAsnSerLeuAlaHisLeuArgAlaIleProCysAsnAspLeu 20
QY 64 CAGCCCAACAAGCTGGCGGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
DB 21 HisAlaAsnIleuAlaProGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 40
QY 124 GGGCCGCTGTGGGACAGCGGTGGCTTGGCTGGCTTACTCGGAGCATCCGCTGGCCGAC 183
DB 41 GlyProLeuLeuGlySerGlyIleGlyPheGlySerValIleArgValAlaAsp 60
QY 184 AACTTGGCGGTGGCCATCAAGCAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
DB 61 AsnIleuProValAlaIleIleValHisValGlyIleAspArgIleSerAspTrpGlyIle 80
QY 244 CCGAAGGAGCAGCGAGTGGCCATGGAAGTGGCTGCTGGAAGAGAGAGAGAGAGAGAG 303
DB 81 ProAsnGlyThrArgValIleProMetGluValValLeuLeuIleuValSerSerGlyPhe 100
QY 304 TCGGGCGCTCATTAAGTCTGACTGGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 363
DB 101 SerGlyValIleIleArgLeuLeuAspTrpPheGlyIleArgProAspSerPheValIleLeu 120
QY 364 GAGAGGCGGAGCAGCGGTGGCAAGCTTCTGACTTCATCACCGAGCGAGAGAGAGAGAG 423
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 424 GAGAGAGTGGCGGAGAGCTTCTTGGCAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 483
DB 141 GluGlnIleuAlaIleArgSerPheIleTrpGlnValLeuIleuAlaValAlaGlySerHisAsn 160
QY 484 TGGCGGGATTCTCCAGCCGAGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
DB 161 CysGlyValIleuIleHisArgAspIleIleValAspGluAsnIleuIleAspLeuAlaGly 180
QY 544 GAACTCAAACTCATTCGACTTGGGGTGGGGGCGCTGGTCAAGAGACAGATCTACAGGAC 603
DB 181 GluIleuIleuIleAspPheGlySerGlyAlaIleuIleuIleAspTrpValIleTrpAsp 200
QY 604 TTGAGCGGAGCAGCGAGTGTACAGTCTCCAGAGTGGATTGGTACCATCGCTACACAGGC 663
DB 201 PheAspGlyThrArgValIleTrpSerProGluTrpIleArgTrpHisAspGlyTrpHisGly 220
QY 664 AGGTGGCGCTGTGGTGGTGGTGGGAGTCTGCTATGACATGGTCTGCGGAGATATT 723
DB 221 ArgSerAlaIleValIleTrpSerLeuGlyIleuIleuIleuIleuIleuIleuIleuIle 240
QY 724 CCATTGGAGCAGCAGAGAGATCGTCAAGGGGCAAGTGAATTGAGCAAGAGGTCTCT 783
DB 241 ProPheGlnIleHisArgIleGluIleValIleValIleGlnAlaIleArgGlnAlaValSer 260
QY 784 TCGAATGTCAACATCTTATTAGATGGTGGCTGTCTCTGAGACCATGGAGCGGCGCTCC 843
DB 261 SerGlyCysGlnIleHisLeuIleArgTrpCysLeuSerIleuArgProSerAspArgProSer 280
QY 844 TTGGAAGAATCCAGAACCATCCGTGGATGACAGATTTCTCTGCGCCGAGGAGCAAGCC 903
DB 281 PheGlnIleuIleGlnAsnHisProTrpMetGlnAspAlaIleuIleuProGlnAlaTrpAla 300
QY 904 GAGATTCATCTGACAGAGCTGTGACCATCAAGCAGCAAA 942
DB 301 GluIleHisLeuHisSerIleuSerProSerIleuSer 313

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RESULT 3

ABR62938 standard; protein; 313 AA.

XX ABR62938;
 XX ABR62938;
 XX DT 04-DEC-2003 (first entry)

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XX DE Rat serine/threonine protein kinase PIM-1.
XX KM Rat; PIM-1; protein kinase; enzyme.
XX OS Rattus norvegicus.
XX PN W02003060130-A2.
XX PD 24-JUL-2003.
XX PF 20-JAN-2003; 2003WO-BE000492.
XX PR 19-JAN-2002; 2002EP-00001401.
XX PA (AVET ) AVENTIS PHARMA DEUT GMBH.
XX PI Korn M, Mueller G, Schneider R, Teschank G;
XX DR WPI; 2003-598536/56.
XX PT New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
XX PT agent for identifying anti-type 2 diabetes mellitus drugs, or for
XX PT treating insulin resistance or type 2 diabetes mellitus.
XX PS Example 2; Page 39; 40pp; English.
XX CC The present sequence is the protein sequence of the rat serine/threonine
XX CC protein kinase and proto-oncogene, PIM-1. PIM-1 proteins are the
XX CC paralogs of novel human and murine PIM-3 proteins (see ABR62932 and
XX CC ABR62933) of the invention, which are therefore expected to be involved
XX CC in cancer and cell growth regulation. PIM-3 is also involved in the
XX CC development of insulin resistance and type 2 diabetes mellitus. The
XX CC invention relates to the use of PIM-3 nucleic acids and proteins in:
XX CC screening assays for compounds that modulate insulin resistance or type 2
XX CC diabetes mellitus; detection assays for detecting insulin resistance or
XX CC type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
XX CC forensic biology); predictive medicine (e.g. diagnostic or prognostic
XX CC assays, monitoring clinical trials, pharmacogenomics); and for the
XX CC preparing a medicament for the treatment of insulin resistance or type 2
XX CC diabetes mellitus
XX SQ Sequence 313 AA;
XX Alignment Scores:
XX Pred. No.: 1,09e-128 Length: 313
XX Score: 1668.00 Matches: 313
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 68.28% Indels: 0
XX DB: 7 Gaps: 0
US-10-705-757-3 (1-1302) x ABR62938 (1-313)
QY 4 ATGCTCTTGTCCAAAGATCAACTCCCTGGCCCACTGGCGGAGCCCTTGCAAGACCTG 63
DB 1 MetIeuLeuSerIysIleAsnSerLeuAlaHisLeuArgAlaIleProCysAsnAspLeu 20
QY 64 CAGCCCAACAAGCTGGCGGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
DB 21 HisAlaAsnIleuAlaProGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGly 40
QY 124 GGGCCGCTGTGGGACAGCGGTGGCTTGGCTGGCTTACTCGGAGCATCCGCTGGCCGAC 183
DB 41 GlyProLeuLeuGlySerGlyIleGlyPheGlySerValIleArgValAlaAsp 60
QY 184 AACTTGGCGGTGGCCATCAAGCAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
DB 61 AsnIleuProValAlaIleIleValHisValGlyIleAspArgIleSerAspTrpGlyIle 80
QY 244 CCGAAGGAGCAGCGAGTGGCCATGGAAGTGGCTGCTGGAAGAGAGAGAGAGAGAGAG 303
DB 81 ProAsnGlyThrArgValIleProMetGluValValLeuLeuIleuValSerSerGlyPhe 100

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QY 304 TCGGGCGCTATTGACTTCTGACTGATTCGAGAGCCCGATAGTTCTGCTGATCTTG 363
    |||||
    |||||
    |||||
Db 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120
QY 364 GAGAGGCCCGAACCCCGTCGACAGACTCTTCTGACTTCATCCGAGCGAGAGCCCTCCAG 423
    |||||
    |||||
    |||||
Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 424 GAGAGCTGGCCGGAGCTTCTTCTGAGAGTGTGAGGCGCGTGGGCGATTCGCCAAC 483
    |||||
    |||||
    |||||
Db 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisAsn 160
QY 484 TCGGGGTTCTCCACCGCGCATCAAGACGAGAACATCTTAACTGACCTGAACCGCGC 543
    |||||
    |||||
    |||||
Db 161 CysGlyValLeuHisArgAspIleIleYAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY 544 GAACTCAAACTCATGCACTTCGGGTCGGGGCGCTGCTCAAGACACAGCTTACAGGAC 603
    |||||
    |||||
    |||||
Db 181 GluLeuIleLeuIleAspPheGlySerGlyAlaLeuLeuIleAspThrValTyrThrAsp 200
QY 604 TTGAGAGAACCCGAGTGTACACTCTCCAGAGTGTGATTCGCTACCATGCTTACCAAGC 663
    |||||
    |||||
    |||||
Db 201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
QY 664 AGCTCGGCTGCTGTTGCTGCTGCGGAGATCTGCTATGACATGCTGCGGAGATATT 723
    |||||
    |||||
    |||||
Db 221 ArgSerAlaIleValIleTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
QY 724 CCATTGAGACGACGAGAGATGCTGACAGGCGCAAGTGTACTTTAGCGAAAGGCTCT 783
    |||||
    |||||
    |||||
Db 241 ProPheGluHisAspGluGluIleValIleValIleValIleValIleValIleValIle 260
QY 784 TCAGAAATGCAATCTTATTAGATGCTGCTGCTGCTGAGACATCGGACCGGCGCTCC 843
    |||||
    |||||
    |||||
Db 261 SerGluCysGluHisLeuIleArgTrpCysLeuSerLeuArgProSerAspArgProSer 280
QY 844 TTGAGAAATCCAGAACATCCGTCGATGACAGATGTTCTCTGCGCCAGGCGCACCGC 903
    |||||
    |||||
    |||||
Db 281 PheGluGluIleGlnHisAspTrpMetGlnAspValLeuLeuProGlnIleThrAla 300
QY 904 GAGATTTCATCTGCAAGCTGTGACCATCAACCCAGCAA 942
    |||||
    |||||
    |||||
Db 301 GluIleHisLeuHisSerLeuSerProSerProSerIle 313

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RESULT 4
ABP54943
ID ABP54943 standard; protein; 313 AA.

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XX AC ABP54943;
XX DT 13-JAN-2003 (first entry)
XX DE Human Pim1.
XX KM Pim1; tyrosine threonine kinase; TTK; protein kinase; enzyme;
XX KM mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;
XX KM human; gene therapy.
XX OS Homo sapiens.
XX PN MO200268444-A1.
XX PD 06-SEP-2002.
XX PF 21-FEB-2002; 2002MO-US005278.
XX PR 21-FEB-2001; 2001US-0271254P.
XX PA (CHIR ) CHIRON CORP.
XX PI Reinhard C, Jefferson AB, Chan WM,
XX

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DR WPI; 2002-698650/75.
DR N-PSDB; ABV733989.
XX
XX Reducing growth of cancer cells comprises reducing Tyrosine Threonine
PT Kinase (TTK) activity, useful in diagnosing and treating disorders with
PT abnormal expression levels and activity of TTK, such as lung, colon,
PT prostate and ovarian cancer.
XX
XX Disclosure; Page 80-81; 113pp; English.
XX
XX The present sequence is the protein sequence of human Pim1, a protein
CC related to tyrosine threonine kinase (TTK, see ABP54938). TTK
CC polynucleotides and polypeptides of the invention encompass
CC polynucleotides and polypeptides having sequence similarity or sequence
CC identity to human TTK and other genes and gene products related to TTK,
CC such as Pim1. The invention is based on the finding that TTK is
CC differentially expressed in various forms of cancer. It provides methods
CC for the identification of cancerous cells, especially breast cancer and
CC colon cancer cells, by detection of expression levels of TTK, as well as
CC diagnostic, prognostic and therapeutic methods. These methods can be used
CC as the basis of rational therapy. Assays for identifying molecules that
CC modulate the activity of these genes in cancers, as well as methods of
CC inhibiting tumour growth by inhibiting the activity of TTK are also
CC provided
XX
XX SQ Sequence 313 AA;
XX
XX Alignment Scores:
XX Score: 4.75e-126 Length: 313
XX Percent Similarity: 1636.00 Matches: 304
XX Best Local Similarity: 99.04% Conservative: 6
XX Query Match: 97.12% Mismatches: 3
XX DB: 66.97% Indels: 0
XX Gaps: 0
XX
XX US-10-705-757-3 (1-1302) x ABP54943 (1-313)

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QY 4 ATGCTCTTGTCCAGATCACTCCCTGCGCCACCTGCGCGACCCCTTGCACGACCTG 63
    |||||
    |||||
    |||||
Db 1 MetLeuLeuSerLeuIleAsnSerLeuAlaHisLeuArgAlaIleProCysAsnAspLeu 20
QY 64 CAGGCCCAACAGCTGGCGCGCGGCAAGAGAGAGCCCTTGAGTCCGACGTACCAAGTG 123
    |||||
    |||||
    |||||
Db 21 HisAlaThrIleValLeuAlaProGluIleValGluIleValGluIleValGluIleVal 40
QY 124 GGGCGCGTGTGGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
    |||||
    |||||
    |||||
Db 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
QY 184 AACTTGCCGTTGGCATCAGACGCTGGAAGAGACCGGATTTCCGACTGGGGAGAACTG 243
    |||||
    |||||
    |||||
Db 61 AsnLeuProValAlaIleIleHisValGluYAspAspArgIleSerAspTrpGlyIleLeu 80
QY 244 CCAACGCGACCCGAGTGCCTGAGAGTGTCTGCTGAGAGAGTGAAGTGTGCGGCTTC 303
    |||||
    |||||
    |||||
Db 81 ProAsnGlyThrArgValProMetGluValValLeuLeuIleValValSerSerGlyPhe 100
QY 304 TCGGGCGCTATTGACTTCTGACTGATTCGAGAGCCCGATAGTTCTGCTGATCTTG 363
    |||||
    |||||
    |||||
Db 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120
QY 364 GAGAGGCCCGAACCCCGTCGACAGACTCTTCTGACTTCATCCGAGCGAGAGCCCTCCAG 423
    |||||
    |||||
    |||||
Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 424 GAGAGCTGGCCGGAGCTTCTTCTGAGAGTGTGAGGCGCGTGGGCGATTCGCCAAC 483
    |||||
    |||||
    |||||
Db 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisAsn 160
QY 484 TCGGGGTTCTCCACCGCGCATCAAGACGAGAACATCTTAACTGACCTGAACCGCGC 543
    |||||
    |||||
    |||||
Db 161 CysGlyValLeuHisArgAspIleIleYAspGluAsnIleLeuIleAspLeuAsnArgGly 180

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QY 544 GAACTCAAACTCATGCACTTCGGGGTGGGGGGCGCTGCTCAAGACACAGTCTACAGGAC 603
 |||||
 DB 181 GILUULYLEULILEAPHPHEGLYSERGLYALALEULYVAPINRVALYTRHASP 200
 |||||
 QY 604 TTGACGGAACCCGAGTGTACAGTCTTCAGAGTGTATGCTACATCGCTACAGCGC 663
 |||||
 DB 201 PHEAPGLYTHARGVALYTRSERPROGLUTRPILEARGYRHSARGYRHSGLY 220
 |||||
 QY 664 AGGTGGCTGCTGTTTGGTCCCTGGGATCTGCTCTATGACATGCTGCGGAGATATT 723
 |||||
 DB 221 ARGSERIALAVALTRPSERLEUGLYILEULYUZYRHPMETVALCYSGLYASPIL 240
 |||||
 QY 724 CCATTGACGACGACGAAGATGTCAGAGGCCCAAGTGTACTTAGCGAAAGGCTCT 783
 |||||
 DB 241 PROPHGLUHSAPGLUGLILEIARGGLYGINVALPHEPHEARGINARGVALSER 260
 |||||
 QY 784 TCAGATGTCACATCTTATAGTGTGCTGCTCCCTGAGACCATCGACCGGCTCC 843
 |||||
 DB 261 SERGLUCYSGINHSLEULILEARGTRPCYLEULALALEUARGPROSERAPARGPROTHR 280
 |||||
 QY 844 TTGGAAGAAATCCAGAACATCCGTGATGACAGATGTTCTCTGCCCAGGCCACGCC 903
 |||||
 DB 281 PHEGLUGLULIEGINAPENHSIPROTRPMEGLINAPVALILEUENPROGLINGLUTRHA 300
 |||||
 QY 904 GAGATTCATCTGACAGGCTGTGACCATCAACCAGCAAA 942
 |||||
 DB 301 GLULIEHLSLEUHSERLEUSERPROGLYPROSERLYS 313
 |||||
 RESULT 5
 ABG33017
 ID ABG33017 standard; protein; 313 AA.
 AC ABG33017;
 DT 20-DEC-2002 (first entry)
 XX Human protein kinase phosphorylation site.
 DE
 KW HKID-1, berline/threonine kinase; cellular proliferative disorder;
 KM differentiative disorder; cancer; haematopoietic neoplastic disorder;
 KM acute promyeloid leukaemia; APL; Chronic myelogenous leukaemia; CML;
 KM Waldenstrom's macroglobulinaemia; WM; human.
 OS Homo sapiens.
 XX
 XX US2002115120-A1.
 PN
 XX
 PD 22-AUG-2002.
 PP 04-OCT-2001; 2001US-00971791.
 XX
 XX 26-JAN-1999; 99US-00237543.
 PR 23-AUG-2000; 2000US-00644450.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;
 XX
 DR WPI; 2002-712471/77.
 XX
 PT Modulating levels or activity of HKID-1 polypeptides, a member of
 PT berline/threonine kinase superfamily, for treating cancer, by contacting
 PT cell expressing the polypeptide with a modulator of the polypeptide.
 XX
 XX Example 3; Page 40-41; 48pp; English.
 PS
 CC The invention describes a method of modulating the level or activity of
 CC human HKID-1 polypeptide, a member of berline/threonine kinase
 CC superfamily. The method involves contacting a cell expressing the
 CC polypeptide or nucleic acid with an agent to modulate the level or
 CC activity of polypeptide, or level of nucleic acid molecule. The method is
 CC useful for modulating the level or activity of HKID-1 polypeptide or
 CC polynucleotide in a subject having or predisposed to having a disorder

CC involving cancer. Modulating HKID-1 expression or activity is useful for
 CC therapeutic purposes, for treating cellular proliferative and/or
 CC differentiative disorders including cancer or hematopoietic neoplastic
 CC disorders e.g. Acute promyeloid leukaemia (APL), Chronic myelogenous
 CC leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
 CC amino acid sequence of a human protein kinase phosphorylation site
 XX
 SQ Sequence 313 AA;
 Alignment Scores:
 Pred. No.: 4,75e-126 Length: 313
 Score: 1636.00 Matches: 304
 Percent Similarity: 99.04% Conservative: 6
 Best Local Similarity: 97.12% Mismatches: 3
 Query Match: 66.97% Indels: 0
 DB: 5 Gaps: 0
 US-10-705-757-3 (1-1302) x ABG33017 (1-313)
 QY 4 ATGCTCTTGTCCAAATCAATCTCCCTGGCCACCTGCGGACCCCTTGCAACGACTGT 63
 |||||
 DB 1 MEULEUENSERLYSILEHNSERLEUALAHLSLEUALRGAIALAProCYSAENAPLEU 20
 |||||
 QY 64 CAGCCCAACAAAGCTGGGCGCGGCAAGAGAGAGCCCTGGAGTCGACGTACAGGTG 123
 |||||
 DB 21 HIALAThrLYLEUALAPROGLYLYSGILVSGILUPROLEUENISERGLYRGLNVAL 40
 |||||
 QY 124 GGCCCGCTTGGGCAAGCGGTGCTTCGCTCGGTACTCGGACATCCGCTCGCGAC 183
 |||||
 DB 41 GLYPROLEUENCLYSERGLYGLYPHEGLYSERVALYTSERGLYILEARGVALSERAP 60
 |||||
 QY 184 AACTTGCCGGTGGCCATCAAGCAGTGTGAGAGAGACCGGATTTCCGACTGGGGGAACTG 243
 |||||
 DB 61 ASNLEUPROVALAIALELYSHLSVALGLULYASPARGLIESTERAPTRPGILULEU 80
 |||||
 QY 244 CCCACGGGACCCGAGTGGCCATGAGAGTGTCTGCTGAAGAGGTGAGCTGGGCTTC 303
 |||||
 DB 81 PROENGLYTHARGVALPROWETGLUVALILEUENLYVALSERSERGLYPHE 100
 |||||
 QY 304 TCGGCGGTATTAAGACTTTCGACTGTTGAGAGGCGCGATAGTTTCGTGATCTGT 363
 |||||
 DB 101 SERGLYVALILEARGLEUENAPTRPHEGLUARGPROASPERPHEVALILEUEN 120
 |||||
 QY 364 GAGAGGCCGGAACCCGTGCAAGACTTTCGACTTATCAACGAGGAGGACCTTCAG 423
 |||||
 DB 121 GUARGPROGLUPROVALGINAPLEUPHEAPPHIEThRGILARGLYALALEUGIN 140
 |||||
 QY 424 GAGGAGCTGGCCGGAGCTTCTTCTGGCAGGTGCTGAGGCGGTGGGCAATTCSCAAC 483
 |||||
 DB 141 GLULILEUALARGSERPHEPETHRPGINVALILEUGINLAVALARIGHISYSHASBN 160
 |||||
 QY 484 TCGGCGGTCTCCACCGGACATCAAGACGAGAACATCTTAATCGACTGAACCGCGC 543
 |||||
 DB 161 CYSGLYVALLEUHSAPGLIILEYVAPRGILUASHLILEUENLEAPLEUENAHARGLY 180
 |||||
 QY 544 GAACTCAAACTCATGCACTTCGGGTGGGGCGCTGCTCAAGACACAGTCTACAGGAC 603
 |||||
 DB 181 GILUULYLEULILEAPHPHEGLYSERGLYALALEULYVAPINRVALYTRHASP 200
 |||||
 QY 604 TTGACGGAACCCGAGTGTACAGTCTTCAGAGTGTATGCTACATCGCTACAGCGC 663
 |||||
 DB 201 PHEAPGLYTHARGVALYTRSERPROGLUTRPILEARGYRHSARGYRHSGLY 220
 |||||
 QY 664 AGGTGGCTGCTGTTTGGTCCCTGGGATCTGCTCTATGACATGCTGCGGAGATATT 723
 |||||
 DB 221 ARGSERIALAVALTRPSERLEUGLYILEULYUZYRHPMETVALCYSGLYASPIL 240
 |||||
 QY 724 CCATTGACGACGACGAAGATGTCAGAGGCCCAAGTGTACTTAGCGAAAGGCTCT 783
 |||||
 DB 241 PROPHGLUHSAPGLUGLILEIARGGLYGINVALPHEPHEARGINARGVALSER 260
 |||||
 QY 784 TCAGATGTCACATCTTATAGTGTGCTGCTCCCTGAGACCATCGACCGGCTCC 843
 |||||

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Db      261 SerGIUCyGlnHISLeuIIeArGTrpCySLeuAlaLeuArGProSerAparProtnr 280
QY      844 TTGAAGAAATCCAGAACCATCCGTGATGACAGATGTTCTCTGGCCCAAGGCCACCGCC 903
Db      281 PheGIuGIuIIeGIInsnHISProTrpMeGIInspValIleuLeuProGIInGIuInrAla 300
QY      904 GAGATTCATCTGCACAGCCTGTGCACCATCAACCCAGCAAA 942
Db      301 GIuIIeHISLeuHISerLeuSerProGIlyProSerIlyS 313

RESULT 6
AA019788 standard; protein; 313 AA.
ID      AA019788;
XX      AA019788;
AC      AA019788;
XX      11-AUG-2003 (first entry)
XX      Human PIM1 kinase.
DE      Human PIM1 kinase.
XX      KM      Human; PIM1 kinase; PIM3 kinase; pain; analgesic.
XX      OS      Homo sapiens.
XX      PN      WO200293173-A2.
XX      PD      21-NOV-2002.
XX      PF      13-MAY-2002; 2002MO-BP005234.
XX      PR      11-MAY-2001; 2001DE-01023055.
XX      PA      (CHEF ) GRUENENTHAL GMBH.
XX      PI      Weihe E, Schaefer MK;
XX      DR      WPI; 2003-120715/11.
XX      N-PSDB; ABZ69186.
XX      PT      Method for identifying analgesics, useful particularly for treating
XX      PT      chronic pain, by screening compounds for interaction with PIM-1 or -3
XX      PT      Kinase, or related compounds.
XX      PS      Claim 1; Fig 1B; 97pp; German.
XX      CC      The present invention relates to a method of identifying pain-regulating
XX      CC      compounds, involving screening candidate compounds for interaction with
XX      CC      PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
XX      CC      useful for treating chronic pain, particularly of neuropathic or
XX      CC      inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
XX      CC      neurodegenerative diseases). The present sequence is human PIM1 kinase
XX      SQ      Sequence 313 AA;

Alignment Scores:
Pred. No.:      4,75e-126      Length:      313
Score:          1636.00      Matches:      304
Percent Similarity: 99.04%      Conservative: 6
Beet Local Similarity: 97.12%      Mismatches: 3
Query Match:    66.97%      Indels:      0
DB:            Gaps:          0

US-10-705-757-3 (1-1302) x AA019788 (1-313)
QY      4 ATGCTCTTGTCAAGATCAACTCCCTGGCCCAAGCCCTTGCACAGACTG 63
Db      1 MetLeuLeuSerIlySIIeAnSerLeuAlaHISLeuArGIaIaIaProCySAnAaPLeu 20
QY      64 CAGGCCAAAGACTGGGCGCGCAAGAGAGAGGCCCTGGAGTGCAGTCCAGGTG 123
Db      21 HIsIaIaThrIlySLeuAlaProGIlyGIuIlySLeuGIuProLeuGIuSerGIInrGIuInAl 40
QY      124 GGCCCGCTGTGGGCAAGCGGTGGCTTGGCTCGGCTTAATCGGACATCCGCTCGCGAC 183

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Db      41 GIyProLeuGIySerGIyGIyPheGIySerValIySerGIyIleArGIaIaSerAaP 60
QY      184 AACTTGGCCGCGTGGCCATCAAGACAGTGGAGAGACCCGGAATTTCCGACCTGGGGGAAACAG 243
Db      61 AenLeuProValAlaIleIySIIeValGIuIyAaPArGIleSerAaPTrpGIyGIuIleu 80
QY      244 CCCAAGCGGACCCGAGTGGCCCATGGAAAGTGTCTCTGTCTAAGAAAGGTGAGTCTCGGCTTC 303
Db      81 ProAnGIyThrArGIaIaProMeGIuValIleValIleuIleuIySIIeValIeSerGIlyPhe 100
QY      304 TCGGGCGTCAATTAAGACTTGTGACCTGGTTCGAGAGGCCGAGATATTTCTGTGATCTTG 363
Db      101 SerGIyValIIeArGIeLeuAaPTrpPheGIuArGIProAaSPSerPheValIleuIIeLeu 120
QY      364 GAGAGGCCGGAACCCGTGGAAGACCTCTTCGACTTCATACACGAGGAGAGACCCCTCCAG 423
Db      121 GIuArGIProGIuProValGIInAaPLeuPheAaPheIIeThrGIuArGIyGIaIaLeuGIIn 140
QY      424 GAGAGACTGGCCGAGCTTCTTGTGACAGTGTGTGAGAGCCGTGCGGACATTTGCCACAAC 483
Db      141 GIuGIuLeuAlaArGIserPheThrGIInValIleuGIuAlaValaIaArGIIScySIIeAaP 160
QY      484 TCGGGGTTTCTCCACCGGCACATCAAGAGAGAACATTTAATGACCTTGAACCGCGGC 543
Db      161 CySIIyValIleuHISArGIaPHeIIeIySIIeAaPHeIIeIleuIIeAaPLeuAaPArGIly 180
QY      544 GAATCAACATCATGACATCTCGGTCGGGGGGGCGCTGCAAGGACACATCTTACAGAGAC 603
Db      181 GIuLeuIyAaPLeuIIeAaPHeIIeSerPheGIySerGIyAlaLeuIyAaPHeIIeThrValIyTrnAaP 200
QY      604 TTGAAGAAATCCAGAACCATCCGTGATGACAGATGTTCTCTGACATCCATCCATCAACAGCC 663
Db      201 PheAaPGIyThrArGIaIyIySerProArGIuInrIleArGIyThIISArGIyTrnISGIly 220
QY      664 AGGTGGCTGTGTTGTTGCTCTGGGATCTGTCTTATGACATGGTCTGGGAGATATT 723
Db      221 ArGIserAlaIaIaValTrpSerLeuGIyIleLeuLeuIyAaPMeValCySIIyAaPHeIIe 240
QY      724 CCATTTGACACAGAGAGATCCGCAAGGGCCAAAGTCAATTTTGGAAAGGCTCTG 783
Db      241 ProPheGIuHISaAaPGIuGIuIIeIleArGIyGIInValIlePheAaPHeIIeArGIaIaSer 260
QY      784 TCGAATGTCAACATCTTATTAAGATGATGCTGTCCCTGAGACCATCGAGCCGCTCC 843
Db      261 SerGIUCyGlnHISLeuIIeArGTrpCySLeuAlaLeuArGProSerAparProtnr 280
QY      844 TTGAAGAAATCCAGAACCATCCGTGATGACAGATGTTCTCTGCCCCAGGCCACCGCC 903
Db      281 PheGIuGIuIIeGIInsnHISProTrpMeGIInspValIleuLeuProGIInGIuInrAla 300
QY      904 GAGATTCATCTGCACAGCCTGTGCACCATCAACCCAGCAAA 942
Db      301 GIuIIeHISLeuHISerLeuSerProGIlyProSerIlyS 313

RESULT 7
ABU61613
ID      ABU61613 standard; protein; 313 AA.
XX      ABU61613;
AC      ABU61613;
XX      11-AUG-2003 (first entry)
XX      Human PIM1 protein.
XX      KM      Human; tyrosine kinase; TTK; cancer; cytostatic;
XX      KM      mitotic checkpoint gene; PIM1.
XX      OS      Homo sapiens.
XX      PN      US2003045491-A1.
XX      PD      06-MAR-2003.

```

XX 21-FEB-2002; 2002US-00081119.
 PF 23-FEB-2001; 2001US-0289813P.
 PR (REIN/) REINHARD C.
 PA (JEFF/) JEFFERSON A B.
 PA (CHAN/) CHAN V W.
 PI Reinhard C, Jefferson AB, Chan VW;
 XX WPI; 2003-45656/43.
 DR N-PSDB; ACA62265.
 XX
 PT Detecting cancer in a subject, by comparing expression levels of tyrosine
 PT threonine kinase polypeptide or polynucleotide in a subject cell and a
 PT normal cell, where an increase in the expression level in the test cell
 PT is indicative of cancer.
 PS
 PS Disclosure; Page 34-35; 79pp; English.
 XX
 XX The invention relates to detecting cancer (other than ovarian cancer) in
 CC a subject, comprising comparing the expression levels of tyrosine
 CC threonine kinase (TRK, a mitotic checkpoint gene) polypeptide or
 CC polynucleotide in a test cell obtained from the subject and in a normal
 CC non-cancer cell, where an increase in the expression level of TRK protein
 CC or nucleic acid in the test cell compared to that in the normal cell,
 CC indicates the presence of cancer other than ovarian cancer. Also included
 CC are reducing growth of a cancerous cell (by contacting a cancerous cell
 CC with an amount of an agent effective to reduce TRK polypeptide activity
 CC in the cell), an assay for identifying a candidate agent that reduces
 CC growth of a cancerous cell (comprising: (i) detecting the activity of a
 CC TRK polypeptide in the presence of a candidate agent; and (ii) comparing
 CC the activity of TRK polypeptide activity in the presence of a candidate agent
 CC relative to TRK polypeptide activity in the absence of the candidate
 CC agent), identifying an agent that reduces TRK activity (comprising: (i)
 CC contacting a cancerous cell displaying elevated expression of a TRK-
 CC encoding polynucleotide with a candidate agent; and (ii) determining the
 CC effect of the candidate agent on TRK polypeptide activity) and assessing
 CC the prognosis of a cancerous disease other than ovarian cancer in a
 CC subject (comprising: (i) detecting expression of TRK -encoding
 CC polynucleotide in a test cancer cell of a subject; and (ii) comparing a
 CC level of expression of TRK-encoding polynucleotide in the test cancer
 CC cell with a level of expression of the polynucleotide in a control non-
 CC cancer cell, where the level of expression of TRK in the test cancer cell
 CC relative to the level of expression in the control non-cancer cell is
 CC indicative of the prognosis of the cancerous disease). The methods are
 CC useful for detecting cancer (other than ovarian cancer) in a subject,
 CC reducing growth of a cancerous cell, identifying a candidate agent that
 CC reduces growth of a cancerous cell, identifying an agent that reduces TRK
 CC activity and assessing the prognosis of a cancerous disease other than
 CC ovarian cancer. The methods are also useful for determining the ability
 CC of a subject to respond to a particular therapy e.g. as a basis of
 CC rational therapy. The present sequence represents a closely related
 CC protein to human TRK, in this case human PIM1 (not defined)
 XX
 XX Sequence 313 AA,
 SO
 Alignment Scores:
 Pred. No.: 4,75e-126 Length: 313
 Score: 1636.00 Matches: 304
 Percent Similarity: 99.04% Conservative: 6
 Best Local Similarity: 97.12% Mismatches: 5
 Query Match: 66.97% Indels: 0
 DB: 7 Gaps: 0
 US-10-705-757-3 (1-1302) x ABU61613 (1-313)
 QY 4 ATGCTCTTTCAGAGTCAACTCCCTGGCCGACAGCCCTTTCAGACGACTG 63
 DB 1 MetLeuLeuSerIySrlaenSerIeulAlhIsIeulrIglAlaIaProCySaenAapIeu 20
 QY 64 CAGGCCAAGAGTGGCGCGGCAAGAGAGAGCCCTGGAGTGCAGTACAGGTG 123

DB 21 HisAlaThrIySleuAlaProGlyIySglIySglIyProIeuGluSerGlnrIglInVal 40
 QY 124 GGCCTGCTGTGGCAGCGGTGGCTTCGGCTCGGTCTACTCGGACATCGCGTCCGAC 183
 DB 41 GlyProIeuLeuGlySerGlyGlyPheGlySerValrIySerGlyIleArgValSerAsp 60
 QY 184 AACTGCGCGTGGCCATTCAGACGCGGAGAGGACCGGATTCGACCTGGGGGAACTG 243
 DB 61 AsnIeuProValAlaIleIyShIeValGluIyAspArgIleSerAspTrpGlyIleu 80
 QY 244 CCCAGCGACCCGAGTGGCCATTCAGAGTGTCTCTGTAAGAAGGTGAGCTCGGCTTC 303
 DB 81 ProAsnGlyThrArgValProMetGluValIleuLeuIySValSerSerGlyPhe 100
 QY 304 TCGGCGTCAATTAGACTTTCGACTGCTGAGAGGCGCGATAGTTTCTGCTGACTG 363
 DB 101 SerGlyValIleArgIeuLeuAspTrpPheGluArgProAspSerPheValIleu 120
 QY 364 GAGAGGCCGAGACCCGTCGAGACCTTCGACTTCATGACCGAGGAGGACCCCTCCG 423
 DB 121 GluArgProGluProValGlnAspIeuPheAspPheIleThrGluArgGlyAlaIeuGln 140
 QY 424 GAGGACTGGCCGAGCTTCTTCTGGCAGGTGCTGAGGCGCGGACATTCGACCAAC 483
 DB 141 GluGluIeuAlaArgSerPhePheTrpGlnValIleuGlnAlaValArgIleScyShIaSn 160
 QY 484 TCGGGGTTCTCCACCGGACATCAAGACGAGACATCTTAATGACCTGAACCGCGGC 543
 DB 161 CyGlyValIleuHisArgAspIleIySAspGluAsnIleuIleAspIeuAsnAArgGly 180
 QY 544 GAACCTCAATCTATGCACTTCGGGTGGGGGCGCTGCTCAAGACACATCTTCACGGAC 603
 DB 181 GluIeuIySleuIleAspPheGlySerGlyAlaIleuIySAspThrValrIyTrnAsp 200
 QY 604 TTGACGGAACCCGAGTGTACAGTCTCCAGAGTGGATTGCTACCATCGCTTCCACGCG 663
 DB 201 PheAspGlyThrArgValrIySerProProGluTrpIleArgTrIyHisArgTrIySgIy 220
 QY 664 AGGTGGCTGCTGTGTTGGTCCCTGGGGAATCTGCTCTATGACATGGTCTGGGATATT 723
 DB 221 ArgSerAlaAlaValrIyPheIleuGlyIleIleuLeuTrIyAspMetValCySgIyAspIle 240
 QY 724 CCATTGACGACGACGAAGATCTGCAAGGGCCAGTGTACTTTGGCAAGGCTCTCT 783
 DB 241 ProPheGluHisAspGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
 QY 784 TCAGATGTCAACATCTTATTAGATGGTGGCTGCTCCCTGAGACATCGGACCGGCTTC 843
 DB 261 SerGluCySgIinHisIleuIleArgTrIyCySleuAlaIeuArgProSerAspArgProThr 280
 QY 844 TTGAAGAATAATCCAGAACCATTCGATGATGACAGATGTTCTCTGCGCCAGGACCGCC 903
 DB 281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValIleuLeuProGlnGluTrnAla 300
 QY 904 GAGATTCATCTGACAGCTCTGTCACATCAACCCAGCAA 942
 DB 301 GluIleHisIeuHisSerIeuSerProGlyProSerIyS 313
 RESULT 8
 ABR62939
 ID ABR62939 standard; protein; 313 AA.
 AC ABR62939;
 XX
 XX 04-DEC-2003 (first entry)
 XX
 DE Human serine/threonine protein kinase PIM-1.
 XX Human; PIM-1; protein kinase; enzyme.
 KW Human;
 XX Homo sapiens.
 OS

PN MO2003060130-A2.
 XX 24-UTL-2003.
 XX 20-JAN-2003; 2003MO-EP000492.
 PF 19-JAN-2002; 2002EP-00001401.
 XX (AVER) AVENTIS PHARMA DEUT GMBH.
 PA Korn M, Mueller G, Schneider R, Tschank G;
 PI WPI; 2003-598536/56.
 DR
 XX
 PT New human or murine P1M-3 DNAs or polypeptides, useful for as a screening
 agent for identifying anti-type 2 diabetes mellitus drugs, or for
 PT treating insulin resistance or type 2 diabetes mellitus.
 XX
 PS Example 2; Page 40; 40pp; English.
 CC The present sequence is the protein sequence of the human
 CC serine/threonine protein kinase and proto-oncogene, P1M-1. P1M-1 proteins
 CC are the paralogues of novel human and murine P1M-3 proteins (see ABR62932
 CC and ABR62933) of the invention, which are therefore expected to be
 CC involved in cancer and cell growth regulation. P1M-3 is also involved in
 CC the development of insulin resistance and type 2 diabetes mellitus. The
 CC invention relates to the use of P1M-3 nucleic acids and proteins in:
 CC screening assays for compounds that modulate insulin resistance or type 2
 CC diabetes mellitus; detection assays for detecting insulin resistance or
 CC type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
 CC forensic biology); predictive medicine (e.g. diagnostic or prognostic
 CC assays, monitoring clinical trials, pharmacogenetics); and for the
 CC preparing a medicament for the treatment of insulin resistance or type 2
 CC diabetes mellitus
 CC
 XX
 SQ Sequence 313 AA;
 Alignment Scores:
 Pred. No.: 4.75e-126 Length: 313
 Score: 1636.00 Matches: 304
 Percent Similarity: 99.04% Conservative: 6
 Best Local Similarity: 97.12% Mismatches: 3
 Query Match: 66.97% Indels: 0
 DB: 7 Gaps: 0
 US-10-705-757-3 (1-1302) x ABR62939 (1-313)
 QY 4 ATGCTTTGTCAAGATCAATCCCTGGCCACCTGGCGCAGCCCTTGCAAGACTTG 63
 DB 1 MetLeuLeuSerIySrlEaNsErLeuAlhIeLnuKrgAlaIaIaProCySaNdAplLeu 20
 QY 64 CAGGCCCAACAAGCTGGGGCGGCGGCAAGAAGAGCCCTGGAGTGCAGTCCAGTGT 123
 DB 21 HlaIaIaThryIySrlEaNsErLeuAlhIeLnuKrgAlaIaIaProCySaNdAplLeu 40
 QY 124 GGGCCGCTGTTGGGAGCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 183
 DB 41 G1PProLeuLeuG1ySrlEaNsErLeuAlhIeLnuKrgAlaIaIaProCySaNdAplLeu 60
 QY 184 AACCTGGCGGTGGCCATCAAGCAGGTGAGAGAGAGCCGATTCGATGGGAGAACTG 243
 DB 61 AsnLeuProValaIaIeLySHIaIaG1uIySaNsErIySrlEaNsErIySrlEaNsEr 80
 QY 244 CCCAAGCGGACCCGAGTGGCCATGGAAGTGTCTGCTGGAAGAAGGTGAGTGGGCTTC 303
 DB 81 ProAsnG1yThryIySrlEaNsErLeuAlhIeLnuKrgAlaIaIaProCySaNdAplLeu 100
 QY 304 TCGGGCGCTGATTGACTTGTGAGTGGTGGAGAGCCGATGTTGCTGCTGATGATCTG 363
 DB 101 SerG1yValIleAlaG1yLeuLeuAAsPTrpPheG1uIyGTrProAspSerPheValIleLeu 120
 QY 364 GAGAGGCCGGAACCCGTGCAAGACCTTTCGACTTTCATCAACGAGCGAGAGCCCTTCAG 423

DB 121 GluArGProGluProValG1nAAsPLeuPheAsPheIleThrG1uArG1yAlaLeuG1n 140
 QY 424 GAGGAGCTGGCCCGAGAGCTTCTTGGCAGAGTGCCTGAGAGCCGCGGATGGCAACAC 483
 DB 141 GluG1uLeuAlaIaArSerPheThrG1nValIleuG1uAlaValaIaArgH1ScySHIaSa 160
 QY 484 TGGCGGGTTCCTCCAGCCGACATCAAGAGCAGAAACATCTTAATGACCTGAAACCGCGCG 543
 DB 161 CyG1yValIleuH1aIaArgAsPrlElySaNsErG1uAaNilIleuIleAsPLeuSaNsErG1y 180
 QY 544 GAATCAAACTCATGACTTCGGGTGGGGCGCTGCTCAAGACACAGTCTACACGAGC 603
 DB 181 GluLeuYleuIleAAsPheG1ySerG1yAlaLeuLeuYAsPThryIyThraAsP 200
 QY 604 TTTGACGGAACCCGAGTGCAGTCTCCAGAGTGGATTCGCTACATGCTACACGAGC 663
 DB 201 PheAsPrlYThraValIySerProG1uIyTrpIleArgTyrH1aIaArgTyrH1aIa 220
 QY 664 AGGTGGCTGCTGTTGGTCCCTGGGAGATCCTGCTATGACATGAGTGTGCGAGATATT 723
 DB 221 ArgSerAlaIaIaValTrpSerLeuG1yIleLeuLeuYrAsPMeValCyG1yAsPrlE 240
 QY 724 CCAATTGACACGAGAGAGATCTCAAGGCGCAAGTCTTATGGCAAGGCTCTT 783
 DB 241 ProPheG1uH1aIaAsPrlG1uIleIleIaArgG1yG1nValPhePheArgG1nArgValSer 260
 QY 784 TCAGAAATGCACATCTTATTAGATGAGTGCCTGCTCCAGACCAATCGAGCCGCGCTCC 843
 DB 261 SerG1uCyG1nH1aIeLeuIleArgTyrCySrlEaNsErAlaLeuArgProSerAsPTrpOmtr 280
 QY 844 TTTGAGAAATCCAGAACCATCCGTGATGACAGATGTTCTCTGCGCCAGGCGCACCGCT 903
 DB 281 PheG1uG1uIleG1nH1aNsH1aProTrpMetG1nAsPValIleuLeuProG1nG1uThraIa 300
 QY 904 GAGATTCATCTGCACAGCTGTCCACCATCAACCCAGCAAA 942
 DB 301 GluIleH1aIeLeuH1aSerLeuSerProG1yProSerIyS 313
 RESULT 9
 AD55368
 ID AD55368 standard, protein, 313 AA.
 XX AC AD55368;
 XX AC
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein AAA60089, SEQ ID NO 1183.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNR; Chung.
 XX
 OS Homo sapiens.
 XX
 PN MO2003016475-A2.
 PD 27-FEB-2003.
 PF 14-AUG-2002; 2002MO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; AAA60089.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for

CC or is modified to contain a reactive group at or near a binding site of
 CC interest, with one or more ligand candidates capable of covalently (C).
 CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
 CC The method is useful for identifying protein kinase inhibitors that
 CC preferentially bind to inactive conformation of a target protein kinase.
 CC The present sequence is a protein kinase which may be modified via an
 CC amino acid substitution, for use in the method of the invention.

XX Sequence 313 AA;

SO Alignment Scores:

Pred. No.: 4,75e-126 Length: 313
 Score: 1636.00 Matches: 304
 Percent Similarity: 99.04% Conservative: 6
 Best Local Similarity: 97.12% Mismatches: 3
 Query Match: 66.97% Indels: 0
 DB: 7 Gaps: 0

US-10-705-757-3 (1-1302) x ADF45083 (1-313)

QY 4 ATGCTCTGTCCAAAGATCAATCCCTGGCCCACTGGCGGACGCCCTTGCAACGACTG 63
 DB 1 MetLeuLeuSerIleLeuSerIleLeuSerIleLeuSerIleLeuSerIleLeuSerIleLeu 20
 QY 64 CACGCCAACAAGCTGGCGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
 DB 21 HisAlaThrIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
 QY 124 GGGCCGCTGTGGGACGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
 DB 41 GlyProLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
 QY 184 AACTTGGCCGCTGGCCCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
 DB 61 AsnLeuProValAlaIleLeuSerIleLeuSerIleLeuSerIleLeuSerIleLeuSerIle 80
 QY 244 CCCAAGCGGACCGGAGTGGCCATGGAAGTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 303
 DB 81 ProAsnIleThrArgValIleProMetGluValIleLeuLeuLeuLeuLeuLeuLeuLeu 100
 QY 304 TCGGGCGCTCAATGACTTCTGAGCTGGTGAAGGCGCGGAGAGAGAGAGAGAGAGAGAG 363
 DB 101 SerGlyValIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
 QY 364 GAGAGCGCCGACCGGCGGAG 423
 DB 121 GluArgProGluProValIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 140
 QY 424 GAGAGCTGGCGGAGAGCTTCTTCTGAGCTGGTGAAGGCGCGGAGAGAGAGAGAGAGAG 483
 DB 141 GluGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 160
 QY 484 TGGCGGGTCTTCCACCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
 DB 161 CysGlyValIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 180
 QY 544 GAATCTGAATCTCACTTCCGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 603
 DB 181 GluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 200
 QY 604 TTGACGGAACCGGAGTGAAGTCTTCCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 663
 DB 201 PheAspGlyThrArgValIleSerProGluIleThrIleArgIleThrIleArgIleThr 220
 QY 664 AGGTGGCTGCTGTTGGTCTTGGGAGTCTGCTTATGACATGCTGCGGAGATATTT 723
 DB 221 ArgSerIleAlaValIlePheSerLeuGlyIleLeuLeuLeuLeuLeuLeuLeuLeuLeu 240
 QY 724 CCATTGAGACGACGAG 783
 DB 241 ProPheGluIleHisArgGluGluIleLeuArgGluIleValIlePhePheArgGluIleVal 260
 QY 784 TCAGAAATGTCAACATCTTATTAGATGTGCTGCTGCTGAGACCATCGACCGGCGCTTC 843

DB 261 SerGluCysGluHisLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 280
 QY 844 TTGGAAGAAATCCAAACATCCCGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 903
 DB 281 PheGluGluIleGluHisIleProIlePheGluIleLeuLeuProGluIleThrAla 300
 QY 904 GAGATTCACTGACAGCGCTGTCACCATCAACCCAGCAAA 942
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerIle 313

RESULT 11

AD019690
 ID AD019690 standard; protein; 313 AA.

AC AD019690;

DT 12-AUG-2004 (first entry)

DE Human PRO polypeptide #308.

KW Human; PRO; immune related disorder; systemic lupus erythematosus;
 KW Rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.

XX Homo sapiens.

PN MO2004043361-A2.

PD 27-MAY-2004.

PF 06-NOV-2003; 2003WO-US035268.

PR 08-NOV-2002; 2002US-0425235P.

XX (GENETH) GENENTECH INC.

PA Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;

PI Wood WI, Wu TD;

XX WPI, 2004-420067/39.

DR N-PSDB; AD019689.

XX Novel PRO polypeptide e.g., PRO9614, PRO71106, or PRO86388 useful for
 PT creating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.

XX Claim 7; SEQ ID NO 616; 1731pp; English.

XX The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.

SO Sequence 313 AA;

Alignment Scores: 4,75e-126 Length: 313
 Pred. No.: 1636.00 Matches: 304
 Score:

Percent Similarity: 99.04%
 Best Local Similarity: 97.12%
 Query Match: 66.97%
 DB: 8
 Gaps: 0

US-10-705-757-3 (1-1302) x ADR88370 (1-313)

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QY 4 ATGCTCTTGTCCAAAGATCAACTCCCTGGCCCACTGGCGGCGAGCCCTTGCAAGCAACTG 63
DB 1 MetleuenuSerlySIIeAmSerleuAlaIleuArgAlaIaProCySAmAspLeu 20
QY 64 CAGCCCAACAAGCTGGCGCGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
DB 21 HisAlaThrlySleuAlaIleuAlaProGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 40
QY 124 GGGCCGCTGTGGGAGCGGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 183
DB 41 GlyProleuenuGlySerGlyGlyPheGlySerValTySerGlyIleArgValSerAsp 60
QY 184 AACTTGGCGGTGGGATCAAGCAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
DB 61 AsnleuProValAlaIleuYHISValGluYAspArgIleSerAspTTPGlyGlyLeu 80
QY 244 CCGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
DB 81 ProAsnGlyThrArgValProMetGlyValValIleuLeuYslySValSerSerGlyPhe 100
QY 304 TCGGCGCTCATTTAGACTTCTTGAGCTGGTTCGAGAGGCGGAGATTTTCGCTGGATCTG 363
DB 101 SerGlyValIleArgLeuLeuAspTTPGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
QY 364 GAGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 423
DB 121 GluArgProGlyProValGlnAspLeuPheAspPheIleThrGlyValAlaLeuGln 140
QY 424 GAGAGGCTGGCGGAGAGCTTCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 483
DB 141 GluIleuAlaIleuArgPhePhePheTTPGlyValIleuGlnAlaValAlaGlnHISVal 160
QY 484 TGGCGGCTTTCACCGGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
DB 161 CyGlyValIleuHISArgAspIleYAspIleuAsnIleuIleuAspLeuAsnArgGly 180
QY 544 GAAGTCAAACTCATTCAGCTTGGGCTGGGCGGCGCTGTCAGAGAGAGAGAGAGAGAGAG 603
DB 181 GluLeuYslySleuIleAspPheGlySerGlyAlaLeuLeuYsAspThrValTyThrAsp 200
QY 604 TTGACGGAAGCCGAGTGTACAGTCTTCAGAGTGGATTCGCTACATCGCTACACAGCG 663
DB 201 PheAspGlyThrArgValTySerProGlyTTPGlyIleArgTyHISArgTyHISGly 220
QY 664 AGGTGGCTGTGTTGGTCCCTGGAGATTCCTGCTATGACATGATCTGGAGAGATAT 723
DB 221 ArgSerAlaIleValTTPSerLeuGlyIleLeuLeuYsAspMetValCySlyAspIle 240
QY 724 CCATTGAGCAGCAGAGAGATGTCAGAGGCGCAAGTGAATTAGGCAAGGCTTCT 783
DB 241 ProPheGlyHISArgGlyGlyIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
QY 784 TCGAAGTCAAGCTTTATAGATGGAGCTGTCCTGGAGAGATTCAGAGAGAGAGAGAGAGAG 843
DB 261 SerIleuYsGlnHISValIleArgTTPCySlyLeuAlaLeuArgProSerAspArgProThr 280
QY 844 TTGAGAGAAATCCAGAAACATCCGTGATGAGAGAGATTTCTCTGCCAGGCGCACGGCC 903
DB 281 PheGlyGlyIleGlnAmHISProTTPMetGlnAspValIleuLeuProGlnGlnThrAla 300
QY 904 GAGATTCACTGCAAGCTGTCATCAGCATCAAGCCAGCAAA 942
DB 301 GluIleHISleuHISSerLeuSerProGlyProSerTyS 313

```

```

ID ADR88370 standard; protein; 313 AA.
XX
AC ADR88370;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human PIM 1 protein.
XX
KW Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW G-protein coupled receptor; methyl transferase; ligase; PIM; human.
XX
OS Homo sapiens.
XX
PN US2004171062-A1.
XX
PD 02-SEP-2004.
XX
PF 28-FEB-2003; 2003US-0037268.
XX
PR 28-FEB-2002; 2002US-0360651P.
PR 16-SEP-2002; 2002US-0411398P.
PR 20-SEP-2002; 2002US-0412341P.
PR 02-JAN-2003; 2003US-0437929P.
XX
PA (PLEX-) PLEXIKON INC.
XX
PT Hirth K, Milburn MV;
XX
DR WPI; 2004-642017/62.
XX
PT Designing a ligand binding to a target molecule, comprises identifying as
PT molecular scaffold compounds binding to members of a molecular family,
PT detecting orientation of scaffolds at a binding site of target, and
PT synthesizing ligand.
XX
PS Disclosure; SEQ ID NO 9; 186bp; English.
XX
CC The present invention relates to a method of designing a ligand binding
CC to a target molecule. The method involves identifying as molecular
CC scaffold compounds binding to members of a molecular family, detecting
CC orientation of scaffolds at a binding site of target, and synthesizing
CC ligand. The invention is useful for designing drug products and for
CC designing ligand binding to target molecules such as nuclear hormone
CC receptors, TNF receptors, G-protein coupled receptors, methyl
CC transferases, ligases, etc. The present sequence is the human PIM 1
CC protein. This sequence is used to illustrate the method of invention.
XX
SQ Sequence 313 AA;
XX
Alignment Scores:
Pred. No.: 4,756-126 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 66.97% Indels: 0
DB: 8 Gaps: 0

```

```

US-10-705-757-3 (1-1302) x ADR88370 (1-313)
QY 4 ATGCTCTTGTCCAAAGATCAACTCCCTGGCCCACTGGCGGCGAGCCCTTGCAAGCAACTG 63
DB 1 MetleuenuSerlySIIeAmSerleuAlaIleuArgAlaIaProCySAmAspLeu 20
QY 64 CAGCCCAACAAGCTGGCGCGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 123
DB 21 HisAlaThrlySleuAlaIleuAlaProGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 40
QY 124 GGGCCGCTGTGGGAGCGGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 183
DB 41 GlyProleuenuGlySerGlyGlyPheGlySerValTySerGlyIleArgValSerAsp 60
QY 184 AACTGCGGCTGGGATCAAGCAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243

```

RESULT 12
 ADR88370

```

Db      61 AsnLeuProValAlaIleIysH1sValGluIysAspArgIleSerAspTrpGlyGluLeu 80
QY      244 CCCAACGGGACCCGAGTGGCCATGGAAGTGATCTCTGCTGAAGAGGAGGCTGGGCTTC 303
XX      |||
XX      81 ProMetGlyThrArgValProMetGluValValLeuLeuIysValIleSerSerGlyPhe 100
QY      304 TCGGGCGCTCATTAAGCTTTGAGCTGGTTGAGAGGCGCCGATAGTTTCGTGATCTTG 363
XX      |||
XX      101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120
QY      364 GAGAGCGCCGACCCCGTGGCAAGACCTTTGACTTTCACCCGAGCGAGGAGCCCTCCAG 423
XX      |||
XX      121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY      424 GAGAGCGTGGCCGGAGCTTCTTGCGCAGTGTGGAGGCGGTGGGAGCTTCCCAACAC 483
XX      |||
XX      141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCysH1sAsn 160
QY      484 TCGGGGGTTTCCACCCGACATCAAGACGAGACGAAATCTTAATCGACCTGAACCGCGC 543
XX      |||
XX      161 CysGlyValLeuH1sArgAspIleIysAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY      544 GAACTCAAACTCATTCGACTTCGGGGTGGGGGCGCTGCTCAAGACACAGTCTACAGGAC 603
XX      |||
XX      181 GluLeuIysLeuIleAspPheGlySerGlyAlaLeuLeuIysAspThrValIlyrThrAsp 200
QY      604 TTGAGAGGAAACCGAGTGTACAGTCTCCGAGTGGATTCGCTACACATGCTGCTACCGGCG 663
XX      |||
XX      201 PheAspIlyrThrArgValIlyrSerProGluTrpIleArgIlyrH1sArgIlyrH1sGly 220
QY      664 AGGTGCGGCTGCTGTTGGTCCCTGGGGATCCTGCTCATGACATGGTCTGGCGAGATATT 723
XX      |||
XX      221 ArgSerAlaIleValIlyrPheLeuGlyIleLeuLeuIlyrAspMetValCysGlyAspIle 240
QY      724 CCAATTGAGACGACGAAAGATGCTCAAGGGCCCAAGTACTTTAGCGAAAGGCTCTCT 783
XX      |||
XX      241 ProPheGluH1sAspGluGluIleIleArgGlyValValPhePheArgGlnArgValIleSer 260
QY      784 TCAGAAATGTCAAATCTTATTAGATGGTGCCTGCTGCTGAGACATCGACCGGCGCTCC 843
XX      |||
XX      261 SerGluCysGlnH1sLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280
QY      844 TTGGAAGAAATCCAGAACCATCCGTGGATGACAGATGTTCTCTGCCCGACGGCCACGCC 903
XX      |||
XX      281 PheGluGluIleGlnAsnH1sProTrpMetGlnAspValLeuLeuProGlnGluThrAla 300
QY      904 GAGATTCATTCGACAGCTGTGTACCACTCACCCAGCAAA 942
XX      |||
Db      301 GluIleH1sLeuH1sSerLeuSerProGlyProSerIlys 313

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RESULT 13
ADP24227
ID ADP24227 standard; protein; 313 AA.

```

XX      AC      ADP24227;
XX      DT      18-NOV-2004 (first entry)
XX      DE      PRO polypeptide SEQ ID NO:1405.
XX      KW      PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
XX      KW      osteopathic; antidiabetic; dermatological; antipneumatic; antiallergic;
XX      KW      antiaesthetic; hepatotropic; respiratory; gene therapy; immune system.
XX      OS      unidentified.
XX      PN      MO2004041170-A2.
XX      PD      21-MAY-2004.
XX      PF      30-OCT-2003; 2003MO-US034312.
XX      PR      01-NOV-2002; 2002US-0423394P.

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XX      XX      (GERTH ) GENENTECH INC.
PA      PA      Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
XX      PI      Wu ID;
XX      PI      MPI; 2004-419628/39.
XX      DR      N-PSDB; ADP24226.
XX      PT      New PRO polypeptides and polynucleotides, useful for treating e.g.
XX      PT      erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
XX      PT      renal disease, or demyelinating diseases of the central or peripheral
XX      PT      nervous system.
XX      PS      Claim 7; SEQ ID NO 1405; 2940bp; English.
XX      CC      The invention relates to a novel isolated nucleic acid and the PRO
XX      CC      polypeptide encoded by it. A protein of the invention has
XX      CC      antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
XX      CC      osteopathic, antidiabetic, dermatological, antipneumatic, antiallergic,
XX      CC      antiaesthetic, hepatotropic, and respiratory activity. A polynucleotide
XX      CC      of the invention may have a use in gene therapy. The PRO polypeptide, its
XX      CC      agonist, antagonist, or antibody that specifically binds to the
XX      CC      polypeptide is useful for treating an immune related disorder such as
XX      CC      systemic lupus erythematous, rheumatoid arthritis, osteoarthritis,
XX      CC      juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
XX      CC      idiopathic inflammatory myopathy, Sjogren's syndrome, autoimmune
XX      CC      vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
XX      CC      thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
XX      CC      disease, a demyelinating disease of the central or peripheral nervous
XX      CC      system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
XX      CC      a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
XX      CC      disease, infectious or autoimmune chronic active hepatitis, primary
XX      CC      biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
XX      CC      inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
XX      CC      disease, an autoimmune or immune-mediated skin disease, a bullous skin
XX      CC      disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
XX      CC      disease, asthma, allergic rhinitis, atopic dermatitis, food
XX      CC      hypersensitivity, urticaria, an immunologic disease of the lung,
XX      CC      eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
XX      CC      pneumonitis, a transplantation associated disease, graft rejection or
XX      CC      graft-versus-host disease. The present sequence represents a PRO protein
XX      CC      of the invention.
XX      SQ      Sequence 313 AA;

```

Alignment Scores:
Pred. No.: 4,75e-126
Score: 1636.00
Percent Similarity: 99.04%
Best Local Similarity: 97.12%
Query Match: 66.97%
DBs: 8
Matches: 313
Conservative: 6
Mismatches: 3
Indels: 0
Gaps: 0

US-10-705-757-3 (1-1302) x ADP24227 (1-313)

```

QY      4 ATGCTCTTGTCCAAATCAACCTCCGCGCCACCTGGCGGACGCCCTTGAACGACGCG 63
XX      |||
XX      1 MetLeuLeuSerLysIleH1sSerLeuAlaH1sLeuArgAlaIleProCysAsnAspLeu 20
QY      64 CAGCGCAACAGACTGGCGCGCGGCAAGAGAGAGCCCTCGAGTGCAGTACGACGAGTG 123
XX      |||
XX      21 H1sAlaThrIlyLeuAlaIleProIlyrGlyIlyrGluProLeuGlnSerGlnIlyrGlnVal 40
QY      124 GGGCGGCTGTTGGGCAAGCGGTGGCTTGGCTGCTACTCGGGCATCCGCGTCCCGAC 183
XX      |||
XX      41 GlyProLeuLeuGlySerGlyIlyrPheGlySerValIlyrSerGlyIlyrArgValSerAsp 60
QY      184 AACTTGGCGGTGGCCATCAAGACGTTGGAGAGACCGGATTTCCGAGGGGGGAAACG 243
XX      |||
XX      61 AsnLeuProValAlaIleIysH1sValGluIysAspArgIleSerAspTrpGlyGluLeu 80
QY      244 CCCAACGGGACCCGAGTGGCCATGGAAGTGTCTGCTGAAGAGTGAAGTCTGGGCTTC 303

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Db      81  ProbenGlyThrArgValPrometGluValValLeuLeuLeuValSerSerGlyPhe 100
Qy      304  TCGGCGCTCATTAAGCTTTCTGAGTGGTGGAGAGCCCGATAGTTTCTGCTGATCTTG 363
Db      101  SerGlyValIleArgLeuLeuLeuAspTrpPheGluArgProAspSerPheValLeuLeu 120
Qy      364  GAGAGCCCGAACCCTGCAAGAGACTCTTGACTTCATCAACCGAGGAGAGCCCTCAG 423
Db      121  GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
Qy      424  GAGAGCTGGCCCGAGACTTTCTTGCAAGGTGCTGAGAGCCGTGCGGACATTCGCAAC 483
Db      141  GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn 160
Qy      484  TCGGGGGTTCTCCACCGGACATTAAGAGAGAAATCTTAATGACTGAAACCGGCGC 543
Db      161  CysGlyValLeuHisArgAspIleLeuAspGluAsnIleLeuIleAspLeuAsnArgGly 180
Qy      544  GAACTCAAACTCATGCACTTCGGGTGCGGGGCGCTGCTCAAGGACAGAGTCTACACGGAC 603
Db      181  GluLeuLeuLeuIleAspPheGlySerGlyAlaLeuLeuLeuAspTrpValTyrThrAsp 200
Qy      604  TTTGACCGAAACCGAGTGTACAGTCTTCAGAGTGTATGCTACATCCGCTACACAGCGC 663
Db      201  PheAspGlyThrArgValTyrSerProGluTrpIleArgTyrHisArgTyrHisGly 220
Qy      664  AGCTCGGCTGCTGTTTGTCCTCGGGGATCTGCTGTATGACATGCTGCGGAGATATT 723
Db      221  ArgSerAlaIleValTrpSerLeuGlyIleLeuLeuLeuLeuAspMetValCysGlyAspIle 240
Qy      724  CCAATTGAGACGACGAGAGATGTCAGAGGCGCAATGTAATTTAGGCAAGGCTCTC 783
Db      241  ProPheGluHisAspGluGluGluIleIleArgGlyGlnAlaPhePheArgGlnArgValSer 260
Qy      784  TCAGAAATGCAACATCTTATTAGATGAGTGCCTGCTCCCTGAGACCATGAGACCGGCTCC 843
Db      261  SerGluCysGlnHisLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280
Qy      844  TTTGAAAGAAATCCAGAACCATCCGTGATGACAGAGATTTCTCTGCCCCAGGCCACCGCC 903
Db      281  PheGluGluIleGlnHisAsnHisProTrpMetGlnAspValLeuLeuProGluGluThrAla 300
Qy      904  GAGATTCATGTCAGAGCTGTGACCACTCAACCCAGCAA 942
Db      301  GlnIleHisLeuHisSerLeuSerProGlyProSerLeu 313

RESULT 14
AAW08139
ID      AAW08139 standard, protein; 313 AA.
AC      AAW08139,
DT      11-MAR-1997 (first entry)
XX      Human cytokine response protein CR7.
DE      Human cytokine response protein CR7.
KW      Cytokine response protein; CR7; interleukin-2; IL-2;
        ligand-stimulated gene expression; diagnosis; therapy; proto-oncogene;
        p1m1; protein kinase; lymphoma.
OS      Homo sapiens.
XX      Homo sapiens.
PN      WO9639427-A1.
PD      12-DEC-1996.
PF      05-JUN-1996; 96MO-US009194.
XX      05-JUN-1995; 95US-00461379.
PR      05-JUN-1995; 95US-00462337.
PR      05-JUN-1995; 95US-00462390.
PR      05-JUN-1995; 95US-00463074.

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PR      05-JUN-1995; 95US-00463081.
PR      05-JUN-1995; 95US-00465585.
XX      (DART-) DARTMOUTH COLLEGE.
PA      Smith KA, Beadling C;
PI      WPI; 1997-043062/04.
XX      DR N-PSDB; AAT43382.
XX      DR N-PSDB; AAT43382.
PT      Cytokine response proteins and genes - used in the detection and therapy
PT      of diseases caused by a mutation in the CR coding region.
XX      Claim 15; Page 32-33; 81pp; English.
PS      Cytokine response proteins CR1-CR8 (AAW08133-40) are encoded by genes
CC      (see also AAT43376-83) isolated from a chiol-selected interleukin-2-
CC      induced human T-cell blast cDNA library. 6 Genes (CR1, 2, 3, 5, 6, 8) are
CC      novel. CR7 is a serine/threonine protein kinase involved in T-cell
CC      lymphomagenesis. The CR7 gene is identical to the putative proto-oncogene
CC      p1m-1, which is over-expressed in about 50% of MuLV-induced T-cell
CC      lymphomas. Recombinant CR7 polypeptides can be produced e.g. as GST
CC      fusions for use as immunogens and as diagnostic and therapeutic agents
CC      XX
SQ      Sequence 313 AA:

Alignment Scores:
Pred. No.: 5,62e-125 Length: 313
Score: 1623.00 Matches: 302
Percent Similarity: 98.40% Conservative: 6
Best Local Similarity: 96.49% Mismatches: 5
Query Match: 66.43% Indels: 0
DB: 2 Gaps: 0

US-10-705-757-3 (1-1302) x AAW08139 (1-313)
Qy      4  ATGCTCTGTGTCCAAAGTCAACTCCCTGCGCCACCTGCGGAGCCCTTGCAAGACCTTG 63
Db      1  MetLeuLeuSerIleHisAsnSerLeuAlaHisLeuArgAlaArgAlaCysAsnAspLeu 20
Qy      64  CACGCCAAGAAGCTGCGCGCGGCAAGAGAGAGACCCCTGAGTGCAGTACAGAGT 123
Db      21  HisAlaThrIleLeuAlaProGlyIleGluIleGluIleProLeuGluSerGlnTyrGlnVal 40
Qy      124  GCGCCGCTGTTGGACGCGGTGCTTGGCTCGGTACTCGGACATCCGCTCGCCGAC 183
Db      41  GlyProLeuLeuGlySerGlyIlePheGlySerValTyrSerGlyIleArgValSerAsp 60
Qy      184  AACTTCCCGGTGGCCATCAAGCACCTGAGAGAACCGGATTTCCGACTGGGGGAACTG 243
Db      61  AsnLeuProValAlaIleLeuHisValGluIleAspArgIleSerAspTrpGlyGluLeu 80
Qy      244  CCAACGAGACCCGAGTGCCTGAGAGTGTCTCTGTAAGAGAGTGAAGCTGGGCTTC 303
Db      81  ProbenGlyThrArgValPrometGluValValLeuLeuLeuValSerSerGlyPhe 100
Qy      304  TCGGCGCTCATTAAGCTTTCTGAGTGGTGGAGAGCCCGATAGTTTCTGCTGATCTTG 363
Db      101  SerGlyValIleArgLeuLeuLeuAspTrpPheGluArgProAspSerPheValLeuLeu 120
Qy      364  GAGAGCCCGAACCCTGCAAGAGACTCTTGACTTCATCAACCGAGGAGAGCCCTCAG 423
Db      121  GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
Qy      424  GAGAGCTGGCCCGAGACTTTCTTGCAAGGTGCTGAGAGCCGTGCGGACATTCGCAAC 483
Db      141  GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn 160
Qy      484  TCGGGGGTTCTCCACCGGACATTAAGAGAGAAATCTTAATGACTGAAACCGGCGC 543
Db      161  CysGlyValLeuHisArgAspIleLeuAspGluAsnIleLeuIleAspLeuAsnArgGly 180
Qy      544  GAACTCAAACTCATGCACTTCGGGTGCGGGGCGCTGCTCAAGGACAGAGTCTACACGGAC 603

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DB 181 GIULEULYLEULLEAPHEPHEGLYSERGLALALEULEULYASPHRVALTYTHRAAP 200
QY 604 TTTGACGGAACCCGAGTGTACAGTCTCCAGAGTGGATTGCTACCATGCTACACGCGC 663
DB 201 PHEASPGLYTHARVALTYRSEPRPROGLUTPRILEARGTYRHARGTYRHISGLY 220
QY 664 AGGTGGGCTGCTTTGGTCCCGGGGATCCCTGCTATGACATGGTCTGCGAGATATT 723
DB 221 ARGSERLAIALAVALTPSERLEUGLYLEULEULTYRHMETVALCYSGLYASPILE 240
QY 724 CCATTGACACGACGAGAGATCGTCAAGGCGCAAGTACTTTAGCAAAAGGCTCTCT 783
DB 241 PROPHGLUHHISAPGLUGLUILEARGLYGLINVALPHEHARGGLNARGVALSER 260
QY 784 TCGAATGTCACATCTTTATAGTGTGCTCCCTGACAGCATCGAGCCGCGCTTCG 843
DB 261 SERGLUCYSGLINHISLEULLEARGTTCYVLEUALALEUARGPROSERAPRPROTHR 280
QY 844 TTTGAAGAATCCAGAACCATCCGTGGATGACAGATGTTCTCTGCGCCAGGCGACGCGC 903
DB 281 PHEGLUGLUILEGLINSHISPRROTTCMETGLINAPVALLEULPROGLINGLUTHRALA 300
QY 904 GAGATTCATCTGCACAGCCTGTGCACCATCACCCAGCAAA 942
DB 301 GLUILEHISLEULHISERLEUSERPROGLYPROSERLYSE 313
RESULT 15
AAV87959
ID AAV87959 standard; protein; 313 AA.
XX
AC AAV87959;
XX
DT 18-SEP-2000 (first entry)
XX
DE Human CR7 protein.
XX
DE CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic;
KW immunosuppressive; antimicrobial; therapy; cell proliferation; treatment;
KW cell differentiation; cancer; immune disease; rheumatologic disease;
KW transplant rejection; anti-infective; CR7.
OS Homo sapiens.
XX
OS US6057427-A.
PN 02-MAY-2000.
XX
PD 05-JUN-1996; 96US-00652446.
PF 20-NOV-1991; 91US-00796066.
PR 10-AUG-1993; 93US-00104736.
PR 27-OCT-1994; 94US-00330108.
PR 05-JUN-1996; 96WO-US008992.
XX
XX (DART-) DARTMOUTH COLLEGE.
XX
PI Beadling C, Smith KA;
XX
XX WPI, 2000-338623/29.
DR N-PSDB; AAA39677.
XX
XX Novel antibody or antibody fragment which selectively binds to a
PT polypeptide encoded by cytokine response gene 2.
XX
XX Example IV; Col 111-114; 66pp; English.
XX
XX This invention describes a novel isolated antibody or antibody fragment
CC (I) which selectively binds to a polypeptide encoded by cytokine response
CC gene 2 (CR2) and modulates CR2 activity. The products of the invention
CC have cytostatic, anti-allergic, immunosuppressive and antimicrobial
CC activity. The antibodies are useful as therapeutic agents for regulating
CC cellular proliferation and differentiation and for treating all kinds of

CC cancer, immune diseases such as allergic, autoimmune, and rheumatologic
CC diseases, transplant rejection, and as anti-infectives for fighting
CC viral, bacterial, parasitic and fungal infections. This sequence
CC represents the human CR7 protein described in the invention

XX
XX Sequence 313 AA;

Alignment Scores:

Pred. No.:	5,626-125	Length:	313
Score:	1623.00	Matches:	302
Percent Similarity:	98.40%	Conservative:	6
Best Local Similarity:	96.49%	Mismatches:	5
Query Match:	66.43%	Indels:	0
DB:	3	Gaps:	0

US-10-705-757-3 (1-1302) x AAV87959 (1-313)

QY 4 ATGCTCTGTTCAGATCACTCCCTGGCCCACTGGCGGACGCCCTTGACACGACTTG 63
DB 1 MetLeuLeuSerLyIleAaSerLeuAlaHISLeuArgAlaArgAlaCyAsnAspLeu 20
QY 64 CACGCCAACAGCTGGCCCGGCGCAAGAGAGAGGCCCTGGAGTCCGACGACAGGTT 123
DB 21 HIsAlaThrLyLeuAlaProGlyLySGIuLySGIuProLeuGlySerGlnThrVal 40
QY 124 GGCCTGCTGGGCGAGCGGTGGCTTCGAGCTGTCTACTCGGCGCATCCGCTCCGAC 183
DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyRserGlyIleArgValSerAsp 60
QY 184 AACCTGCGGTGGCCATCAAGCAGTGAAGAGAACCCGAGATTCGAGCTGGGGGAACTG 243
DB 61 AenLeuProValAlaIleValHisValGluLyAspArgIleSerAspTrpGlyIuLeu 80
QY 244 CCCAACGGCAGCCCGAGTCCCATGGAAGTGTCTGGAAGAGTGAAGTGGCTTCG 303
DB 81 ProAaNGlyThARValProMetGluValValLeuLeuLyValValSerSerGlyPhe 100
QY 304 TCGGCGTCATTAAGACTTCTGAGTGTTCGAGAGGCCCGAATGTTCTGCTGATCTTG 363
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluAArgProAspSerPheValLeuLeu 120
QY 364 GAGAGGCCGGAACCCGTGCAGACTCTTTCATTCATCACCGAGCGAGACCTTCAG 423
DB 121 GluArgProGluProValGlnAspPheArgPheIleThrGluArgGlyAlaLeuGln 140
QY 424 GAGAGCTGGCCCGGAGCTTCTTCGAGAGTGTGCGAGGCCGCGGATGGCCACAC 483
DB 141 GluGluLeuAlaArgSerPheThrGlnValValLeuGluAlaValArgHisCyAsnAsn 160
QY 484 TCGGGGGTCTTCACCGCGCAGCATCAAGAGAGAACATCTTAATGACCTGGAACCGCGC 543
DB 161 CySGlyValLeuHISArgAspIleLyAspArgIuAaHISLeuHISAspLeuAsnArgGly 180
QY 544 GAATCAAACTCATGACTTCGAGGTGGGGCGCTGCTCAAGACACAGTCTACACGAGC 603
DB 181 GIULEULYLEULLEAPHEPHEGLYSERGLYALALEULEULYASPHRVALTYTHRAAP 200
QY 604 TTTGACGGAACCCGAGTGTACAGTCTCCAGAGTGGATTGCTACCATGCTACACGCGC 663
DB 201 PHEASPGLYTHARVALTYRSEPRPROGLUTPRILEARGTYRHARGTYRHISGLY 220
QY 664 AGGTGGGCTGCTTTGGTCCCGGGGATCCCTGCTATGACATGGTCTGCGAGATATT 723
DB 221 ARGSERLAIALAVALTPSERLEUGLYLEULEULTYRHMETVALCYSGLYASPILE 240
QY 724 CCATTGACACGACGAGAGATCGTCAAGGCGCAAGTACTTTAGCAAAAGGCTCTCT 783
DB 241 PROPHGLUHHISAPGLUGLUILEARGLYGLINVALPHEHARGGLNARGVALSER 260
QY 784 TCGAATGTCACATCTTTATAGTGTGCTCCCTGACAGCATCGAGCCGCGCTTCG 843
DB 261 SERGLUCYSGLINHISLEULLEARGTTCYVLEUALALEUARGPROSERAPRPROTHR 280

Qy	844	TTTGAAGAAATCCAGAACATCCGTGATGCGATGTTCTCTGCCCCAGCCACCGCC	903
Db	281	PheGluGluIleGlnAsnHisProTPrMetClnbpyValLeuLeuProGlnGluThrAla	300
Qy	904	GAGATTGATCTGCACAGCCTGTTCACCATCACCAGCAAA	942
Db	301	GluIleHisLeuHisSerLeuSerProGlyProSerLys	313

Search completed: September 22, 2005, 16:47:54
 Job time : 178.006 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_blue_n2p model

Run on: September 22, 2005, 16:17:56 ; Search time 42.6688 Seconds
(without alignments)
5871.937 Million cell updates/sec

Title: US-10-705-757-3
Perfect score: 2443
Sequence: 1 gggatgctctctgcacagat.....ggattaaactgcacacat 1302

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgr2_1/USPRO.spool_p/US10705757/runac.22092005.115015.22141/app.query.fasta_1.5333
-DB=PIR -OPMT=faetan -SUFFIX=n2p.rpx -MINMATCH=0.1 -LOOPT=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=spct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPRM=ppc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USPR=US10705757_QCGN_1.1-256_@runac.22092005.115015.22141 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1668	68.3	313	1 S26298	protein kinase (BC
2	1636	67.0	313	1 TVHUP1	protein kinase (BC
3	1584	64.8	313	1 TVMSPI	protein kinase (BC
4	878	35.9	370	1 S55333	protein kinase p1m
5	622.5	25.5	363	2 T22255	hypothetical prote
6	495	20.3	409	2 T15435	hypothetical prote
7	381.5	15.6	504	2 T10449	probable serine/th
8	380	15.6	512	1 JCI146	serine/threonine-s
9	380	15.6	1398	2 T13741	hypothetical prote
10	378	15.5	481	2 I49072	protein kinase - m
11	374	15.3	1101	2 S66730	hypothetical prote
12	372	15.2	512	2 T52633	serine/threonine-s
13	370.5	15.2	511	1 A56009	serine/threonine-s
14	366.5	15.0	887	2 T20941	hypothetical prote

15	366	15.0	1358	2 S33653	probable serine/th
16	358.5	14.7	512	2 T07788	probable serine/th
17	358.5	14.7	651	2 S52244	p59eg3 protein - A
18	358	14.7	798	2 UC7500	gik protein - chic
19	355.5	14.6	469	2 B84644	probable protein k
20	355	14.5	726	2 T33998	hypothetical prote
21	353.5	14.5	513	1 S60304	serine/threonine-s
22	350.5	14.3	414	2 JN0323	Ca2+/calmodulin-de
23	350.5	14.3	504	2 T07415	probable serine/th
24	348	14.2	472	2 B90100	SNF-related kinase
25	338.5	13.9	1518	2 S37928	probable purine nu
26	338	13.8	445	2 T50802	serine/threonine p
27	337.5	13.8	502	2 T02306	probable protein k
28	336.5	13.8	489	2 T04862	probable serine/th
29	336	13.8	713	2 S27966	probable serine/th
30	336	13.8	1558	2 T29253	hypothetical prote
31	334.5	13.7	339	2 S56719	serine/threonine-s
32	334	13.7	435	2 E84707	probable threonine-s
33	333.5	13.7	746	2 S62365	SMF1-related prote
34	333	13.6	520	2 G86414	probable protein k
35	331.5	13.6	513	2 S60303	serine/threonine-s
36	330	13.5	461	2 T14822	probable serine/th
37	330	13.5	774	2 T48609	probable serine/th
38	328	13.4	442	2 T48203	hypothetical prote
39	328	13.4	745	2 G01025	serine/threonine p
40	326	13.3	423	2 T40224	protein kinase - f
41	326	13.3	591	2 S54788	calcium-activated
42	325	13.3	1246	2 G89287	protein H39E23.1 f
43	323.5	13.2	713	2 T37886	probable serine/th
44	323	13.2	622	1 S44859	serine/threonine-s
45	322.5	13.2	473	1 S59941	serine/threonine-s

ALIGNMENTS

RESULT 1

S26298

protein kinase (BC 2.7.1.37) p1m-1 - rat

N/Alternate names: kinase-related transforming protein p1m-1; p1m-1 proto-oncogene prot

C/Species: Rattus norvegicus (Norway rat)

C/Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004

C/Accession: S26298

R/Wingett, D.; Reeves, R.; Magnuson, N.S.

Nucleic Acids Res. 20, 3183-3189, 1992

A/Title: Characterization of the testes-specific p1m-1 transcript in rat.

A/Reference number: S26298; MUID:92319652; PMID:1620615

A/Accession: S26298

A/Molecule type: mRNA

A/Residues: 1313 <MIN>

A/Cross-references: UNIPROT:P26794; EMBL:X63675; NID:956902; PIDN:CAA5214.1; PID:95690

A/Experimental source: testis

A/Note: testis-specific transcript is shorter and more stable than the somatic transcript.

C/Comment: p1m-1 autophosphorylates at unknown sites.

A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine.

A/Note: In testis may be involved in signal transduction events of normal germ cell matu

C/Superfamily: Kinase-related transforming protein; protein kinase homology

C/Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen

F/36-290/Domains: protein kinase homology <KIN>

F/44-52/Region: protein kinase ATP-binding motif

F/67/Active site: Lys #status predicted

Alignment Scores:

Pred. No.: 5.33e-70 Length: 313
Score: 1668.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 68.28% Indels: 0
DB: 1 Gaps: 0

US-10-705-757-3 (1-1302) x S26298 (1-313)

QY 4 ATGCTCTTGCAAGATCAACTCCCTGGCCACCTGGCGGACAGCCCTTGCAAGACCTG 63

Db 1 MetLeuLeuSerLysIleAsnSerLeuAlaIleLeuAlaArgAlaAlaProCysAsnAspLeu 20

QY 64 CAGCGCAACAAGCTGGCGCCGGGCAAGAGAGAGAGCCCTGAGTGGCAATGCAAGTGT 123

Db 21 HisAlaAsnLysLeuAlaLeuProGlyLeuGlyLysLeuProLeuGlnSerGlnTyrGlnVal 40

QY 124 GGGCCGCTGTTGGGCGAGCGGTGGCTTCGGCTCTACTCTGGGCAATCCGGGTGGCCGAC 183

Db 41 GlyProLeuLeuGlnLysSerGlyGlyPheGlySerValTyrSerGlyIleArgValAlaAsp 60

QY 184 AACTTGGCCGGTGGCCATGACGACGATGGAGAAAGACCGGAAATTCCTGGATGGGGGAACTG 243

Db 61 AsnLeuProValAlaIleLysHisValGlyLysAspArgIleSerAspTyrGlyGlyLeu 80

QY 244 CCCAAGCGACACCCGAGTGGCCCATGAGAAAGTGGCTCTGTCGAGAAAGTGAAGCTCGGCTTC 303

Db 81 ProAsnGlyThrArgValProMetGlyValValLeuLeuLysValValSerSerGlyPhe 100

QY 304 TCGGGCGCTCATTTAGAATTCTTGAGACTGGTTCGAGAGGCGCCGATAGTTTCGTGCTATCTG 363

Db 101 SerGlyValIleArgLeuLeuAspTyrPheGlyLysArgProAspSerPheValLeuIleLeu 120

QY 364 GAGAGGGCCGCAACCCGTCAGAGACTCTTCTGACGATTCATCAACCGAGCGAGAGCCCTCAG 423

Db 121 GlnArgProGlnProValGlnAspLeuPheAspPheIleThrGlyLysArgValAlaLeuGln 140

QY 424 GAGAGCTGGAGCCCGAGAGCTTCTTCTGACGATGGTGGAGAGCCCTGGCGGCAATGGCAAC 483

Db 141 GlnGlyLeuAlaIleArgSerPhePheThrGlnValLeuGlnAlaValAlaGlnIleCysHisAsn 160

QY 484 TCGCGGGGCTTCTCACCCGCAATCATAGAGACGAGAAACATTATATGACTGAAACCGCGGC 543

Db 161 CysGlyValLeuHisArgAspIleLysAspArgIleAsnIleLeuIleAspLeuAsnArgGly 180

QY 544 GAAGTCAAACTCATGACTTTCGGGGTGGGGGGCGTGGTCAAGACACAGTCTACAGCGAC 603

Db 181 GlnLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200

QY 604 TTTCAGCGAACCAGTGTACAGTCTTCCAGAGTGGATTCGCTACATCGCTACACAGCGC 663

Db 201 PheAspGlyThrArgValTyrSerProGlnTyrIleArgTyrHisArgTyrHisGly 220

QY 664 AGGTGGCTGCTGTTGGTCCCTGGGGGATCCTGCTCTATGACAGTGGTGGCGAGATTT 723

Db 221 ArgSerAlaAlaValTyrPheSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240

QY 724 CCATTTCAGCAGAGAGAGATGCTCAAGGGGCAAGTGAATCTTAGCGAAAGGCTCT 783

Db 241 ProPheGlnHisAspGlnGlyIleValLysGlyGlnValTyrPheArgGlnArgValSer 260

QY 784 TCAGATGTCAACATCTTATTTAGATGATGTCCTGTCCTCCAGACCATCGGACCGGCTCC 843

Db 261 SerGlnCysGlnHisLeuIleArgTyrCysLeuSerLeuAspProSerAspArgProSer 280

QY 844 TTGAGAGAAATCCAGAACCATCCGTGATGACAGATGTTCTCTGCGCCAGCGCACCGCC 903

Db 281 PheGlnGlnIleGlnAsnHisProTyrMetGlnAspValLeuLeuProGlnAlaThrAla 300

QY 904 GAGATTCATTCGACACGCTGTGCACCATCACCCACGAA 942

Db 301 GlnIleHisLeuHisSerLeuSerProSerProSerLys 313

RESULT 2

TVHUP1

protein kinase (EC 2.7.1.37) p1m-1 - human

N/Alternate names: kinase-related transforming protein p1m-1; p1m-1 proto-oncogene protein

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1989 #sequence revision 07-Oct-1994 #text_change 09-Jul-2004

C/Accession: J00327; A46554; A27476; I58412

R/Rever: R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.

Gene 90, 303-307, 1990

A/TITLE: Primary structure of the putative human oncogene, p1m-1.

A:Reference number: J00327; MUID:90382681; PMID:2205533
A:Accession: J00327
A:Molecule type: DNA
A:Residues: 1-313 <RES>
A:Cross-references: UNIPROT:P11309; GB:M27903; NID:g189956; PIDN:AAA60090.1; PID:g387022
R:Meeker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M.
J. Cell. Biochem. 35, 105-112, 1987
A:Title: Cloning and characterization of the human PIM-1 gene: a putative oncogene related to src
A:Reference number: A46554; MUID:88115604; PMID:3429489
A:Accession: A46554
A:Molecule type: mRNA
A:Residues: 1-313 <RES>
A:Cross-references: GB:M24779; NID:g1066790; PIDN:AAA61553.1; PID:g1066791
R:Zakut-Houri, R.; Hazum, S.; Girol, D.; Telemann, A.
Gene 54, 105-111, 1987
A:Title: The cDNA sequence and gene analysis of the human pim oncogene.
A:Reference number: A27476; MUID:87277423; PMID:3475233
A:Accession: A27476
A:Molecule type: mRNA
A:Residues: 1-14, 'RA', 17-313 <ZAK>
A:Cross-references: GB:M16750; NID:g189956; PIDN:AAA60089.1; PID:g189957
R:Domèn, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.
Oncogene Res. 1, 103-112, 1987
A:Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immunologic cross-reactivity
A:Reference number: I58412; MUID:88217305; PMID:3329709
A:Accession: I58412
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-313 <DOM>
A:Cross-references: GB:M54915; NID:g189961; PIDN:AAA6447.1; PID:g189962
C:Comment: Pim-1 autophosphorylates at unknown sites.
C:Genetics:
A:Gene: GDB:PIM1
A:Cross-references: GDB:119495; OMIM:164960
A:Map position: 6p21.2-6p21.2
A:Introns: 28/2; 63/3; 80/3; 203/1; 262/1
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate
A:Superfamily: kinase-related transforming protein; protein kinase homolog
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F,36-290/Domain: protein kinase homolog <KIN>
F,44-52/Region: protein kinase ATP-binding motif
F,67/Active site: Lys #statue predicted

Alignment Scores:
Pred. No.: 1,59e-68 Length: 313
Score: 1636.00 Matches: 304
Percent Similarity: 99.04% Conservative: 6
Best Local Similarity: 97.12% Mismatches: 3
Query Match: 66.97% Indels: 0
Gaps: 1

US-10-705-757-3 (1-1302) x TVHUP1 (1-313)

QY 4 ATGCTCTTGTCCAAAGTCAACTCCCTGGCCCACTGGCGGAGCCCTTGCAGACCTG 63
Db 1 MetLeuLeuSerLyLeaAnsSerLeuAlaHisLeuAlaAlaProCyAsnAspLeu 20
QY 64 CACGGCAACAACGTGGCGCGCGGCAAGAGAAGAGCCCTCGAGTCGACAGCCAGGTG 123
Db 21 HisAlaThrLyLeuAlaProGlyLySgIuLySgIuProLeuGluSerGlnTyrAlaVal 40
QY 124 GGGCCGCTGTGGGCGCGCGGTGCGCTCGCTGCTTACTCGGCGATCCGCGTCGCGAC 183
Db 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
QY 184 AAATTGGCCGTGGCCATCAAGACGCTGGAGAGAAGACCGGATTTCCGACTCGGGGGAACCTG 243
Db 61 AsnLeuProValAlaIleLyHisValGluLyAspArgIleSerAspIleGlyIuLeu 80
QY 244 CCCAAGCGGACCGCGAGTGGCCATGAAAGTGTCCTGCTGAAGAAGTGAGCTCGGGCTTC 303
Db 81 ProAsnGlyThrArgAlaProMetGluValAlaLeuLeuLysValSerSerGlyPhe 100

QY 304 TCGGGCGCTACCTAGACTTCTGCACTGGTTCGAGAGCCGATAGTTCTGCTGATCTCTG 363
 |||||
 Db 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
 |||||
 QY 364 GAGAGCCCGACCCCGTCGAAGACTCTTCTGACTTCAACCGAGCGAGGCCCTTCAG 423
 |||||
 Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 |||||
 QY 424 GAGAGCTGGCCCGGAGCTTCTTCTGGCAGGTGCTGAGAGCCGTCGGGCACTTGGCAAC 483
 |||||
 Db 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
 |||||
 QY 484 TGGGGGGTTCTCCACCGCAGCATCAAGAGAGAGAACTTTAAATCGACTGAAACCGGCGC 543
 |||||
 Db 161 CysGlyValLeuHisArgAspIleLeuAspGluAsnIleLeuIleAspLeuAsnArgGly 180
 |||||
 QY 544 GAACTCAAACTCATCGACTTCGAGGTCGGGGCGCTGCTCAAGACACAGTCTACACGAGC 603
 |||||
 Db 181 GluLeuLeuLeuLeuLeuAspPheGlySerGlyAlaLeuLeuLeuAspThrValTyrThrAsp 200
 |||||
 QY 604 TTTGACGGAACCCGAGTGTACAGTCTTCCAGAGTGGATTGCTAACCATCGCTACACAGGC 663
 |||||
 Db 201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
 |||||
 QY 664 AGGTCCGCTGCTGTTGGTCCCTGGGGATCTGCTCTATGACATGGCTGGGAGATATT 723
 |||||
 Db 221 ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuLeuArgPheValCysGlyAspIle 240
 |||||
 QY 724 CCATTGAGCAGCAGAGAGATCGTCAGAGGCGCAAGTACTTAAAGCAAGGCTCT 783
 |||||
 Db 241 ProPheGluHisIleAspGluGluIleIleArgGlyGlnAlaPhePheArgGlnArgValSer 260
 |||||
 QY 784 TCGAATGTCAACATCTTATTAGATGGTGCCTCCCTGAGACCATGGAACCGGCTCC 843
 |||||
 Db 261 SerGluCysGluHisIleLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProHis 280
 |||||
 QY 844 TTGGAAGAATTCGAGAACATCCGCTGGATGACAGATGTTCTCGGCCCGGAGCGCCG 903
 |||||
 Db 281 PheGluGluIleGluHisAspTrpTrpMetGlnAspValLeuLeuProGluGlnTrpAla 300
 |||||
 QY 904 GAGATTTCATTCGACAGCCTGTGCACATCAACCGAGCAA 942
 |||||
 Db 301 GluIleHisIleHisSerLeuSerProGlyProSerIys 313
 |||||
 RESULT 3
 TVMSPI
 protein kinase (BC 2.7.1.37) p1m-1 - mouse
 N:Alternate names: kinase-related transforming protein p1m-1; p1m-1 proto-oncogene prote
 C:Species: Mus musculus (house mouse)
 C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
 C:Accession: A24169
 R:Seiten, G.; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen, J.;
 Cell 46, 603-611, 1986
 A>Title: The primary structure of the putative oncogene p1m-1 shows extensive homology w
 A:Reference number: A24169; PMID:86272109; PMID:3015420
 A:Accession: A24169
 A:Molecule type: DNA
 A:Residues: 1-313 <SE>
 A:Cross-references: UNIPROT:P06803; GB:M13945; GB:M13946; NID:g200352; PIDN:AAA3930.1;
 C:Comment: P1m-1 autophosphorylates at unknown sites.
 C:Genetics:
 A:Gene: p1m-1
 A:Introns: 28/1; 63/3; 80/3; 203/1; 262/1
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; autophosphorylation; phosphotransferase; proto-oncogene; serine/threonin
 P:36-280/Domain: protein kinase homology <KIN>
 F:44-52/Region: protein kinase ATP-binding motif
 F:67/Active site: Lys #status predicted

Alignment Scores:

	Pred. No.:	3, 94e-66	Length:	313
QY	Score:	1584.00	Matches:	295
Db	Percent Similarity:	96.81%	Conservative:	8
	Best Local Similarity:	94.25%	Mismatches:	10
	Query Match:	64.84%	Indels:	0
	DB:	1	Gaps:	0

US-10-705-757-3 (1-1302) x TVMSPI (1-313)

QY	4	ATGCTTTGTTCGAAGTCAACTCTCTGGCCACCTTCGGGACGCCCTTGGCAAGACTTG 63
Db	1	MetLeuLeuSerIysIleAsnSerLeuAlaHisLeuArgAlaArgProCysAsnAspLeu 20
QY	64	CACGCCAACAGCTGGCGCGCGGCAAGAGAGAGACCCCTTGAGTCGAGTACAGGTG 123
Db	21	HisAlaThrLysLeuAlaProGlyLysGluLysGlnProLeuIleSerGlnTyrGlnVal 40
QY	124	GGCCCGCTGTGGGCGAGCGGTGCTTCGAGTCCGCTGCTACTCGGCGCATCCGCTCGCGAC 183
Db	41	GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValAlaAsp 60
QY	184	AACCTGCCGTCGCTCATCAAGCAGTGAAGAGACCGGATTTCCACTGGGGGAACTG 243
Db	61	AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyLeu 80
QY	244	CCCAAGCGACCCGAGTCCCATGGAAGTGCCTCTGCTGAAGAAGTGAAGTCCGGCTTC 303
Db	81	ProAsnGlyThrArgValAlaProMetGluValValLeuLeuLysValSerSerAspPhe 100
QY	304	TCGGCGCTATTAAGACTTCTGCACTGGTTCGAGAGGCGCGGATAGTTCTGCTGATCTG 363
Db	101	SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120
QY	364	GAGAGGCCGGAACCCGTCGAAGACTCTTGCACCTTCATCAACCGAGCGAGAGCCCTTCAG 423
Db	121	GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY	424	GAGGAGCTGGCCCGGAGCTTCTTCTGGCAGGTGCTGGAAGCCGTCGGGCACTTGGCCAAC 483
Db	141	GluAspLeuAlaArgGlyIlePhePheTrpGlnValLeuGlnAlaAlaArgHisCysHisAsn 160
QY	484	TGGGGGGTTCTCCACCGCAGCATCAAGAGAGAGAACTTTAAATCGACTGAAACCGGCGC 543
Db	161	CysGlyValLeuHisArgAspIleLeuAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY	544	GAACTCAAACTCATTCGACTTCGAGGTCGGGGCGCTGCTCAAGACACAGTCTACACGAGC 603
Db	181	GluIleLeuLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200
QY	604	TTTGAAGGAACCCGAGTGTACAGTCTTCCAGAGTGGATTGCTAACCATCGCTACACAGGC 663
Db	201	PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
QY	664	AGGTCCGCTGCTGTTGGTCCCTGGGGATCCGCTCTATGACATGGCTGGGAGATATT 723
Db	221	ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
QY	724	CCATTGAGCAGCAGAGAGATCGTCAGAGGCGCAAGTACTTAAAGCAAGGCTCTCT 783
Db	241	ProPheGluHisIleAspGluGluIleIleLysGlyGlnAlaPhePheArgGlnThrValSer 260
QY	784	TCGAATGTCAACATCTTATTAGATGGTGCCTCCCTGAGACCATGGAACCGGCTCC 843
Db	261	SerGluCysGluHisIleLeuLysTrpCysLeuSerLeuArgProSerAspArgProSer 280
QY	844	TTTGAAGAATTCGAGAACATCCGCTGGATGACAGATGTTCTCGGCCCGGAGCGCCG 903
Db	281	PheGluGluIleArgAsnHisProTrpMetGlnGlyAspLeuProGluAlaAlaAsp 300
QY	904	GAGATTTCATTCGACAGCCTGTGCACATCAACCGAGCAA 942
Db	301	GluIleHisIleHisSerLeuSerProGlyProSerIys 313

RESULT 4

S55333

protein kinase pim-2 (EC 2.7.1.-) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Oct-1995 #sequence revision 21-Jan-1997 #text_change 09-Jul-2004

C:Accession: S55333; A43093; B43093

R:van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Janders, K.; van der Gulden, H.; Allen

EMBO J. 14, 2536-2544, 1995

A:Title: Proviral tagging in E-mu-myc transgenic mice lacking the Pim-1 proto-oncogene

A:Reference number: S55333; MUID:95300786; PMID:7781606

A:Accession: S55333

A:Molecule type: mRNA

A:Residues: 1-370 <V>

A:Cross-references: UNIPROT:Q62070; GB:L41495; NID:G765065; PID:AAA98922.1; PID:G765066

A:Note: 40K form

A:Accession: A43093

A:Molecule type: mRNA

A:Residues: 'M', 27-370 <VA3>

A:Cross-references: GB:L41495; NID:G765065; PID:AAA98922.1; PID:G765068

A:Note: 34K form

C:Comment: Pim-2 autophosphorylates at unknown sites.

C:Genetics:

A:Gene: Pim-2

A:Map position: X

A:Start codon: CTG

A:Note: locus between A-raf and Act-7, near Kv4.1

C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine

C:Superfamily: kinase-related transforming protein; protein kinase homology

C:Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotrans

F:89-345/Domain: protein kinase homology <KIN>

F:97-105/Region: protein kinase ATP-binding motif

F:120/Active site: Lys #status predicted

Alignment Scores:

Pred. No.:	1,256-33	Length:	370
Score:	878.00	Matches:	173
Percent Similarity:	69.93%	Conservative:	41
Best Local Similarity:	56.54%	Mismatches:	79
Query Match:	35.94%	Indels:	13
DB:	1	Gaps:	4

US-10-705-757-3 (1-1302) x S55333 (1-370)

QY	27	CTTGCCACCACTGCGCGAGCCCTTGCAACGACTTGACCAAGAGTGGCCGGG	86
DB	69	ProSerProProVal---ThrProThrGlnProPro-----Gly-Gl	81
QY	87	CAAAAGAGAGAGCCCTGAGTGCAGTACCAAGGTGGCCCGCTGTGGCAACGGTGG	146
DB	81	LYLSAsprgrAlaAlaPheGlnAlaGluTyrTargenGlyProLeuGlnGlyGlyG1	101
QY	147	CTTGCGCTCGCTCTACTCGCGGCATCCGCGTGCACAACTTGCCTGGGACATCAACA	206
DB	101	YPheG1yThrValIPheAlaG1yHisArgValThrsprgrArgGlnValAlaIleLeuVa	121
QY	207	CGTGAGAGAGAGCCGAGATTTCGCACTGGGGGGGAATGCGCAACGAGCACCCAGAGCCAT	266
DB	121	IIleSerArgAnaArgValIleuGlyTTrpSerThrValSerAspSerValThrcysProLe	141
QY	267	GGAGTGTCTCTGCTGAAGAGGTG-----AGCTCGGGCTTCTCGGCGTCATTAGCT	320
DB	141	UG1uValAlaLeuLeuTTrpLysValIG1uG1uYanG1yHisProG1yValIIleArgLe	161
QY	321	TCTGACATGCTTCAGAGAGCCCGGATAGTTCGTCTGTATCTCGAGAGAGCCCGAACCCGT	380
DB	161	UleuAspTrpPheG1uThrProG1uG1yPheMetLeuValIleuG1uArgProMetProAl	181

[illegible]


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Db      235 lyleuProphlearghngliuleglnileCyleuGlyAanVallyserPheProAap 254
QY      778 GTTCTTCAGAAATGCAACATTTATTAAGTGTGCTGCTCCAGACATTCGACCG 837
Db      255 LeuSerlyseGluValCyseGlnleuVallyserCyseuThrThrSerThrsAlaArg 274
QY      838 CCTCTTCAGAAATTCAGAACATCCCTGATGCAG----- 876
Db      275 AlaSerleuAlaInleAlaAlaHleProTPrMetGluThrAspLyserProPheNegly 294
QY      877 ---GATGTTCTCTGCCCCAGCCGACCCGACGATT 909
Db      295 GlyAspLeuThrPheGlnGluAlaLeuMetGluIle 306

RESULT 7
T10449
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber
N/Alternate names: SNF1-related protein kinase
C/Species: Cucumis sativus (cucumber)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T10449
R/Gumpel, N.J.
submitted to the EMBL Data Library, December 1996
A/Reference number: Z17020
A/Accession: T10449
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residue: 1-504 <GDM>
A/Cross-references: UNIPROT:P91113; EMBL:Y10036
A/Experimental source: cv. Maeterpiece; cotyledon
C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C/Keyword: AMP-activated protein kinase; protein kinase homology
C/Keyword: AMP; phosphotransferase; serine/threonine-specific protein kinase
F/6-260/Domain: protein kinase homology <KIN>

Alignment Scores:
Pred. No.:      8,69e-11      Length:      504
Score:          381.50      Matches:      124
Percent Similarity: 46.39%      Conservative: 69
Best Local Similarity: 29.81%      Mismatches: 165
Query Match:      15.62%      Indels:      58
DB:              2          Gaps:      16

US-10-705-757-3 (1-1302) x T10449 (1-504)
QY      115 TACCAGGTGGCGCGCTGTTGGGACGCGTGGCTTGGCTGCTTACTCGGCGATCCG 174
Db      8 TylrlyseuGlylyThrleuGlylleglyserPheGlylyVallyleAlaGluHls 27
QY      175 GTGGCGGACAACTTGGCGGTCATGACGACGATGAGAAAGGACCGGATTCGACGTG 234
Db      28 AlaLeuThrGlyHlslyValAlaIlelyleleuAanArgArglyserIlelyValan--- 46
QY      235 GGGGAACTGGCCCAACGCGACCCGATGCCATGAGAGTGTCTCTGCTGAAGAGAGTGA 294
Db      47 -----leuAspMetGluGluValArgArgGluIlelyleleuAanArgleuPheMet 64
QY      295 TCGGGCTTCTCGGCGCTCATTTAATCTTGAAGTGTGTCGACAGCCCGATGCTTCG 354
Db      65 -----HisProHlsIleIleArgleuIleValIleGluThrProserAapIleTy 82
QY      355 CTGATCTCTGAGAGAGCCCGCAACCCGTGCAAGACTCTTGCATCTTACACCGACGAG 414
Db      83 ValValMetGluIlyrVallyser---GlyGluLeuPheAspLyrlleValGluLyGly 101
QY      415 GCCCTCCAGAGAGAGCCCGGAGCTTCTTGCAGAGTGTGAGAGCCGTGCGGAGAT 474
Db      102 ArgleuGlnGluAspGluAlaArgAanPhePheGlnIleIleIleSerGlyValGlyTy 121
QY      475 TGCCCAACAAGTGGCGGGTCTTCCACCGGACATCAAGACGAGAAATCTTAATGACCTG 534
Db      122 CyHlsIleArgAanMetValIleHisArgAspLeuLyserProIleuIleuLeuAap--- 140

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QY      535 AACCGGGGCAACTCAATCATGACTTGGGTTGGGGGCGCTGCTCAAGACAGATC 594
Db      141 SerLyserCyAanVallyleAlaAspPheGlyLeuSerAanIleMetArgAspGlyHls 160
QY      595 TACAGGACTTTGAC---GGAACCCGAGTGAACAGTCTCCAGAGTGAATTCGATCAAT 651
Db      161 PheleuLythrSerCyGlyserProAanTyrlaAlaProGluValIleSerGlyLy 180
QY      652 CGCTACACGAGAGGTGCGCTGCTGTTGTCCTCCGAGATCTGCTCATGACATGTC 711
Db      181 LeuTyrlaGlyProGluValAspValIlyserCyGlyValIleLeuTyrlaLeuLeu 200
QY      712 TCGGAGATATTCATTGAGACGACGAAAGATC-----GTCAAG 753
Db      201 CyseGlyThrleuProPheAsp---AspGluAanIleProAanLeuPheLyserIleLy 219
QY      754 GGCCAAGTGTAC---TTTAGCAAAAGGTCTCTTCAAGATTCACATCTTAATTAGATG 810
Db      220 GlyGlyIleTyThrleuProserHlsleuSerSerGlyAlaArgGluIleuIleProser 239
QY      811 TGCTGTCTCTGAGACATCGGACCGGCTCTTGAAGAAATCCAGAACATCCGTG 870
Db      240 MetleuValValAspProMetLyserGlyIleThrIleProGluIleArgGlnHlsProIty 259
QY      871 ATGCAAGATGTTCTCTGCCCCAGCCGACCGGAGATCATCTGACACAGCCTGTACCA 930
Db      260 PheGln-----AlaHlsleuProArgTyrlleuAlaValPro 271
QY      931 TCACCCAGCAATAGACGACATCTGTGACAGCTTCACAGGAAAGAGAGCTTGTCTGCT 990
Db      272 ProPro-----AapThrMetGlnGlnAlaIlelyserIleAspGlu 284
QY      991 GGCCTTCACACAGACCTGCTTACAGTACAGGACAGAAAGACAACTCATTCAGAGCT 1050
Db      285 AspIleleuGlnGluValVallyserGlyPheAspArgAan-----Glnleu 300
QY      1051 CCGGGGTCCCTGAGACAACTCCCTCAAGAGAAAGAGATTAAGTCA-----CTCGTCT 1104
Db      301 ValGlnSerleuAanArgAanArgIleGlnAanGlnAlaThrValAlaTyThrleuLeu 320
QY      1105 GGAACCCGCTTTGCCCTTCACAGACTCACTGAGCGTTCAGTGTGCTGCGTCCGCAAGT 1164
Db      320 uAspAanArgPhe-----ArgValserSerGlyTyrlleGlyAlaGluPheG 336
QY      1165 CCGGCTGTGGGGGGGAGAGTGGAGAGTGGGTGACAGCCCTTCATGAACTTAAGTCAC 1224
Db      336 nGluThrMet-----GluThrGlyPheAanArgMetHlsProserAapProth 352
QY      1225 CATGAGACTGTGGTCAACAA-----GATGGGCGCCAGGTTAGGGG----- 1264
Db      352 kAsnProAlaValGlyHlsArgleuProGlyTyrlMetAapTyrlGlnGlyMetGlyleuAan 372
QY      1265 -----AAAAACATTTGGGGGTTGGGATTAATAAACT 1294
Db      372 gAlaGlnPheProValGluArglyThrAlaIleuGlyleuGlnSer 387

RESULT 8
JC1446
serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana
N/Alternate names: protein kinase SNF1 homolog
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JC1446; S58266; S66334
R/LeGuen, L.; Thomas, M.; Blanchi, M.; Halford, N.G.; Kreis, M.
Gene 120, 249-254, 1992
A/Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protei.
A/Reference number: JC1446; MUID:93013041; PMID:1339373
A/Accession: JC1446
A/Molecule type: DNA
A/Residue: 1-512 <DEG>
A/Cross-references: UNIPROT:Q38997; GB:M93023; NID:g166599; PIDN:AAA32736.1; PID:g16660
R/Thummler, F.; Kirchner, M.; Teuber, R.; Dietrich, P.

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US-10-705-757-3 (1-1302) x T13741 (1-1398)

QY 3 GATGCTCTTGTCCAGATCACTC-----CCTGGCCCACT 38
   |||||
Db 94 AApAlaLeuLeuLaIaGlnLyLeuPheAlaSerGlyGlySerThrProGlyPro---- 112
   |||||
QY 39 GCGCGAGAGCCCTTGGACAGCTGCACCGCAACAGCTGGGCGCGGGC----- 87
   |||||
Db 113 -----SerProThrSerSerAlaValAlaGlyAla-----GlyGlyIleSerGly 126
   |||||
QY 88 -----AAGAGAGAGAGCCCTCGAG-----TCGCACTACAGAGTGGCGCCGCT 131
   |||||
Db 126 yLySaPheLeuLeuLeuLyLeuLeuGluProMetArgValGlyPheTyAlaSerIleGluArgTh 146
   |||||
QY 132 GTTGGGCGAGCGGTGGCTTCGAGCTCGGTC---TACTGGGGGATCCGGCTCGCGCAACAATT 188
   |||||
Db 146 rIleGlyLyGlyAlaSerPheAlaValLyLeuAlaArgHisArgIleThrLySerAsn-- 165
   |||||
QY 189 GCGGCTGGCATCAGACGTGGAGAGAGACCGGATTTCCGACTGGGGGGGAACCTGGCCAA 248
   |||||
Db 166 -GluValAlaAlaIleLyLeuIleAlaPheLySerGlnLeu-----AspGlnThrAs 181
   |||||
QY 249 CCGGACCCGAGTCCGACATGAGAGTGTCTCTGAAAGAGTGAAGCTCGGCTTCGCGG 308
   |||||
Db 181 nLeuGlnLyValIlyArgGluValGluIleMetLySerGluLeuLy-----HisProH 199
   |||||
QY 309 CGTCATTAGACTTCTGAGCTGTGTCCAGAGCCCGATGTTGTCTGTATCTGTAGAGAG 368
   |||||
Db 199 sIleIleLyLeuLyGlnValMetGlnThrLySerMetIleTyIleValSerIleLy 219
   |||||
QY 369 GCCCGAACCCGTCAGAGACTTCTGCATTCACCGAGCGAGAGCCCTCCAGAGAGA 428
   |||||
Db 219 rAlaSerGln---GlyGluIlePheAspTyIleAlaLySerGlyAlaArgMetSerGlnSe 238
   |||||
QY 429 GCTGGCCCGAGGCTTCTTGGCAGGTGTGAGGCGCGTGGCAGCTTCCCAACAATGCGG 488
   |||||
Db 238 rAlaAlaArgPheLyPheThrGlnIleIleSerAlaValAlaGluTyCyHisIleLySerG 258
   |||||
QY 489 GGTTCCTCCACCGGACATCAAGACGAGAACATTTATAGACTTGAACCGCGGCAACT 548
   |||||
Db 258 yIleValHisArgHisPheLeuLyAlaGluAlaLeuLeuAlaSerLeuAlaSerMet---AsnI 277
   |||||
QY 549 CAAACTCATGCACTTCGCG---TCGGGGGCGCTGCTCAAGACACAGACTTACACGAGACT 605
   |||||
Db 277 eLySerIleAlaSerPheGlyPheSerAsnHisPheLySerProGlyGluLeuLeuAlaThrTr 297
   |||||
QY 606 TGAAGAAACCGAGTACAGTCTCTCCAGAGTGAGATTCCGTAACATCCATCCACGCGAG 665
   |||||
Db 297 pCySerGlySerProProTyAlaAlaProGluValPheGluGlyLyGlnIlyThrGlyP 317
   |||||
QY 666 GTGGGCTGTGTGGTTCCTGGGAGATCCGTCTATAGACATGTCTGCGGAAATATTC 725
   |||||
Db 317 oGluIleAspIleTrpSerLeuGlyValIleValIleuTyValIleuValCySerGlyAlaLeuP 337
   |||||
QY 726 ATTGAGACAGAC-----GAAGAGATGTCAGAGGCGCAAGTGTACTT 767
   |||||
Db 337 oPheAspGlySerThrLeuGlnSerLeuArgAspArgValLeuSerGlyArgPheArgI 357
   |||||
QY 768 TAGGCAAAAGGCTCTTCAAGATGTCACATCTTATTAGATGGTGGCTGTCTGAGACC 827
   |||||
Db 357 eProPhePheMetSerSerGlnCySerGlnHisIleuIleArgArgMetLeuValIleuGluP 377
   |||||
QY 828 ATGAGACCGGCGCTCTTGAAGAAATCCAGAACATCCGCGATGAGAGATTTCTCC 887
   |||||
Db 377 oThrArgAlaGlyTyThrIleAspGlnIleLySerGlnHisArgIlyPheCysProGluLeu 397
   |||||
QY 888 GCCCAGAGCGACCGGATTCATCTGACAGAGCTGTACCATCCAGCAATAGCA 947
   |||||
Db 397 u-----Glu-HisValLeuIleAlaLySerTyArgnLeuGlyAlaGluArg 412
   |||||
QY 948 GCCATTCTGTCAAGCCTCCAGGGAA----- 973
   |||||

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Db 412 InThrSerValGluProSerGluAspIleLeuArgIleMetAlaGluTyValGlyIleG 432
QY 974 -----GAGAGAGCTGTCTG-----CTGGGCTCCACA 1001
   |||||
Db 432 LySerAspLyThrArgAlaSerLeuLyLySerAsnThrTyArgAspHisValAlaAlaIleT 452
   |||||
QY 1002 GGACCTGCTCTTACAGATGAGGAGACAGAAATGACATCATTCATCCAGCTCCGGGGTCCCT 1061
   |||||
Db 452 yLeuLeuLeuGlnAsp-----ArgValSerHisLyLySerGluGlnSer-Asn 467
   |||||
QY 1062 GGA-----GCAACTTCCTCAAGAGAGAGAGACTAGTTCACTTCGTC 1103
   |||||
Db 468 GlnGluGlyAlaSerAlaLeuAlaSerThrSerAlaSerArgMetIleTySerSer 487
   |||||
QY 1104 TGGACCCGCTTGGCCCTCACAAGACTGAG 1133
   |||||
Db 488 ArgAsnAspHisGlnProThrGlnGlnGln 497

RESULT 10
I49072
protein kinase - mouse (fragment)
Cispecies: Mus musculus (house mouse)
Cidate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
Cidaccession: I49072
R/Ruiz, J.C.; Conlon, P.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A>Title: Identification of novel protein kinases expressed in the myocardium of the deve
A|Reference number: I49071; MUID:95200798; PMID:7893599
A|Accession: I49072
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: mRNA
A|Residues: 1-481 <RBS>
A|Cross-references: EMBL:U11494; NID:9595420; PIDN:AAA67926.1; PID:9595421
C|Superfamily: protein kinase homology
C|Keywords: ATP
F|71-324/Domain: protein kinase ATP-binding motif
F|79-87/Region: protein kinase ATP-binding motif

Alignment Scores:
pred. No.: 1,276-10 Length: 481
Score: 378.00 Matches: 97
Percent Similarity: 51.37% Conservative: 53
Best Local Similarity: 33.22% Mismatches: 116
Query Match: 15.47% Indels: 26
DB: 2 Gaps: 10

US-10-705-757-3 (1-1302) x I49072 (1-481)

QY 28 CTGGCCCACTTGGCGGCGACCCCTTGCACGACCTGCACGCGCAACAGCTGGCGCGGC 87
   |||||
Db 51 MetSerGluPheArgAlaValProSer-----GlyThrGly 62
   |||||
QY 88 AAAAGAGAGAGACCCCTGAG---TCGCAGTACAGTGGGCGCGCTGTGGAGCGGT 144
   |||||
Db 63 ArgSerGlnLySerProLeuArgValGlyPheTyArgValGluArgThrLeuGlyLyGly 82
   |||||
QY 145 GGTTCGGCTCGGTC---TACTGGGATCCCGCTGCGAGACAACTTGGCGGCGCATC 201
   |||||
Db 83 AsnPheAlaValValLyLeuArgGlyHisArgValThr---LyThrGlnValAlaIle 101
   |||||
QY 202 AAGCAGTGAAGAGACCGGATTTCCGACTGGGGGAACTCCCAACGCGACCGGAGT 261
   |||||
Db 102 LyIleIleAspLyThrArgLeu-----AspSerSerAsnLeuGluLyIle 117
   |||||
QY 262 CCCATGAGATGTGCTCTGTGAAGAGTGAAGTGAAGTCTCGGCTTCTCGGCGCTTATGACTT 321
   |||||
Db 118 TyArgGluValAlaGlnMetLySerLeuAsn-----HisProAsnIleIleLySer 135
   |||||
QY 322 CTGAGCTGTTGAGAGGCGCGATGATTCTGCTGATCTGAGAGAGCGCGAACCGGT 381
   |||||
Db 136 TyArgValMetGlnThrLySerPheMetLeuTyIleValThrGluPheAlaLySerAsn--- 154
   |||||
QY 382 CAAGACTTCTGACTTCATCAACGAGAGAGCGCTTCAGAGAGAGCTGGCGCGAGC 441
   |||||

```


C: Superfamily: AMP-activated protein kinase; protein kinase homology
C₁: Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Alignment Scores:
Pred. No.:

Pred. No.:	2.37e-10	Length:	51
Score:	372.00	Matches:	66
Percent Similarity:	45.61%	Conservative:	11
Best Local Similarity:	29.07%	Mismatches:	15
Query Match:	15.23%	Indels:	66
DB:	2	Gaps:	15

US-10-705-757-3 (1-1302) X T52633 (1-512)

QY	97	GAGCCCTCGAGTCCGACGATCAAGAGTGGGCGCGCTGTGGGACGCGTGGCTTCGGCTCG	156
Db	14	GUSeSTLeLeuProaenTyrluVleuGluYvThrLeuIdlylIleGlySerPheGluYv	33
QY	157	GTCTACTCGGGATCCGCGCTCGCGGCAACTTCGTCGGAGCCATCAAGACGCTGGAGAAG	216
Db	34	VallvPleAlaGluHstValValThrGluHleYvAlaAlaIleYvStleuAenAng	53
QY	217	GACCGATTCCGATCGAGGGGAACTGCCCAACGCGAACCCGAGTCCCATGAGTGC	276
Db	54	ArgYvStleYvAen-----MetGluMetGluGluYvAlaValArgArgGluIleYv	70
QY	277	CTGCTGAAGAAGGTAGAGCTCGGGCTTCGCGGCGTCAATTGATTCGAGCTGGTTCAG	336
Db	71	IleLeuAArgLeuPheMet-----HisProHstIleIleArgGluYvrgIuValIleGlu	88
QY	337	AGCGCCGATAGTTCGTGCTGATCTCGAAGAGCCGGAACCCGATCGAGAAGACTTTGCAC	356
Db	89	ThrlThrSerAAspIleTyvAlValMetGluTyvValIlySer---GluIleuPheAer	107
QY	397	TTGATTCACCGACGAGACCCCTCCAGAGAGACTGGCGGAGCTTCCTTCGCGAGTg	456
Db	108	TyrlIleValGluYvStleYvArgLeuGluGluAAspGluAlaArgAenPhePheGluGluIle	127
QY	457	CTGAGGCGCGTGGCTGGATTCGCAACTGCGGGGTTCGCAACCGGACATCAAGACGAG	516
Db	128	IleSerGluYvAlGluYvrcYvHstAArgAenMetValValHstAArgAenIlyvProGlu	147
QY	517	AACATCTTATGACTGCTGAACCGCGGCGAACTCAAACTCATGACTTCGGGTGGGGCG	576
Db	148	AenIleuLeuAAsp---SerArgCyvAenIleYvAlleAlaAAspPheGluLeuSerAen	166
QY	577	CTGCTCAAGACACAGCTTACACGAGACTTGAC---GAACCCGAGGTACAGTCTCCCA	633
Db	167	ValMetAArgAAspGluHstPheLeuYvThrSerCyvStleYvSerProAenTyrlAlaAPro	186
QY	634	GAGTGATTCGCTTACCATCGCTACCAACGCGAGGTGGGCTGTGGTTCCTCGGGAGT	693
Db	187	GluValIleSerGluYvLeuTyrlAlaGluYvProGluValAlaAAspIlyvSerCyvStleYvAl	206
QY	694	CTGCTCTTACGACATGCTGCGGAGATTCATTCATTTGAGACAGACGAAGAAGATC-----	747
Db	207	IleLeuTyrlAlaLeuLeuCyvStleYvThrlLeuProPheAer---AAspGluAenIleProAen	225
QY	748	-----GTCAAGGCGCCAAAGTGAC---TTTAGCGAAAGGCTCTTCAGATGT	792
Db	226	LeuPheIlyvStleYvStleYvStleYvIleTyvThrlLeuProSerHstIlyvSerStleGluAla	245
QY	793	CACATCTTATTAAGATGAGTGCCTGCTCCCTGAGACATCGACCGGCGCTCTTGAAGA	852
Db	246	ArgAAspLeuIleProAenMetLeuIleValAAspProValIlyvArgIleThrlIleProGlu	265
QY	853	ATCCGAACACATCCGAGATGACGAGATGTTCTCTGCGCCAGGCGACCGCGAGATTGAT	912
Db	266	IleArgGluHstAArgTlrPheGlu-----ThrlHst	275
QY	913	CTG---CACAGCTGTCAACCATCAACCCAGAAATAGACGACCATTTGTGACACCTTCAG	968
Db	276	LeuProAArgTyrlleuAlaValSerProPro-----AAspThrlValGlu	289

QY	970	GGAAGAGAGAGCTGTGTCTGGCGCTCCACAGAC-----	1005
		::: ::: ::: :::	
Db	290	GlAlaLySvIleAenGluGlnIleAlaGlnIleValAlaMetGlyPheAspArg	309
		::: ::: ::: :::	
QY	1006	-----CCTGCCTACGATGACGGACGCAAAAT-----	1032
		::: ::: ::: :::	
Db	310	AsnGlnValLeuGlnIuSerLeuArgAsnArgThrGlnIleAsnAlaIatnValIthrTyTyr	329
		::: ::: ::: :::	
QY	1033	-----GACACTCATTCACAGGCTCCG-----GGGTCCCTGGAGCAACT-----	1071
		::: ::: ::: :::	
Db	330	LeuLeuLeuAspAsnArgPheArgValProSerGlyTyrLeuGlnIuSerGlnPheGlnIu	349
		::: ::: ::: :::	
QY	1072	-----CCCTCAAGAGAAAGACTGATTCACCTCGTCTGACCC	1110
		::: ::: ::: :::	
Db	350	ThrIhrAspSerGlySerAsnProMetArgIhrProGlnIuAlaGlyAlaSerProValGly	369
		::: ::: ::: :::	
QY	1111	CGCTTTGGCCCTCACAGACTCAGTGGCGCTCCAGTGGCGGTCCGCAAGTCCC	1167
		::: ::: ::: :::	
Db	370	HisIrrPleProAlaHisValAspIleItyrGlyLeuGlnAlaArgSerGlnValPro	388
		::: ::: ::: :::	

RESULT 13

serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco
C:Species: Nicotiana glauca (common tobacco)
C:Date: 28-Apr-1995 #sequence_rev1995 #text_change 09-Jul-2004
C:Accession: A56009
R:Murataka, T.; Banno, H.; Machida, Y.
Mol. Cell. Biol. 14, 2958-2965, 1994
A:Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces cerevisiae.
A:Reference number: A56009; MUID:94217693; PMID:8164654
A:Accession: A56009
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-511 <MR>
A:Cross-references: UNIPROT:Q00544; GB:D26602; NID:G496384; PTDN:BA005649.1; PID:G496385
C:Function:
A:Description: catalyzes the formation of peptidyl-L-serine-phosphate or peptidyl-L-threonine-phosphate
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F:117-271/Domain: protein kinase ATP-binding motif
F:25-33/Region: protein kinase ATP-binding motif
F:148,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F:147,151/Binding site: magnesium (Aen, Asp) #status predicted

Alignment Scores:	
Pred. No.:	2.78e-10
Score:	370.50
Percent Similarity:	47.79%
Best Local Similarity:	28.91%
Query Match:	15.17%
DB:	1
	9
	3
	5
	511
Length:	
Matches:	98
Conservative:	64
Mismatches:	142
Indels:	35
Gaps:	9

US-10-705-757-3 (1-1302) x A56009 (1-511)

```

QY      85  GGCAGAAAGAGAGAGACCCCTGGAGTCGCAAGTCCAGAGTGGGCCCGCTGTTGGGCAACGCT 144
Db      9   GlySerSerValGluSerPheLeuArgaenTYrLYSLenGLiLYrThrLeuGLiLYgly 28
QY      145 GGGCTTCGGCTCGGTCTACTCCGGGCAATCCGCTCGCGCAACATTGGCCGGTGCCATCAAG 204
Db      29  SerPheGLiLYrValLYrLeaLagLuihIsthrLeuthrGLYhiLYrValaLYaLYrLYs 48
QY      205 CACGGAGAGAAAGACCCGATTTCCAGCTGGGGGAAACTGCCCAAGCGCACCCGAGAGCCC 264
Db      49  IleLeuAenArgArgLYrLeLYsAsn-----MetGluMetCuiGLiLYrValArg 65
QY      265 ATGGAAGTGGCTCTGCTGAAGAAGGTGAAGCTCGGGCTTCGGGCGCTCATTAGCTTCTG 324
Db      66  ArgGluIleLYrIleLeuArgLeuPheMet-----HisProhIstIleLeaLYrLYr 83
QY      325 GACTGGTTCGAAGAGCCCGCATGTTTCGTCGATTCCTGAGAGAGCCCGCAACCCGTGCA 384

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Db 84 GluValValGluThrProSerAspIleTyrValValMetGluTyrValIleSer---Gly 102
 QY 385 GACCTCTTGCATTGCACCGGAGAGCCCTCCAGAGAGAGCGGCCGAGCTTC 444
 Db 103 GluLeuPheAspTyrIleValGluValArgLeuIleGluPheGluValAspGlyPhe 122
 QY 445 TTTCGAGGTTGTCGAGGCGGTCGATTCGACAACTGCGGGGTTCTCAACCGGAG 504
 Db 123 PheGlnIleIleIleSerGlyValGluTyrCysHisArgAspMetValHisAspArg 142
 QY 505 ATCAAGACGAGAAACATTTAATGACGTGAACCGCGCGAACTCAAACTCATGACTTC 564
 Db 143 LeuIleProGluLeuLeuLeuLeuAsp---SerIleTyrAsnValIleAlaAspPhe 161
 QY 565 GGGTCGGGGCGCTGCACAGACAGCTACAGCACTTTGAC---GGAACCCGAGTG 621
 Db 162 GlyLeuSerAsnIleMetArgAspGlyHisPheLeuIleTyrSerCysGlySerProAsn 181
 QY 622 TACAGTCTCCAGAGTGATTCGCTACATCGCTACACGAGGAGTGCGGCTGTTTG 681
 Db 182 TyrAlaIleProGluValIleSerGlyLeuLeuTyrAlaGlyProGluValAspValTyr 201
 QY 682 TCCCTGGGATCTCTGTATGACATGCTGCGAGATATTCATTGACAGCAGC--- 738
 Db 202 SerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspArgIleAsn 221
 QY 739 -----GAAGAGTGTGACAGGCGCAAGTGTATTTAGCAAAAGGCTCT 783
 Db 222 IleProAsnLeuPheLeuValIleValGlyMetIleSerLeuProSerHisLeuSer 241
 QY 784 TCAGAAATGCACATCTTATTAGATGCTGCTCCAGACCATGAGACCGGCTTC 843
 Db 242 AlIGlyAlaArgAspLeuIleProArgMetLeuIleAlaProMetIleValArgMetTyr 261
 QY 844 TTGAAAGAAATCCAGAACATCCGCTGATGACAGATGTTCTCTGCCCCAGGACCGCC 903
 Db 262 IleProGluIleArgMetHisProTyrPheGln-----Ala 273
 QY 904 GAATTCATCTGCACAGCCCTGTACCATCCAGCAAAATAGCAGCATTTCTGTACAGCC 963
 Db 274 HisLeuProArgTyrLeuAlaValProProPro-----AspThr 286
 QY 964 CTCGAGGAGAGAGAGCTGTCTGTGCTGCAACAGACCCCTGTCTAAGTAGAGG 1023
 Db 287 MetGlnGlnAlaLeuValIleAspGluAspIleLeuGlnIleValIleValAspGlyPhe 306
 QY 1024 GACAGAAATGAC-----AACTCATTTCCAGGCTCCGGGCTCCCTG 1062
 Db 307 AspArgAsnSerLeuValAlaSerLeuCysAsnArgValGlnAsnGluGlyThrVal 325
 RESULT 14
 T20941
 hypothetical protein F15A2.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T20941
 R:Category: J.
 submitted to the EMBL Data Library, March 1996
 A:Reference number: Z19349
 A:Accession: T20941
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-887 <MIL>
 A:Cross-references: UNIPROT:Q19469; EMBL:Z70207; PIDN:CAA94127.1; GSPDB:GN00028; CESP:F1
 A:Experimental source: clone F15A2
 C:Genetics:
 A:Gene: CESP:F15A2.6
 A:Map position: X
 A:Functions: 32/1; 63/3; 92/2; 139/2; 189/3; 328/2; 448/2; 516/3; 604/2; 684/3; 735/2; 777
 Alignment Scores: 3.92e-10 Length: 887
 Pred. No.: 366.50 Matches: 119
 Score:

Percent Similarity: 44.37% Conservative: 70
 Best Local Similarity: 27.93%
 Query Match: 15.00% Indels: 71
 DB: 2 Gaps: 15
 US-10-705-757-3 (1-1302) x T20941 (1-887)
 QY 115 TACAGATGGAGCGCGCTTTGGGACCGGCTTGGCTCGCTGCTTACTCGGCACTCCG 174
 Db 20 TyrLeuLeuGluIleThrLeuGluIleValGlnIleThrGlyLeuValIleThrArgIleHis 39
 QY 175 GTGCGGCAACAATTGCGCGGTCATTAAGACAGCATGTAAGAGACGAGATTTCCGACTG 234
 Db 40 CysIleThrGlyArgValAlaIleValIleValAsnValGluIleValSerGlu--- 58
 QY 235 GGGAAATGCCCAACGAGCAACCGAGTCCCAAGATGCTCTGCTGAAGAGTGAGC 294
 Db 59 -----SerValLeuGlnIleValGluArgGluIleAlaIleMetIleValIleGlu 75
 QY 295 TCGGCTTCGAGGCTCATTAAGATTTGAGATGCTGTTGAGAGGCGCGATTTGCTG 354
 Db 76 -----HisProHisValLeuHisIleValTyrAspValTyrGluAsnValIleValTyr 93
 QY 355 CTGATCTGAGAGAGCGCCGCAACCGTGAAGACCTTCTGCAAGTGTGAGCGCTGCGGAT 474
 Db 94 LeuLeuLeuGluIleHisValSerGly---GlyGluLeuPheAspTyrLeuValArgIleVal 112
 QY 415 GCGCTCCAGAGAGAGCTGCGCGGAGCTTCTTGTGCAAGTGTGAGCGCTGCGGAT 474
 Db 113 ArgLeuMetSerIleGluIleAlaArgIlePhePheArgGlnIleIleSerHisLeuAspPhe 132
 QY 475 TGCCCAACATGCGGGGTTCTCCACCGGACATAGAGAGCAATTTATTCAGCTG 534
 Db 133 CysHisAlaHisAsnIleCysHisAspArgLeuIleProGluAsnLeuLeuAsp--- 151
 QY 535 AACCGGCGGCAATCAACATTCATCGACTTCGAGGTCGCGGCGCTG---CTCAAGACCA 591
 Db 152 GluArgAsnAsnIleLeuValAlaAspPheGlyMetAlaSerLeuGlnValGluGlySer 171
 QY 592 GTGTACACGACATTTGACGAGAACCGAGTGTACAGTCTCCAGAGTGTGCTGCTCAT 651
 Db 172 MetLeuGluIleThrSerCysGlySerProHisTyrAlaCysProIleValIleAspGlyGlu 191
 QY 652 CGGTACACAGGAGAGCTGCGCTGCTTTGGTCCCTGGGATCTGCTTATGACAGCTG 711
 Db 192 LysTyrAspGlyArgIleValAspValIleTyrSerCysGlyValIleLeuTyrAlaLeu 211
 QY 712 TCGGAGATATTCATTTAGACAGCAGC-----GAAGAGATGTGACG 753
 Db 212 ValGlyAlaLeuProPheAspArgAspArgAsnLeuAspValLeuGluIleValIleValArg 231
 QY 754 GGCAGATGATCTTTAGGCAAGAGGCTCTTCAATGTCACATCTTATTAGATGCTG 813
 Db 232 GlyValPheHisIleLeuProHisPheValProHisAspValGlnSerLeuAspArgLamet 251
 QY 814 CTGTCCTGACAGCATGCGAGCGGCTCTTTGAAGAAATCCAGAACCATCCGCTGAGT 873
 Db 252 IleGluValAspProGluLysArgTyrSerLeuAlaAspValPheLeuHisProTyrVal 271
 QY 874 CAGGATGTTCTGCTGCGGCAAGCGGCGGAGATTCATCTGACAGCGCTGTACATCA 933
 Db 272 SerGlyThr-----ThrValAspProGluIleLeu----- 283
 QY 934 CCCAGCAAAATAGACAGCATTTGTGACAGCTCCAG-----GGAAGAGAG 978
 Db 284 -----PrometSerGlnValValGlnIleThrHisValIleProGluGluAsp 298
 QY 979 AGTTTGTCTGCTGCG---CTCCAAAGAGACCTGCTTACAGTGC---AGGACAGAAAT 1032
 Db 299 SerIleAspProAspValLeuArgHisMetAsnCysValLeuGlyCysPheLysAspLys-Gl 318
 QY 1033 GACAACTATTCAGGCTCCGCGGCTCCGAGCAACCTC----- 1072

Db 318 nlyslleuileAenGluleuLeuSerProlyshIsaenThrGlulylMetValtyr-Phele 338
 QY 1073 -----CCTCAGAGAAAGAGACTAGTACTGCTGCTG-- 1105
 Db 338 uleuLeuAparGlysaArgaArgProAlaInglnuAparThGlulileuLear 358
 QY 1106 -----GACCCGCTTTGGCCCTCAGAGCTCAGTGGCTCAGTGT 1146
 Db 358 gGlyAlaAlaInglnAenAparProProlyslYsaArgThrAparSerArgThrSer-- 377
 QY 1147 GCGTGGCTGCCAGAGTCCCGGCTTTGGGGGGAGGTGGAGTGGGTCAAGCCCTG 1206
 Db 378 -----ArgTyrProMetGlySerIleAlaAparGlySerProIleAasnPro-- 392
 QY 1207 TCATGAACTTATAGTACCATGAGACTGTGGGTACCAAGATGGCCAGGTAGGGGAA 1266
 Db 393 -----ArglyeThrTyrGlyArg-AenGlnYsaSerGlyArgHis 406
 QY 1267 AAACATTGGGGGG 1280
 Db 406 erSerleuclGly 410

RESULT 15

S33653

probable serine/threonine protein kinase (EC 2.7.1.-) - Yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YAL002; protein YAL017w; secretory protein SPP138

C:Species: Saccharomyces cerevisiae

C>Date: 30-Sep-1993 #sequence_revision 02-Aug-1994 #text_change 16-Aug-2004

C/Accession: S33653; S36717; S36732; U00486

R:Clark, M.W.; Zhong, W.W.; Keng, T.; Storme, R.K.; Ouellette, B.F.F.; Barton, A.; Kabac

Yeast 9, 543-549, 1993

A>Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae enc

A:Reference number: S33653; MUID:93311122; PMID:8322517

A:Accession: S33653

A:Structure: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-1358 <CLA>

R:Ouellette, F.; Clark, M.W.; Keng, T.; Storme, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; D

submitted to the EMBL Data Library, January 1993

A:Description: Sequencing of Chromosome I from Saccharomyces cerevisiae: analysis of a 3

A:Reference number: S36711

A:Accession: S36717

A:Molecule type: DNA

A:Residues: 1-864,867-1358 <ONE>

R:Clark, M.W.; Zhong, W.W.; Keng, T.; Storme, R.K.; Barton, A.; Kaback, D.B.; Bussey, H.

Yeast 8, 133-145, 1992

A>Title: Identification of a Saccharomyces cerevisiae homolog of the SNF2 transcriptiona

A:Reference number: S22266; MUID:92221690; PMID:1561836

A:Accession: S36732

A:Structure: translation not shown

A:Molecule type: DNA

A:Residues: 1-862 <CL2>

R:Sidhu, R.S.; Mathewes, S.; Bollon, A.P.

Gene 107, 111-118, 1991

A>Title: Selection of secretory protein-encoding genes by fusion with PHOS in Saccharomy

A:Reference number: JH0483; MUID:92077420; PMID:1743509

A:Accession: JH0486

A:Molecule type: DNA

A:Residues: 1-72, 'E', 74-154 <SID>

C:Genetics:

A:Gene: SGD:FUN31; SSP138

A:Cross-references: SGD:S0000015; MIPS:YAL017w

A:Map position: 1L

C:Superfamily: protein kinase homology

C:Keywords: ATP; glycoprotein; phosphotransferase; serine/threonine-specific protein kin

F:1096-1356/domain: protein kinase homology <KIN>

F:1104-1112/region: protein kinase ATP-binding motif

F:8,128/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:1232/Active site: Asp #status predicted

Alignment Scores:
 Pred. No.: 3,886-10 Length: 1358
 Score: 366.00 Matches: 86
 Percent Similarity: 55.04% Conservative: 56
 Best Local Similarity: 33.33% Mismatches: 100
 Query Match: 14.98% Indels: 16
 DB: 2 Gaps: 6

US-10-705-757-3 (1-1302) x S33653 (1-1358)

QY 133 TTGGCAGCGGTGGCTTGGCTCGGTCTAATCGGCAATCCGGTCCGACACTTGGCG 192
 Db 1104 MetGlyGlnGlyAlaTyrGlyValAenLeuCyIleHleIleYsaAsnArgTyrIle 1123
 QY 193 GTGGCATTCAAGCAGCTGAGAGAGCGGATT-----TCGACGTGGGGGGAATCGGCC 246
 Db 1124 ValValIleYsaMetIlePheYsaGlnTyrGlyIleValAparThrTyrValArgAparG 1143
 QY 247 AACGCGACCCGAGTCCCATGTGAGAGTGGTCTGTGAAAGAGTAGC--TCGGGCTTC 303
 Db 1144 LysLeuGlyThrIleProSerGlnIleGlnIleMetAlaThrLeuAsnLysProHis 1163
 QY 304 TCGGCGTCATTAGACTTCTGACTGTTCAGAGAGCCGATAGTTGTGCTGATCTCG 363
 Db 1164 GlnAenIleLeuArgLeuAparPhePheGlnAparAparTyrTyrIle----- 1181
 QY 364 GAGAGCCCGAACCCTGCAG-----GACCTTCGACTTCATCAC 405
 Db 1182 -----GlnThrProValHisGlyGlnTyrGlyCyIleAparPhePheIleGln 1199
 QY 406 GAGCGAGAGCCCTCAGAGAGAGTGGCCCGGACTTCTTGTGCAAGTGTGAGAGCC 465
 Db 1200 PheYsaThrAenMetThrGlnPheGlnAlaLysLeuIlePheYsaGlnValValAagly 1219
 QY 466 GTGGCGCAATTCGCAACTCGCGGCTTCCACCCGCACTCAAGAGAGAGAACTCTTA 525
 Db 1220 IleYsaHleYsaHleAparGlnIleValHisAparIleYsaAparIleAparValIle 1239
 QY 526 ATCGACCTGGAACCGGCGGAGAACTCAAACTCACTCGGCTCGGGGCGCTGCAG 585
 Db 1240 ValApar---SerYsaGlyPheValYsaIleIleAparPheGlySerAlaIaTyrValYsa 1258
 QY 586 GACACAGTCTACACGCACTTTGACCGAAACCGAGGTACAGTCTCCAGAGTGTATCGC 645
 Db 1259 SerGlyProPheAparValPheValGlyThrIleAparTyrAlaAlaProGlnValLeugly 1278
 QY 646 TACCATTCGCTACACGAGAGTGGCTGTGTTGCTCCCTGGGATCTGCTTATGAC 705
 Db 1279 GlnAenProTyrGlnGlyGlnProGlnAparIleTyrAlaIleGlyIleLeuLeuTyrThr 1298
 QY 706 ATGTCCTGGAGATATTCATTGAGACGACGAAAGATGTCAGAGGCGCAAGTGTAC 765
 Db 1299 ValValIleYsaPheYsaPhePheTyrAenIleAparGlnIleGlnGlnLysPheLys 1318
 QY 766 TTTAGG-----CAAAGGCTCTTTCAGAAATCAACTTTATAGATGTCCTGTC 819
 Db 1319 PheAenAenAlaGlnGlnValSerGlnAparCyIleGlnLeuIleYsaSerIleLeuAen 1338
 QY 820 CTGAACCATCGGAGCGGCTCTTGAAGAAATCCAGAACATCCGTGATG 873
 Db 1339 ArgCyValProYsaArgProThrIleAparIleAenAenAparYsaPheLeu 1356

Search completed: September 22, 2005, 17:20:31

Job time : 58.6688 secs

[illegible]

i		ORGANISM: Mus musculus	
US-05-644-450-7			
Alignment Scores:			
Pred. No.:	4.9e-144	Length:	313
Score:	1668.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.37%	Indels:	0
DB:	3	Gaps:	0
US-10-705-757-5 (1-942) x US-09-644-450-7 (1-313)			
QY	1	ATGCTCCCTGCATCAAGATCAACTCCCTGGCCCAACCTGGCGCCGCCCTTGCAACGACCTTG	60
DB	1	McteuLeuSerLyVleIaSnSerLeuAlaHsLeuAArgAlaArgProCyShmShpLeu	20
QY	61	CACGCCAACCAAGCTGCGCCGCCGGAAGAAAGAGAGCCCTTGAGTCGACGATCAACGAGTG	120
DB	21	HlsAlaThrLySLeuAlaProGlyLySgLuLySgLuProLeuGlnSerLInTyrgLInVal	40
QY	121	GAGCCCGCTGTGTGGGACGCGGTGGCTTGCGCTCGGTACTCTGGCATCCGCGTCCGCCAG	180
DB	41	GlyProLeuLeuGlySerGlyGlyPheGlySerValTySerGlyIleArgValAlaAsp	60
QY	181	AACTTGGCCGGTGGCCATTAAGACGATGAGAAAGACCGGATTTCCGATTGGGGAGAACTG	240
DB	61	AbmLeuProValAlaIleLyShHsValGluLyShAspArgLsSerShpTrpGlyGluLeu	80
QY	241	CCCAATGACACCCGAGTGCCCATGGAGTGTCTCTGTGAAGAAAGGTGAGCTCGACCTTC	300
DB	81	ProAnGlyThrArgValProMetGluValLeuLeuLyLysLeuValSerserAspPhe	100
QY	301	TGCGGCGCTCATTAAGCTTGTGACCTGTTCGAGAGAGCCCGATAGTTTCGTCTGATCTCG	360
DB	101	SerGlyValIleArgLeuLeuAspTrpPheGlyuArgProAspSerHsValLeuIleLeu	120
QY	361	GAGAGAGCCCGAACCGGTGACAGACTCTTCGACTTATCAACGAAAGAGAGCCCTACAG	420
DB	121	GluArgProGluProValGlnShpLeuHsPheIleThrGluArgGlyAlaLeuGln	140
QY	421	GAGGACCTGGCCCGAGATTCTTCTGGAGGTGCTGAGAGCCGTGGCGGATTTGCCAACC	480
DB	141	GluShpLeuAlaArgGlyPhePheTrpGlnValLeuGluAlaValAlaArgHsCyShHsAsn	160
QY	481	TGCGGGGCTTCCACCCGCGACATCAAGACGAGAACTTTAATGACCTTGAGCGCGCGC	540
DB	161	CysGlyValLeuHsIAspArgSprLeyAspGlyuAnIleLeuIleAspLeuSerAspGly	180
QY	541	GAATCAACTCATGACATTCGAGTGGGAGGCGGCTGCTCAAGACACAGTCTTACAGCGAC	600
DB	181	GluIleLySLeuIleAspPheGlySerGlyAlaLeuLeuLyAspPhrValTyTrpThrAsp	200
QY	601	TTTGATGGAGCCCGAGTGAAGTCTTCCAGAGTGAGATTGCTTACCATGCTTACACAGGC	660
DB	201	PheAspGlyThrArgValTySerProProGluTrpLleArgTyxHsIAspGlyxHsIAspGly	220
QY	661	AGTGGCGGACGCTGTGGTCCCTTGAGATCCGCTCTAAGATAGATGCTTCGCGGAGATATT	720
DB	221	ArgSerAlaValAlaValTrpSerLeuGlyIleLeuLeuTyAspMetValCySgLyAspIle	240
QY	721	CGATTGAGACGATGAGAGATCATCAAGGGCCCAAGTCTTCTTCAAGGCAACTGTCTCT	780
DB	241	ProPheGlyuHsIAspGlyGluIleIleLySgLyGlnValPhePheArgGlnThrValSer	260
QY	781	TCAGAGTGCAGACCTTATTAAATGTGTGCTGTCCCTTGAGACCGTCAGATCGCCCTTC	840
DB	261	SerGlyuCySgLyHsIleLeuIleLyTrpCySleuSerLeuArgProSerAspArgProSer	280
QY	841	TTTGAAGAAATCCCGAACAACATCCGATGATGCAAGGGTGAACCTTCGCCGACGAGCTTC	900
DB	281	PheGlyGluIleArgAspHsIAspTrpMetGlnGlyAspLeuLeuProGlnAlaAsp	3000

QY	301	TCGGGGCGTCATTAAGACTTCTGGACCTGGTTCGAGAGGCCCGGATGATGTTTCGGTCGATCCG	360
Db	101	SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu	120
QY	361	GAGAGGCCCGGAACCGGTGGCAAGACCTCTTGCATTTATGACCCGAAAGAGAGCCCTACAG	420
Db	121	GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln	140
QY	421	GAGAACCTGGCCCCGAGGATTTCTTTGGCAGAGTCTGGAGGCCGTGGGGCATTTGCCAAGC	480
Db	141	GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValAlaArgHisCysHisAsn	160
QY	481	TGCGGGGGTCTCCACCGCGACACATCAAGAGACGAAACATCTTAATCGACCTGAGCCCGCGC	540
Db	161	CysGlyValLeuHisArgAspIleIleAspGluAsnIleLeuIleAspLeuAsnArgGly	180
QY	541	GAATCAAACTCATGCACTTCGGGTGGGGGGCGCTGCTCAAGGACACAGCTTACACGAGC	600
Db	181	GluLeuValLeuIleAspPheGlySerGlyAlaLeuLeuAspPheThrValTyrThrAsp	200
QY	601	TTTGATGGGACCCGAGTGTACAGTCTCTCCAGATGGATTCGCTACCAATCGCTTACCAAGCGC	660
Db	201	PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly	220
QY	661	AGGTGGCGACGTGTGTGATCCCTTGGGATCCGCTGTATGACATGAGTCTGGCAGATATT	720
Db	221	ArgSerHisAlaIleValTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle	240
QY	721	CCGTTTGACGACGATGAAAGAGATCATCAAGGCCCAAGTGTCTTTCAGGCCAACTGTCTCT	780
Db	241	ProPheGluHisAspTrpGluIleValIleValIleValIleValIleValIleValIleValSer	260
QY	781	TCAGAGTGCACACCTTATTAATGATGCGTGTCCCTGAGACCGTCAGATCGGCCCTCC	840
Db	261	SerGluCysGlnHisLeuIleArgTrpCysLeuSerLeuArgProSerAspArgProSer	280
QY	841	TTTGAAGAAATCCGGAACCATCCGTGGATGACAGGATGACCTCTGCCCCAGGACGTTCT	900
Db	281	PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGlnAlaThrAla	300
QY	901	GAGATCCATCTGCACAGTCTGTACACCGGGATTCACGACAG	939
Db	301	GluIleHisLeuHisSerLeuSerProSerProSerIys	313
RESULT 5			
US-09-237-543-9			
Sequence 9, Application US/09237543A			
Patent No. 613540			
GENERAL INFORMATION:			
APPLICANT: Kappelier, Rosana			
TITLE OF INVENTION: NOVEL MOLECULES OF THE HK1D-1-RELATED PROTEIN FAMILY			
TITLE OF INVENTION: AND USES THEREOF			
FILE REFERENCE: 035800/175631			
CURRENT APPLICATION NUMBER: US/09/237,543A			
NUMBER OF SEQ ID NOS: 11			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO 9			
LENGTH: 313			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-09-237-543-9			

Alignment Scores:

Pred. No.:	3,57e-136	length:	313
Score:	1582.00	Matches:	294
Percent Similarity:	97.12%	Conservative:	10
Best Local Similarity:	93.93%	Mismatches:	9
Query Match:	90.45%	Indels:	0
DB:	3	Gaps:	0

US-10-705-757-5 (1-942) x US-09-237-543-9 (1-313)

[illegible]

US-09-644-450-9

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: Sequence 9, Application US/09644450
: Patent No. 6383791
: GENERAL INFORMATION:
: APPLICANT: Kapeller, Rosana
: TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: 035800/175631

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/ CURRENT APPLICATION NUMBER: US/09/644,450
/ CURRENT FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 9
/ LENGTH: 313
/ TYPE: PROT
/ ORGANISM: Homo sapiens
US-09-644-450-9

Alignment Scores:
Pred. No.: 3,57e-136 Length: 313
Score: 1582.00 Matches: 294
Percent Similarity: 97.12% Conservative: 10
Best Local Similarity: 93.93% Mismatches: 9
Query Match: 90.45% Indels: 0
DB: Gaps: 0

US-10-705-757-5 (1-942) x US-09-644-450-9 (1-313)

QY 1 ATGCTCTGTCCAGATCAATCCCTGCGCCACCTGCGCCGCCCTTGCAACGACTTG 60
DB 1 MetLeuLeuSerIysIleAsnSerLeuAlaHleuArgAlaIaProCysAsnAapLeu 20
QY 61 CAGCCCAACCAAGCTGGCGCCGCGCAAGAGAGAGCCCTTGAGTCCGACTACAGT 120
DB 21 HlaIaIaThryLeuAlaProGlyLysGluLysGluProLeuIuSerGlnIyGlnAla 40
QY 121 GCGCCCTGTGGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 41 GlyProLeuLeuIuSerGlyIleGlyPheGlySerValIySerGlyIleArgValSerAap 60
QY 181 AACTTCCCGGTGGCCATTAAAGACGTGAGAGAGACCGGATTTCCGATTGGGAGAACTG 240
DB 61 AenLeuProValAlaIleLysHleValGluLysAapArgIleSerAapTrpGlyLysLeu 80
QY 241 CCCAATGGGACCCGAGTGGCCCATGGAAGTGTCTGTGAAGAGAGTGGAGCTTGCACTTC 300
DB 81 ProAenGlyThryArgValIleProMetGluValValLeuLeuLysValSerSerGlyPhe 100
QY 301 TCGGGCGCTATTAGACTTCTGCACTGGTTGAGAGAGCCGATAGTTCTGCTGATCTTG 360
DB 101 SerGlyValIleArgLeuLeuAapTrpPheGluArgProAspSerPheValLeuIleLeu 120
QY 361 GAGAGGCCCGGACCCGCTGCAAGACTTCTGCACTTTATCAACGAGAGAGCCCTTACAG 420
DB 121 GluArgProGluProValGlnAapLeuPheAapPheIleThryGluArgGlyAlaLeuGln 140
QY 421 GAGGACCTGGCCCGGAGATCTTCTGCACTGCTGAGAGCCGCTGCGGCACTTCCCAAC 480
DB 141 GluGlnLeuAlaIaArgSerPhePheTrpGlnValLeuGlnIaValAlaTrpHlaSerHlaSer 160
QY 481 TGGGGGTTCTCCAGCGGACATCAAGAGAGAGAACTTTAATCGACTGAGCCGCGG 540
DB 161 CysGlyValLeuLeuHlaArgAapIleLysAapGluAsnIleLeuIleAapLeuAaHlaArgGly 180
QY 541 GAAATCAAACTCATTCGACTTGGGGTGGGGGCGCTGCTCAAGAGACAGTCTACAGGAC 600
DB 181 GluLeuLysLeuIleAapPheGlySerGlyAlaLeuLeuLysAapTrpValIyTrpHlaAap 200
QY 601 TTTGATGGGACCCGAGGTGTAAGTCTTCCAGAGTGGATTGGCTAACCTACCTACAGGCG 660
DB 201 PheAapGlyThryArgValIySerProGluTrpIleArgTrpHlaSerGlyTrpHlaSerGly 220
QY 661 AGGTCCGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 221 ArgSerHlaIaIaValIleTrpSerLeuGlyIleLeuLeuTrpAspMetValCysGlyAapPhe 240
QY 721 CCGTTTGAGCAGCATGAAGATCATCAAGAGCCCAAGTGTCTTTCAGGCAAACTGTCTCT 780
DB 241 ProPheGluHlaIaAapGluGlnIleIleArgGlyGlnValPhePheArgGlnAaValSer 260
QY 781 TCAGAGTGTGACGACCTTATTAAATGATGCTGCTGCTGAGACCGTCAAGATCGGCTCTC 840
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DB 261 SerGluCysGlnHlaIaSerLeuIleArgTrpCysLeuAlaLeuArgProSerAapTrpHla 280
QY 841 TTTGAAGAATCCGAGACCAATCCCTGATGACAGGAGTACCTCTGCGCCAGGACGCTTCT 900
DB 281 PheGluGlnIuIleGlnAsnHlaIaProIleMetGlnAapValLeuLeuProGlnIuTrpAla 300
QY 901 GAGATCCATCTGACAGCTGTGTCAACCGGATCCAGCAAG 939
DB 301 GluIleHlaIaSerLeuSerProGlyProSerLys 313

RESULT 7
US-08-463-081B-26
/ Sequence 26, Application US/08463081B
/ Patent No. 5871960
/ Patent No. 5871960 5837487
/ GENERAL INFORMATION:
/ APPLICANT: Smith, Kendall A. & Beadling, Carol
/ TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
/ TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ STREET: 444 South Flower St. - Suite 1900
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: USA
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0,
/ SOFTWARE: Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/463,081B
/ FILING DATE: 5-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/104,736
/ FILING DATE: 10-AUG-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/796,066
/ FILING DATE: 20-NOV-91
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Vaviana Amzel, Ph. D.
/ REGISTRATION NUMBER: 30,930
/ REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 622-7700
/ TELEFAX: (213) 489-4210
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 313 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: n.a.
/ TOPOLOGY: n.a.
/ MOLECULAR TYPE: peptide
/ US-08-463-081B-26

Alignment Scores:
Pred. No.: 5,44e-136 Length: 313
Score: 1580.00 Matches: 294
Percent Similarity: 97.12% Conservative: 10
Best Local Similarity: 93.93% Mismatches: 9
Query Match: 90.34% Indels: 0
DB: Gaps: 0

US-10-705-757-5 (1-942) x US-08-463-081B-26 (1-313)

QY 1 ATGCTCTGTCCAGATCAATCCCTGCGCCACCTGCGCCGCCCTTGCAACGACTTG 60
DB 1 MetLeuLeuSerIysIleAsnSerLeuAlaHleuArgAlaIaProCysAsnAapLeu 20
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Oy      61  CACGGCCACCAACGTGGCGCGCGGCAAAAGAAAGAGACCCCTGGAGTGCAGATCCAGGTC 120
Db      21  HIsAlatmLyLeuLlaIaProGlyLbVgSLVgSLbProLeuLbSerGlnTyGlnVal 40
Oy      121  GGCCTCGCTGTTGGAGCAGCGGTGGCTTCGCGCTCGGTCTACTGTGGCAATCCGCTCGCGCAC 180
Db      41  GLyProLeuLeuGLySerGlyGlyPheGLySerValTySerGlyLLehrGValSerbAP 60
Oy      181  AACTTGGCCGGTGGCCATTTAAGCAGGTGAGAAAGAGACCGGATTTCCGATTGGGGAGAACTG 240
Db      61  AsnLeuProValAlaLeuYshbValGlnLysbAPaGllLeSerbAPTrpGlyGluLeu 80
Oy      241  CCCAATGGCAGCCCGAGTCCCATGGAAAGTGCCTCTTGAAGAAAGGTAGAGCTCGAGCTTC 300
Db      81  ProAsnGLyThraArgValaPrometGlnValValLeuLeuYshValSerSerGlyPhe 100
Oy      301  TCGGGCGTCATTAGAATCTTGAGTCTGTTCGAGAGGCGCGATAGTATTCGTGCTGATCTGT 360
Db      101  SerGlyValIllaArgLeuLeuAspTrpPheGlnArgProAspSerPheValLeuIleLeu 120
Oy      361  GAGAGGCCCCGAAACCGGTGCAGACCTTTTGAATTATGACCGAGCAGAGAGCCCTTACAG 420
Db      121  GlnaArgProGlnProValGlnbAPLeuPheAspPheIleThrGlnArgGlyAlaLeuGln 140
Oy      421  GAGGACCTTGGCCCCGAGGAGATTTCTTCTGGCAGGTGCTGTGAGAGCCGTGGCGGCTTCGCAAC 480
Db      141  GlnGlnLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValaArgbAPsCyshbAPaAsn 160
Oy      481  TGGCGGGGTTCTCCACCGGACACATCAAGAGCAGAAACATCTTAATCGACCTGAGCGCGG 540
Db      161  CybGlyValLeuHlaArgbAPlleuYsbAPGlnAsnIleLeuIleAspLeuAsnArgGly 180
Oy      541  GAAATCAAACTCATGACTTCGCGGTGCGGCGCGCTGCTCAAGAGCACAAGTTACACGAGAC 600
Db      181  GlnLeuLysLeuIleAspPheGlySerGlyAlaLeuLysbAPhPheValTyThrAsp 200
Oy      601  TTTGATGGGACCCGAGGTGAACAGTCCCTCCAGAGTGATTCGCTACACATCGCTACACAGCG 660
Db      201  PheAspGLyThraArgValaTySerProProGlnTrpIlaArgTyThbAPGly 220
Oy      661  AGGTGGCGAGCTGTCTGATCCCTTGGGAGTCTGCTCTATAGACATGAGTTCGGAGATATT 720
Db      221  ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyThbAPMetValCybGlyAspIle 240
Oy      721  CCGTTTGAGCAGATGAGAGATCATCAAGAGGCGCAAGTGTCTTTCAGGCAAACTGTCTCT 780
Db      241  ProPheGlnHlaAspGlnGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
Oy      781  TCAAGGTGTCAAGACCTTTATTAATGTGTGCTGCTCCCTGAGACCGTCAAGTCCGCGCTTC 840
Db      261  SerGlnCybGlnHlaIshLeuIleArgTrpCybLeuAlaLeuArgProSerbAPaProthr 280
Oy      841  TTTGAAGAATCCGGAGACCATCGGTGGAGTGCAGAGGAGTGCCTCTGCGCCAGAGAGTTC 900
Db      281  PheGlnGlnIleGlnbAPhAsnIleProTrpMetGlnAspValLeuLeuProGlnGlnTrpAla 300
Oy      901  GAGATCAATCTGCACAGTCTGTCAACCGGAGATCCAGCAAG 939
Db      301  GlnIleHlaIshLeuIshSerLeuSerProGlyProSerLys 313

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CITY: Valley Forge
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19482
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0,
 SOFTWARE: Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/461,379A
 FILING DATE: 5-JUNE-1995
 PRIOR APPLICATION DATE:
 APPLICATION NUMBER: US2N 08/330,108; 08/104,736
 APPLICATION NUMBER: & 07/796,066
 FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
 ATTORNEY/AGENT INFORMATION:
 NAME: Viviana Amzel, Ph. D.
 REGISTRATION NUMBER: 30,930
 REFERENCE/DOCKET NUMBER: DART-070
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610)470-0700
 TELEFAX: (610)470-0701
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 313 amino acids
 TYPE: peptide
 STRANDEDNESS: n.a.
 TOPOLOGY: n.a.
 MOLECULE TYPE: peptide
 US-08-461-379A-26

Alignment Scores:

Pred. No.:	5,44e-136	Length:	113
Score:	150.00	Matches:	294
Percent Similarity:	97.12%	Conservative:	10
Best Local Similarity:	93.93%	Mismatches:	9
Query Match:	90.34%	Indels:	0
DB:	2	Gaps:	0

US-10-705-757-5 (1-942) X US-08-461-379A-26 (1-313)

[illegible]


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Db      141  GUGUleuAlaArgSerPhePheTrpGlnValIleuGlnAlaValArgHisCysHisAsn 160
Qy      481  TGGGGGGTTTCCACCGCGACATCAAGAGAGAAATTTTATTCAGCTGAGCCGGCC 540
Db      161  CysGlyValIleuHisArgSerPheIleuArgGlnAsnIleuIleuArgLeuAsnArgGly 180
Qy      541  GAATCAAACTCATGCACTCGGGGTGGGGGGCGGTGTCAAGGACAGCTCTACAGGAC 600
Db      181  GlnIleuValIleuIleuAspPheGlySerGlyAlaIleuIleuValAspPheValIleuAsp 200
Qy      601  TTTGATGGACCCGAGTGTACAGTCTCTCAGAGTGTACATTCATCCATCCCTACAGCG 660
Db      201  PheAspGlyThrArgValIleuSerProPheGlnIleuTrpIleuArgGlyHisGly 220
Qy      661  AGGTGGACAGCTGTCTGTCTCTGGATCTGTCTGTATGACATGGTCTCGGAGATATT 720
Db      221  ArgSerAlaIleuValIleuSerIleuGlyIleuIleuValIleuValIleuValIleuVal 240
Qy      721  CGGTTTGAGACAGATGAAGATCATCAAGGGCCAAAGTCTTTTCAAGGCAAGCTGTCT 780
Db      241  ProPheGlnHisAspGlnIleuGlnIleuArgGlyGlnAlaPhePheArgGlnArgValSer 260
Qy      781  TCAGAGTGTACAGCACTTATTAATGTGTCTGTCTCTGAGACCGTCTCAGATCCGCTCC 840
Db      261  SerGlnCysGlnHisIleuIleuArgTrpCysIleuAlaIleuArgProSerAspArgProThr 280
Qy      841  TTTGAAGAATCCGGAACCATCCGTGTGATGACAGGGTGAACCTCTGCCCGAGGAGCTTCT 900
Db      281  PheGlnGlnIleuIleuHisAspProIleuMetGlnAspValIleuIleuProGlnIleuTrpAla 300
Qy      901  GAGATCATCTGACAGTCTGTCAACGGGATCCAGCAAG 939
Db      301  GlnIleuHisIleuHisSerIleuSerProGlyProSerIleu 313

RESULT 9
US-08-462-3908-26
Sequence 26, Application US/084623908
Patent No. 5682894
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding Cms Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Ractner & Prestia
ADDRESS: (B) STREET: One Westlakes-Berwyn
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 26:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULAR TYPE: peptide
US-08-462-3908-26

Alignment Scores:
Pred. No.: 5,44e-136 Length: 313
Score: 1580.00 Matches: 294
Percent Similarity: 97.12% Conservation: 10
Best Local Similarity: 93.93% Mismatches: 9
Query Match: 90.34% Indels: 0
DB: 2 Gaps: 0

US-10-705-757-5 (1-942) x US-08-462-3908-26 (1-313)

Qy      1  ATGCTCTGTCCCAAGATCAATCCCTGGCCACCTGGGCGCCCTGCAAGCACTTG 60
Db      1  MetLeuIleuSerIleuHisSerIleuAlaHisIleuArgAlaArgAlaCysAsnAspLeu 20
Qy      61  CACGCCAACAGCTGGCGCGCGCAAGAGAAAGAACCCCTGAGTGTGAGTACAGTGT 120
Db      21  HisAlaThrIleuValIleuAlaProGlyIleuValIleuValIleuValIleuValIleuVal 40
Qy      121  GGGCGCGTGTGGGACAGCGGTGTGGCTGTGCTTACTCTGACATCCGCGTCCGAC 180
Db      41  GlyProIleuGlnIleuSerIleuGlyPheGlySerValIleuSerGlyIleuArgValSerAsp 60
Qy      181  AACTTCCCGGTGGCCATTAAGACACGTGAGAAAGAACCCGATTTCCGATTGGGGAGAACTG 240
Db      61  AsnLeuProValAlaIleuHisValGlnIleuValAspArgIleuSerAspTrpGlyIleu 80
Qy      241  CCCAATGACACCCGAGTGGCCATGAGAGTGTCTCTGTAAGAGAGTGTGAGTCTTC 300
Db      81  ProHengIleuThrArgValIleuMetGlnValIleuIleuValIleuValIleuValIleuVal 100
Qy      301  TGGGGCGTCAATTAAGCTTGTGACCTGTGTGAGAGGCGCGATAGTTTGTCTGATCTTG 360
Db      101  SerGlyValIleuIleuArgLeuIleuAspTrpPheGlnArgProAspSerPheValIleuIleu 120
Qy      361  GAGAGCGCCGGAACCGGTGGAAGACCTTCGACTTATACGGAAGAGAGCCCTACAG 420
Db      121  GlnArgProGlnProValGlnAspLeuPheAspPheIleuThrGlnArgGlyAlaIleuGln 140
Qy      421  GAGGACCTGAGCCGAGAGATTTCTTGGCAGGTGTGTGAGAGCGGTGGGATTCGCAAC 480
Db      141  GlnGlnIleuAlaArgSerPhePheTrpGlnValIleuGlnAlaValArgHisCysHisAsn 160
Qy      481  TGGGGGGTTTCCACCGCGACATCAAGAGAGAAATTTTATTCAGCTGAGCCGGCC 540
Db      161  CysGlyValIleuHisArgSerPheIleuArgGlnAsnIleuIleuArgLeuAsnArgGly 180
Qy      541  GAATCAAACTCATGCACTCGGGGTGGGGGGCGGTGTCAAGGACAGCTCTACAGGAC 600
Db      181  GlnIleuValIleuIleuAspPheGlySerGlyAlaIleuIleuValAspPheValIleuAsp 200
Qy      601  TTTGATGGACCCGAGTGTACAGTCTCTCAGAGTGTACATTCATCCATCCCTACAGCG 660
Db      201  PheAspGlyThrArgValIleuSerProPheGlnIleuTrpIleuArgGlyHisGly 220
Qy      661  AGGTGGACAGCTGTCTGTCTCTGGATCTGTCTGTATGACATGGTCTCGGAGATATT 720
Db      221  ArgSerAlaIleuValIleuSerIleuGlyIleuIleuValIleuValIleuValIleuVal 240
Qy      721  CGGTTTGAGACAGATGAAGATCATCAAGGGCCAAAGTCTTTTCAAGGCAAGCTGTCT 780
Db      241  ProPheGlnHisAspGlnIleuGlnIleuArgGlyGlnAlaPhePheArgGlnArgValSer 260
Qy      781  TCAGAGTGTACAGCACTTATTAATGTGTCTGTCTCTGAGACCGTCTCAGATCCGCTCC 840
Db      261  SerGlnCysGlnHisIleuIleuArgTrpCysIleuAlaIleuArgProSerAspArgProThr 280

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: USN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: peptide
STRANDEDNESS: n.a.
TOPOLOGY: n.a.
MOLECULE TYPE: peptide
US-08-465-585C-26
Alignment Scores:
Pred. No.: 5,44e-136 Length: 313
Score: 1580.00 Matches: 294
Percent Similarity: 97.12% Conservative: 10
Best Local Similarity: 93.93% Mismatches: 0
Query Match: 90.34% Indels: 0
Gaps: 0
US-10-705-757-5 (1-942) x US-08-465-585C-26 (1-313)
QY 1 ATGCTCTGTGCAAGATCACTCCCTGGCCACCTGGCCGCCGCCCTGCAAGCACTTG 60
DB 1 MetLeuLeuSerIySrlLeuAsnSerIeulAlhIleuAlgrhIaIaCySaMaAplre 20
QY 61 CAGCCCAACCAAGTGGCGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 21 HleAlaThrIyLeuAlaIleuAlaProglIySrlGluIyProleuGlIySerGlIyGlnVal 40
QY 121 GGGCCGCTGTGGGCAAGCGGTGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 41 GlyProleuLeuSrlYserGlIyPheGlySerValIySrlYlealgrValIserAap 60
QY 181 AACTTCCCGGTGGCAATTAAGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 61 AenLeuProValAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAla 80
QY 241 CCCAATGGCAAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 81 ProAsnGlIyThrIyAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAla 100
QY 301 TGGGGGTGCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 101 SerGlIyValIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAla 120
QY 361 GAG 420
DB 121 GluArgProglIyProValIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAla 140
QY 421 GAG 480
DB 141 GluGluLeuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAla 160
QY 481 TGGGGGTGCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

DB 161 CyseGlIyValIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAla 180
QY 541 GAAATCAACTCATTCGAGTCTGGGCGCGCTGCTGCAAGAGAGAGAGAGAGAGAGAGAG 600
DB 181 GluLeuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAla 200
QY 601 TTTGATGGGAGCGGAGTGTACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 201 PheAspGlIyThrIyAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAla 220
QY 661 AGGTCCGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 221 ArgSerAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAla 240
QY 721 CCGTTGAGCAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 241 ProPheGlIyAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAla 260
QY 781 TCAGAGTGTACAG 840
DB 261 SerGlIyCyseGlIyAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAla 280
QY 841 TTTGAG 900
DB 281 PheGluGluIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAla 300
QY 901 GAGATCCATCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 939
DB 301 GluIleAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAlaIleuAla 313
RESULT 12
US-08-652-446-26
Sequence 26, Application US/08652446
Patent No. 6057427
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CRS
TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PRETTY, SCHROEDER & POPILMSKI 444 South Flower St. - Suite 190
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,446
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/462,390

FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,585
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: PP66 40035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: peptide
STRANDEDNESS: n.a.
TOPOLOGY: n.a.
MOLECULE TYPE: peptide
US-08-652-446-26

Alignment Scores:

Pred. No.: 5,44e-136 Length: 313
Score: 1580.00 Matches: 294
Percent Similarity: 97.12% Conservative: 10
Beet Local Similarity: 93.93% Mismatches: 9
Query Match: 90.34% Indels: 0
DB: 3 Gaps: 0

US-10-705-757-5 (1-942) x US-08-652-446-26 (1-313)

QY 1 ATGCTCTGTCCAAAGTCACTCCCTGAGCCCGCCCGCCCTGCAACGACTTG 60
DB 1 MetLeuLeuSerLysIleAsnSerLeuLAlaIleuAlaArgAlaCysAsnAspLeu 20
QY 61 CAGGCCACCAAGCTGGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 21 HAlaIAlaThrLysLeuAlaProGlyLysGluLysGluProLeuLysGlnIAlaVal 40
QY 121 GGGCCGCTGTGGGAGCGGCTGCTCGGCTCGGCTCTACTCTGGCATCCGCTGGCGAG 180
DB 41 GlyProLeuLeuGlySerGlyLysPheGlySerValTyrSerGlyIleArgValSerAsp 60
QY 181 AACTTGGCGGCTGGCCATTAAAGCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 61 AsnLeuProValAlaIleLysHAlaValGluLysAspArgIleSerAspTrpGlyGluLeu 80
QY 241 CCAATGGGAGCGGAGTGGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysValSerSerGlyPhe 100
QY 301 TCGGGCGTCACTAGACTTCTGAGCTGGTCTGAGAGAGCGCCGATATTCTGCTGATCTTG 360
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleuIleLeu 120
QY 361 GAGAGGCCGAGACCGGCTGCAAGACTTTTGAAGCTTTATCCAGAGAGAGAGAGAGAG 420
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 421 GAGAGACTGGCGCGAGAGATCTTCTGGCAGAGTGTGAGAGCGGCGGAGATTGGCAAC 480
DB 141 GluGluLeuLysAlaArgSerPhePheTrpGlnValLeuLysValAlaLysHAlaSer 160
QY 481 TGGGGGTTCTCCAGCGGAGATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

DB 161 CysGlyValLeuHAlaArgAspIleLysAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY 541 GAATCAAACTGATGCACTTCGGGCTGGGCGGCTGTCAAGAGACAGTCAACGAGAC 600
DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValIlyrThrAsp 200
QY 601 TTTGATGGAGCCGAGGTGACAGTCTTCAGAGTGGATTCGCTACCATGCTTACCAAGCG 660
DB 201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
QY 661 AGTGGGAGAGCTGTCTGCTTCCTTGGGATCCGCTCTTGAATGATGTCGCGAGATATT 720
DB 221 ArgSerAlaAlaValIleTrpSerLeuGlyIleLeuLeuLysAspMetValCysGlyAspIle 240
QY 721 CGGTTGAGCAGATGAGAGATCATCAAGAGGCGCAAGTGTCTTCAAGCAACTGTCTCT 780
DB 241 ProPheGluHAlaAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
QY 781 TCAGAGTGCAGACCTTATTAATGTGCTGTCTGCTGAGACCGTCAAGATCGGCCCTTC 840
DB 261 SerGluCysGlnHAlaLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280
QY 841 TTTGAAGAAATCCGGAACCATCCGTGATGACAGGAGTACCTTCGCCAGAGCACTTCT 900
DB 281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGluGlnIAla 300
QY 901 GAGATCCATCTGCACAGTCTGCACCGGAGATCCAGCAAG 939
DB 301 GluIleHAlaLeuHisSerLeuSerProGlyProSerLys 313

RESULT 13
US-07-857-224B-41
Sequence 41, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSER: Steven A. Benner
STREET: Hadlabastrasse 151
CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
ORGANISM: rat
FEATURE: Protein kinase; Table 8 Column 46
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Hanke, S. K.
AUTHORS: Quim, A. M.

```

AUTHOR: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
PAGES: 42-52
DATE: 1988
US-07-857-224B-41

Alignment Scores:
Pred. No.: 1.67e-115 Length: 257
Score: 1355.50 Matches: 256
Percent Similarity: 98.84% Conservative: 0
Beet Local Similarity: 98.84% Mismatches: 0
Query Match: 77.50% Indels: 3
DB: Gaps: 2

US-10-705-757-5 (1-942) x US-07-857-224B-41 (1-257)

QY 106 TCCGAGTACAGAGGCGCGCTGTTGGGAGCGGTGGCTTCGGCTCGCTACTGCGC 165
DB 1 SerGlnTrpGlnValGlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGly 20
QY 166 ATCCGCTCCGCGCAACTGCGGTGCGCATTAAGACGCTGGAAGACCGGATTTCC 225
DB 21 IleArgValAlaIleAspLeuLeuProValAlaIleIleValGlnIleValAspArgIleSer 40
QY 226 GATTGGGAGAACTGCCCAATGGCACTCGAGTGGCCATGGAAAGTGTCTGTGAAGAG 285
DB 41 AspTrpGlyGlu-----AenGlyThrArgValProMetGluValValLeuLeuValys 58
QY 286 GTAGAGCTGGGACTTCTGGGCGTCATTAAGACTTCTGGAAGTGTGGAGGCGCGATG 345
DB 59 ValSerSerAspPheSerGlyValIleArgLeuLeuAspTrpPheGlyIleValProAspSer 78
QY 346 TTGCTGCTGATCTCGAGAGGCGCGCAACCGGTGCAAGACTTCTGCACTTTATCAGCA 405
DB 79 PheValLeuLeuLeuGlnIleValProGluProValGlnIleAspPheAspPheIleMetGlu 98
QY 406 CGAAGACCTTACAGAGAACTTGGCCCGCAAGACTTCTTGGCAGGTGTGGAAGCGCGTG 465
DB 99 ArgGlyAlaLeuGlnGlnIleAspLeuAlaArgGlyPhePheTrpGlnValLeuGlnAlaVal 118
QY 466 CGGATTTGGCAAACTGCGGGGTCTTCACCGGCACTCAAGACGCAAGCAATCTTAATC 525
DB 119 ArgHisGlyHisIleAsnGlyValLeuHisArgAspIleLeuAspGlyIleValLeuIle 138
QY 526 GACCTGACGCGCGCAAACTCAACTGACTTGGGTGCGGGGCGGTCTCAAGAC 585
DB 139 AspLeuSerArgGlyIleIleValLeuLeuIleAspPheIleSerGlyAlaLeuLeuValAsp 158
QY 586 ACAAGTACACGACTTTGATGGGACCGGAGTGTACAGTCTTCCAGAGTGGATTGCTTAC 645
DB 159 ThrValTyrThrAspPheAspGlyThrArgValTyrSerProProGluTrpIleArgTyr 178
QY 646 CATGCTACACGCGCAAGTGGCGAGCTGTGCTGCTTGGGACTTCTGCTTATGACATG 705
DB 179 HisArgTyrHisGlyArgSerAlaIleValTyrSerLeuGlyIleLeuLeuTyrAspMet 198
QY 706 GTGCGCGAGATATTCCGTTT---GAGCAGATGAAGAGATCATCAAGGCGCAAGTTC 762
DB 199 ValCysGlyAspIleProPheAspGlnHisAspGlnIleIleIleValGlnValPhe 218
QY 763 TTGAGGAACTGTCTTCAAGATGTCAAGCTTATTAATGATGCTGTGCTTGAAGA 822
DB 219 PheArgGlnThrValIleSerSerGlnCysGlnHisIleLeuIleValTyrCysLeuSerLeuArg 238
QY 823 CCGCAGATGCGCGCTCTTGAAGAAATCCGGAACCATCCGCGAGATGCGAGGAGAC 879
DB 239 ProSerAspArgProSerPheGlnGlnIleArgHisIleProTrpMetGlnGlyAsp 257

```

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Patent No. 6143540
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 455
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-237-543-5

Alignment Scores:
Pred. No.: 4.3e-94 Length: 455
Score: 1122.50 Matches: 213
Percent Similarity: 81.33% Conservative: 31
Beet Local Similarity: 71.00% Mismatches: 43
Query Match: 64.18% Indels: 13
DB: Gaps: 5

US-10-705-757-5 (1-942) x US-09-237-543-5 (1-455)

QY 1 ATGCTCTGTCAGATCAATCTCTGCGCCACCTGCGCGCCCTGC----- 51
DB 130 MetLeuLeuSerIleAspPheGlySerLeuAlaIleLeu-----CysGlyProGly 145
QY 52 -----AAGACCTTGACCGCAACCAAGCTGGGCGCGGCAAA---GAGAGGAGCGCCGTG 102
DB 146 GlyValAlaAspIleLeuProValIleValGlnProAlaValAlaAspIleValSerPhe 165
QY 103 GAGTCCAGTACCAAGTGGGCGCGCTGTTGGGAGCGGTGCGTTCGCTCGATCTA 162
DB 166 GlnIleValTyrGlnValGlnIleValAlaValLeuGlySerGlyGlyPheGlyThrValTyrAla 185
QY 163 GGCATCGCGGTGCGCGCAACTTGGCGGTGCGCATTAAGACGCTGGAAGACCGGATT 222
DB 186 GlySerArgGlyLeuIleAspGlyLeuProValAlaValIleHisValValIleGlnIleVal 205
QY 223 TCCGATTTGGGGAAGTGGCCCAATGGCACTGGCCGATGGCCATGAGTGTGTTGAAG 282
DB 206 ThrGlnTrpGlySerLeu---GlyGlyMetAlaValProLeuGlnValValLeuLeuArg 224
QY 283 AAGGTG-----AGCTCGGACTTCTCGGCGGTCTTGAAGTGTGAGAGG 336
DB 225 IysValGlyAlaIleGlyAlaArgGlyValIleArgLeuLeuAspTrpPheGlnIleArg 244
QY 337 CCGGATGATTTGCTGCTGATCTTGGAGAGCGCGCAACCGGTGCAAGACTTTCGACTTT 396
DB 245 ProAspGlyPheLeuLeuValLeuGlnIleValProGluProAlaGlnIleAspPheAspPhe 264
QY 397 ATACCGGAACGAGAGACCTTACAGAGACCTTGGCCCGGAGATTTCTTGGCGAGGTG 456
DB 265 IleThrGlnArgGlyAlaLeuLeuAspGluProLeuAlaArgArgPhePheAlaGlnValLeu 284
QY 457 GAGCGCGTGGGATTTGCCCAACTGCGGGGTCTTCACCGCGCACTCAAGACGAGAAC 516
DB 285 AlaIleValAlaArgHisGlyHisIleAsnGlyValValHisArgAspIleIleAspGlnIle 304
QY 517 ATCTTAATGCACTTGAAGCGCGGCAAACTCAACTGACTTGGGTGCGGGGCGCTG 576
DB 305 LeuLeuValAlaAspLeuArgSerGlyGlnLeuValLeuIleAspPheGlySerGlyAlaVal 324
QY 577 CTCAAGACACAGTCTACACGCACTTGAATGGGACCGGAGTGTACAGTCTCCAGAGTGG 636
DB 325 LeuIleAspPheThrValTyrThrAspPheAspGlyThrArgValTyrSerProProGluTrp 344
QY 637 ATTCGTAACATGCTACCAAGGAGAGTGTGCTGTGCTGCTTGGAGATCTGCTC 696
DB 345 IleArgTyrHisArgTyrHisGlyArgSerAlaThrValTrpSerLeuGlyValLeuLeu 364

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RESULT 14
US-09-237-543-5
Sequence 5, Application US/09237543A

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QY 697 TATGACATGCTCTGCGAGATATATTCGTTTGAACGATGAGATCATCAAGGCGCA 756
DB 365 TTAAspMetValCysGlyAspIleProPheGlnGlnAspIleuIleuAspArgIAsp 384
QY 757 GTGTTCTTCAGGCAAACTGTCTCTTCAGAGTGTACAGCCTTAATTAATGTCCTGTC 816
DB 385 LeuPhePheArgArgValSerProGluCysGlnGlnLeuIleGluTrpCysLeuSer 404
QY 817 CTGAAGACCTCAATCGGCGCTCTTGAAGAAATCCGAAACCATCCGTGATGACAGGT 876
DB 405 LeuArgProSerGluArgProSerLeuAspGlnIleAlaIleAspTrpMetLeuGly 424

RESULT 15
US-09-644-450-5
; Sequence 5, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-644-450-5
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Alignment Scores:
Pred. No.: 4,3e-94 Length: 455
Score: 1122.50 Matches: 213
Percent Similarity: 81.33% Conservative: 31
Best Local Similarity: 71.00% Mismatches: 43
Query Match: 64.18% Indels: 13
DB: 3 Gaps: 5
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US-10-705-757-5 (1-942) x US-09-644-450-5 (1-455)

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QY 1 ATGCTCTGTCAAGATCAATCTCCCTGGCCCACTTGCGCGCCGCTGC----- 51
DB 130 MetLeuLeuSerIysPheGlySerLeuAlaIleLeu-----CysGlyProGly 145
QY 52 -----AACGACTGCACGCGCACCAAGCTGGCCCGGCGCAA---GAGAAAGAGCCCTG 102
DB 146 GlyValAspHisLeuProValIleLeuGlnProAlaIleAspIysGlnSerPhe 165
QY 103 GAGTCGAGTACCAAGGAGGCGCGCTGTGGGCGAGGCTTGCGGCTCGGTCTACTCT 162
DB 166 GlnIleValIleTyrGlnValIleGlyAlaValIleuGlySerGlyIlePheGlyTrpValIleTyrAla 185
QY 163 GGCATCCGCGCTCGCCGCAACATTGCGCGTGCGCATTAAGCAGCTGGAAGAAGACCGGATT 222
DB 186 GlySerArgIleAlaAspGlyLeuProValAlaValIleHisValIleValIleArgVal 205
QY 223 TCCGATTGGGAGAACTGCCCAATGAGCAACCGAGTGCCTGGAAGTGGTCTGTGAAG 282
DB 206 ThrGluTrpIleGlySerLeu---GlyGlyMetAlaValProLeuGluValIleLeuArg 224
QY 283 AAGGTG-----AGCTCGGACTTCTCGGGCGTCAATTGACTTTCGAGCTGCGAGAG 336
DB 225 LysValIleValAlaIleGlyAlaArgGlyValIleArgLeuLeuAspTrpPheGluArg 244
QY 337 CCCGATAGTTTCGTGCTGATCTGAGAGAGCCGAAACGGGTGCAAGACTTTCGACTTT 396
DB 245 ProAspGlyPheLeuLeuValIleuGluArgProGluTrpAlaGlnAspLeuPheAspPhe 264
QY 397 ATGACCGAAGAGAGGCGCTTACAGAGAGACCTGGCCCGAGAGATTCTTGGCAGGTGCTG 456
DB 265 IleThrGluArgGlyAlaLeuAspGluProLeuAlaArgArgPhePheAlaGlnValLeu 284
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QY 457 GAGCGGTGCGGCAATTGCGCAAACTGCGGGGTTCTCCACCGGACATCAAGAGCGAAG 516
DB 285 AlaAlaValAlaHisCysHisAsnCyseGlyValIleAlaHisArgAspIleLysAspGluAsn 304
QY 517 ATCTTAATGACTGAGCCGCGGCAAAATCAACTCATCTGACTTCGGGTGCGGGCGCTG 576
DB 305 LeuLeuValAspLeuArgSerGlyGluLeuLysLeuIleAspPheGlySerGlyAlaVal 324
QY 577 CTGAAGACACAGCTCTACACGAGCCTTGAATGGGACCCGAGTGTACAGTCTCTCAAGTGG 636
DB 325 LeuLysAspTrpHisValIleTyrHisPheAspGlyTrpArgValIleSerProProGluTrp 344
QY 637 ATTGCTACCATCGCTACCAACGAGGTCGAGCTGTCTGCTCCCTTGGAATCTGTCTC 696
DB 345 IleArgTyrHisArgTyrHisGlyArgSerAlaIleHisValTrpSerLeuGlyValIleLeu 364
QY 697 TATGACATGCTCTGCGAGATATTCGTTTGAACGATGAAGAATCATCAAGGCGCA 756
DB 365 TTAAspMetValCysGlyAspIleProPheGlnGlnAspIleuIleuAspArgIAsp 384
QY 757 GTGTTCTTCAGGCAAACTGTCTCTTCAGAGTGTACAGCCTTAATTAATGTCCTGTC 816
DB 385 LeuPhePheArgArgValSerProGluCysGlnGlnLeuIleGluTrpCysLeuSer 404
QY 817 CTGAAGACCTCAATCGGCGCTCTTGAAGAAATCCGAAACCATCCGTGATGACAGGT 876
DB 405 LeuArgProSerGluArgProSerLeuAspGlnIleAlaIleAspTrpMetLeuGly 424
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Search completed: September 22, 2005, 17:24:43
Job time : 32.7742 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 15:57:45 ; Search time 123 Seconds
(without alignments)
5924.037 Million cell updates/sec

Title: US-10-705-757-5

Perfect score: 1749
Sequence: 1 atgcctctctccagatca.....caccggagatccagcaagtag 942

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+n2p.model -DEV=xlp
-Q/cg2.1/USPTO.epool_p/US10705757/runat_22092005.115014.22122/app_query.fasta_1.5333
-DB=A.GeneSeq -QMT=fastcan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPRT=prco -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10705757_QCGN_1_1_753_Qrunat_22092005.115014.22122 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A_GeneSeq_16Dec04:.*
1: geneSeqp19808:.*
2: geneSeqp19808:.*
3: geneSeqp20008:.*
4: geneSeqp20018:.*
5: geneSeqp20028:.*
6: geneSeqp20038:.*
7: geneSeqp20038:.*
8: geneSeqp20048:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1668	95.4	313	5	ABG33015
2	1668	95.4	313	6	AAO19788
3	1668	95.4	313	7	ABR62939
4	1668	95.4	313	8	ADN97347
5	1668	95.4	313	8	ADR88371
6	1584	90.6	313	5	ABR62938
7	1584	90.6	313	6	AAO19789
8	1584	90.6	313	7	ABR62938
9	1582	90.5	313	5	ABP54943
10	1582	90.5	313	5	ABG33017

11	1582	90.5	313	6	AAO19788	AAO19788 Human PIM
12	1582	90.5	313	7	ABR62939	ABR62939 Human PIM
13	1582	90.5	313	7	ABR62939	ABR62939 Human ser
14	1582	90.5	313	7	ADP55368	ADP55368 Human pro
15	1582	90.5	313	7	ADP55368	ADP55368 Human kin
16	1582	90.5	313	8	ADP55368	ADP55368 Human PRO
17	1582	90.5	313	8	ADP55368	ADP55368 Human PIM
18	1582	90.5	313	8	ADP55368	ADP55368 Human PIM
19	1580	90.3	313	2	AAO08139	AAO08139 Human cys
20	1580	90.3	313	3	AAO08139	AAO08139 Human CR7
21	1580	90.3	313	3	AAO08139	AAO08139 Human PIM
22	1580	90.3	313	8	ADN03170	ADN03170 Human PIM
23	1355.5	75.2	253	8	ADP55368	ADP55368 Rat prote
24	1315	75.2	253	8	ADP55368	ADP55368 Rat prote
25	1215.5	69.5	254	8	ADR88376	ADR88376 Human kin
26	1131	64.7	323	6	AAO19792	AAO19792 Murine PI
27	1123.5	64.2	326	6	ABR62933	ABR62933 Mouse pro
28	1123.5	64.2	326	6	ABR62933	ABR62933 CRH signa
29	1123.5	64.2	326	8	ADR88375	ADR88375 Mus muscu
30	1123.5	64.2	326	5	AAO20524	AAO20524 Protein 8
31	1122.5	64.2	326	6	AAO19791	AAO19791 Rat PIM3
32	1122.5	64.2	326	6	ABR62936	ABR62936 Rat prote
33	1122.5	64.2	326	7	ABR62936	ABR62936 Rat KID-1
34	1122.5	64.2	455	5	ABG33013	ABG33013 Rat prote
35	1122.5	64.2	455	5	ABG33013	ABG33013 Rat prote
36	1122.5	64.2	455	7	ADP55368	ADP55368 Rat prote
37	1119	64.0	326	2	AAO06886	AAO06886 HWHU20 p
38	1119	64.0	326	4	AAO29788	AAO29788 Human ser
39	1119	64.0	326	5	AAE23834	AAE23834 Human HKI
40	1119	64.0	326	5	ABG33011	ABG33011 Human ser
41	1119	64.0	326	7	ABR62932	ABR62932 Human pro
42	1119	64.0	326	8	ADP55368	ADP55368 Human cal
43	1119	64.0	326	8	ADP55368	ADP55368 Human PIM
44	1119	64.0	382	8	ADP55368	ADP55368 Human PIM
45	1119	64.0	382	8	ADP55368	ADP55368 Human PRO

ALIGNMENTS

RESULT 1	ABG33015	standard; protein; 313 AA.
ID	ABG33015	
AC	ABG33015	
XX		
DT	20-DEC-2002	(first entry)
XX		
DB	Mouse protein kinase phosphorylation site.	
XX		
KW	HKID-1; serine/threonine kinase; cellular proliferative disorder;	
KW	differentiative disorder; cancer; haematopoietic neoplastic disorder;	
KW	acute promyeloid leukaemia; APL; Chronic myelogenous leukaemia; CML;	
KW	Waldenstrom's macroglobulinaemia; WM; mouse.	
XX		
OS	Mus musculus.	
XX		
PN	US2002115120-A1.	
XX		
PD	22-AUG-2002.	
XX		
PF	04-OCT-2001; 2001US-00971791.	
XX		
PR	26-JAN-1999; 99US-00237543.	
XX		
PR	23-AUG-2000; 2000US-00644450.	
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
XX		
PI	Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;	
XX		
DR	WPI; 2002-712471/77.	
XX		
PT	Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting	

US-10-705-757-5 (1-942) x AAO19790 (1-313)

```

QY 1 ATGCTCTGTCGAAGATCAACTCCCTGGCCCACTGGCGCCGCCCTCTGCAAGACTTG 60
DB 1 MetLeuLeuSerIySrlleAsnSerIeulAhlleuArlgAlaArgProCyAsnAspLeu 20
QY 61 CAGCCCAAGAGCTGGCGCGCGGCAAGAGAAGAGAGCCCTGGAGTGGCAAGTACAGTGT 120
DB 21 HisAlaThrIySleuAlaProGlyIySglulysGluProLeuGluSerGlnIyrglnVal 40
QY 121 GGCCTGCTGTGGGACGCGGTGGCTTGGCTCTGCTACTCTGGCATCCGCTGCGCGAC 180
DB 41 GlyProLeuLeuGlySerGlyIyPheGlySerValIySerGlyIleArgValAlaAsp 60
QY 181 AACTTGCGCGTGGCCATTAAAGCAGTGGAGAGAGACCGGATTTCCGATTGGGAGAACTG 240
DB 61 AsnLeuProValAlaIleIyShIeValGluIySAspArgIleSerAspTrpGlyGluLeu 80
QY 241 CCCAATGGCAACCGAGTGGCCATGGAAGTGGTCTGTTGAAGAAGAGAGTGGAGCTTC 300
DB 81 ProAsnGlyThrArgValIProMetGluValIleuLeuIySlyValSerSerAspPhe 100
QY 301 TGGCGCGCTATTGAAGTCTTGAAGTGGTGGAGAGCCGAGTATGTTCTGCTGATCTTG 360
DB 101 SerGlyValIleArgIleuLeuAspTrpPheGluArgProAspSerPheValIleuLeu 120
QY 361 GAAGAGCCCGCAACCGGTGGCAAGACTTCTTGACTTTATCCGAAAGAGAGCCCTTACAG 420
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluIyArgIyAlaLeuGln 140
QY 421 GAGGACCTGGCGCGGAGTCTTCTGGCAGGTGGTGGAGGCGCGGCGGCAATTCGCAAC 480
DB 141 GluAspLeuAlaArgIyPhePheTrpGlnValIleuGlnAlaValAlaArgIyScyShIeAsn 160
QY 481 TGGCGGAGTCTTCCACCGCAGCATCAAGAGAGAGAACTTTAATCGACTGACCCGCGGC 540
DB 161 CyGlyIyAlaLeuIyShIeAspArgIleIyAspGluAsnIleuLeuIleAspLeuSerArgGly 180
QY 541 GAAATCAAACTCATCGACTTCGGGTGGGGGCGCTGCTCAAGACACAGTCTACAGGAC 600
DB 181 GluIleIySleuIleAspPheGlySerGlyAlaIleuLeuIySAspThrValIyTrpAsp 200
QY 601 TTTGATGGGACCGGAGTGTACAGTCTCCGAGAGTGGATTCGCTACCATGCTACCAAGC 660
DB 201 PheAspGlyThrArgValIySerProGluTrpIleArgIyTrhIeArgIyTrhIeGly 220
QY 661 AGGTGGCAGCTGTGGTCTCTGGAGTCTGCTCTATGACATGGTCTCGAGATATT 720
DB 221 ArgSerAlaIleValIleTrpSerIleuGlyIleIleuLeuIyTrhAspMetValIySglIyAspIle 240
QY 721 CCGTTTGAGCAGATGAGATCATCAAGAGGCGCAAGTGTCTTTCAGGCAAACTGTCTCT 780
DB 241 ProPheGluIyShIeAspGluGluIleIleIySglIyGlnIyAlaPhePheArgGlnTrhValSer 260
QY 781 TCAGAGTGTAGAGACCTTATTAAATGGTGTGCTCTCCCTGAGACCGTCAAGATCGGCCCTCC 840
DB 261 SerGlnIySglIyShIeIleuIleIyTrpCyIleuSerIleuArgProSerAspArgProSer 280
QY 841 TTTGAAGAAATCCGGAACATCCGTGGATGACAGGTGACTCTGCGCCAGCAGCTTCT 900
DB 281 PheGluGluIleIleArgIyShIeAspTrpMetGlnIyIyAspLeuLeuProGlnIleAlaIleAsp 300
QY 901 GAGATCCATGTGCAAGTCTGTCAACGGGATTCAGCAAG 939
DB 301 GluIleIySleuIyShIeSerIleuSerProGlySerSerIyS 313

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RESULT 3

ABR62940 standard, protein; 313 AA.

AC ABR62940;
XX
DT 04-DEC-2003 (first entry)

```

XX XX
DE Mouse serine/threonine protein kinase PIM-1.
KW Mouse; PIM-1; protein kinase; enzyme.
XX KW
XX Mus musculus.
XX PN W02003060130-A2.
XX PD 24-JUL-2003.
XX PF 20-JAN-2003; 2003WO-EP000492.
XX PR 19-JUN-2002; 2002EP-00001401.
XX PA (AVET ) AVENTIS PHARMA DEUT GMBH.
XX PI Korn M, Mueller G, Schneider R, Techank G;
XX DR WPI; 2003-598536/56.
XX PT New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
XX PT agent for identifying anti-type 2 diabetes mellitus drugs, or for
XX PT treating insulin resistance or type 2 diabetes mellitus.
XX PS Example 2; Page 40; 40pp; English.
XX CC The present sequence is the protein sequence of the murine
XX CC serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins
XX CC are the paralogs of novel human and murine PIM-3 proteins (see ABR62932
XX CC and ABR62933) of the invention, which are therefore expected to be
XX CC involved in cancer and cell growth regulation. PIM-3 is also involved in
XX CC the development of insulin resistance and type 2 diabetes mellitus. The
XX CC invention relates to the use of PIM-3 nucleic acids and proteins in:
XX CC screening assays for compounds that modulate insulin resistance or type 2
XX CC type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
XX CC forensic biology); predictive medicine (e.g. diagnostic or prognostic
XX CC assays, monitoring clinical trials, pharmacogenomics); and for the
XX CC preparing a medicament for the treatment of insulin resistance or type 2
XX CC diabetes mellitus
XX SQ Sequence 313 AA;
XX Alignment Scores:
XX Pred. No.: 5.03e-139 Length: 313
XX Score: 1668.00 Matches: 313
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 95.37% Indels: 0
XX DB: 7 Gaps: 0

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US-10-705-757-5 (1-942) x ABR62940 (1-313)

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QY 1 ATGCTCTGTCGAAGATCAACTCCCTGGCCCACTGGCGCCGCCCTCTGCAAGACTTG 60
DB 1 MetLeuLeuSerIySrlleAsnSerIeulAhlleuArlgAlaArgProCyAsnAspLeu 20
QY 61 CAGCCCAAGAGCTGGCGCGCGGCAAGAGAAGAGAGCCCTGGAGTGGCAAGTACAGTGT 120
DB 21 HisAlaThrIySleuAlaProGlyIySglulysGluProLeuGluSerGlnIyrglnVal 40
QY 121 GGCCTGCTGTGGGACGCGGTGGCTTGGCTCTGCTACTCTGGCATCCGCTGCGCGAC 180
DB 41 GlyProLeuLeuGlySerGlyIyPheGlySerValIySerGlyIleArgValAlaAsp 60
QY 181 AACTTGCGCGTGGCCATTAAAGCAGTGGAGAGAGACCGGATTTCCGATTGGGAGAACTG 240
DB 61 AsnLeuProValAlaIleIyShIeValGluIySAspArgIleSerAspTrpGlyGluLeu 80
QY 241 CCCAATGGCAACCGAGTGGCCATGGAAGTGGTCTGTTGAAGAAGAGTGGAGCTTC 300
DB 81 ProAsnGlyThrArgValIProMetGluValIleuLeuIySlyValSerSerAspPhe 100

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QY 301 TCGGGGCTATTAGACTTCTGAGCTGGTTGAGAGGCCCGATAGTTTCGTCGATCTCTG 360
    |||||
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
QY 361 GAGAGGCCCGAACCCGGTGCAGACCTCTTGCATTTATACCGAACGAGAGCCCTACAG 420
    |||||
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 421 GAGAGCTTGGCCCGAGAGATTCTTCTGACAGTCTGAGAGGCCCTGGGGCATTTGCCAAC 480
    |||||
DB 141 GluAspLeuAlaArgGlyPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
QY 481 TCGGGGCTTCTCCACCGCAGCATCAAGAGAGAACATCTTATTCAGCTGAGCCCGCGC 540
    |||||
DB 161 CysGlyValLeuHisArgAspIleArgAspGlnAsnIleLeuIleAspLeuSerArgGly 180
QY 541 GAATCAAACTCATCGACTTCGGGTCGGGGCGCTCTCAAGGACACAGCTTACACGAGAC 600
    |||||
DB 181 GluIleIleLeuIleAspPheGlySerGlyAlaIleLeuIleAspThrValIleThrAsp 200
QY 601 TTTGATGGGACCCGAGTGTACATCTCTCCAGAGTGTGATTCGTAACGCTTACACGGC 660
    |||||
DB 201 PheAspGlyThrArgValIleSerProProGluIleArgGlyHisArgIleHisArgGly 220
QY 661 AGGTCCGACAGCTGTCTGATCTCTGGGATCTGCTCTATGACATGCTGCGGAGATATT 720
    |||||
DB 221 ArgSerHisAlaValIleTrpSerLeuGlyIleLeuLeuIleArgMetValCysGlyAspIle 240
QY 721 CCGTTTGAGACGACATGAAGATCATCAAGGCGCAAGTCTTCTTCAAGCAACTGTCTCT 780
    |||||
DB 241 ProPheGluHisArgGluGluIleIleArgGlyGlnValPhePheArgGlnThrValSer 260
QY 781 TCAGAGTGTACAGACCTTATTAATGCTGCTGCTGCTGAGACCGTCAAGATCGGCCCTCC 840
    |||||
DB 261 SerGluCysGlnHisLeuIleIleArgIleArgCysLeuSerLeuArgProSerAspArgProSer 280
QY 841 TTTGAGAAGAAATCCGGAACCATCCGTGATGACGAGTGAACCTCTGCGCCACGAGCTTCT 900
    |||||
DB 281 PheGluGluIleArgHisAsnIleProTrpMetGlnGlyAspLeuLeuProGlnAlaIleAsp 300
QY 901 GAGATCCATCTGCACAGTCTGTCAACCGGAGATCCAGCAAG 939
    |||||
DB 301 GluIleHisLeuHisSerLeuSerProGlySerSerIle 313

```

RESULT 4

```

ADN97347
ID ADN97347 standard; protein; 313 AA.
XX
AC ADN97347,
XX
DT 01-JUL-2004 (first entry)
XX
DE Murine Plm1 SEQ ID NO:6.
XX
KW mouse; probasin; promoter; transgenic mouse; c-myc; prostate cancer;
    Plm1.
OS Mus musculus.
XX
PN MO2004000010-A2.
XX
PD 31-DEC-2003.
XX
PF 23-JUN-2003; 2003MO-US019818.
XX
PR 21-JUN-2002; 2002US-0390692P.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Sawyers CL, Ellwood-Yen KB,
XX
DR WPI; 2004-099050/10.

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XX
PT New transgenic mouse, useful as model system for the study of prostate
PT cancer and its progression comprising a nucleic acid construct comprising
PT a promoter operably linked to c-myc gene encoded in prostate cells of
PT transgenic mouse.
XX
XX Claim 7; SEQ ID NO 7; 65bp; English.
XX
CC The invention relates to a novel transgenic mouse whose genome comprises
CC a nucleic acid construct comprising 310 bp (ADN97347), where the promoter is
CC nucleotide sequence comprising 310 bp (ADN97347), where the promoter is
CC operably linked to c-myc having a fully defined nucleotide sequence
CC comprising 1320 bp (ADN97342) where the c-myc protein encoded is
CC expressed in prostate cells of the transgenic mouse at detectable levels.
CC The transgenic mouse can be used as an in vivo model system for the study
CC of prostate cancer and its progression. It can also be used in
CC preclinical and clinical models to test novel diagnostic and therapeutic
CC modalities including drug therapies relevant to prostate cancer
CC prevention and progression. The transgenic animal can also be used to
CC identify molecular markers that can be mediators of progression.
CC Identification of the mediators is useful since they are potential
CC therapeutic targets. The present sequence represents murine Plm1.
XX
SQ Sequence 313 AA;

```

Alignment Scores:	Pred. No.:	Length:	Matches:
Score:	5,036-139	313	1668,00
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatch:	0
Query Match:	95.37%	Indels:	0
DB:	8	Gaps:	0

```

US-10-705-757-5 (1-942) x ADN97347 (1-313)
QY 1 ATGCTCTGTCTCCAAATCACTTCCTGGGCCACTGCGCGCCCTCTGCAACGACTTG 60
    |||||
DB 1 MetLeuLeuSerIleIleAsnSerLeuAlaHisLeuArgAlaArgProCysAsnAspLeu 20
QY 61 CACGCCACCAACCTGCGCGCGCGGCAAGAGAGAGGCCCTCGAGTGCAGTACCGAGT 120
    |||||
DB 21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGlnSerIleArgIleVal 40
QY 121 GGCCTGCTGTTGGGAGCGAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
    |||||
DB 41 GlyProLeuLeuGlySerGlyIlePheGlySerValIleSerGlyIleArgValAlaAsp 60
QY 181 AACTGCGGTGGCCATTAAAGCAGTGAAGAGAACCGGATTTCCGATTGGGAGAACTG 240
    |||||
DB 61 AsnLeuProValAlaIleIleHisValGluLysAspArgIleSerAspTrpGlyIleLeu 80
QY 241 CCCAATGGACCCCGAGTGCCTTGAAGTGTCTTGAAGAGTGTGAGTCCGACTTC 300
    |||||
DB 81 ProAsnGlyThrArgValProMetGluValValIleLeuLeuLysValSerSerAspPhe 100
QY 301 TCGGGGCTATTAGACTTCTGAGCTGGTTGAGAGGCCCGATAGTTTCGTCGATCTCTG 360
    |||||
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
QY 361 GAGAGGCCCGAACCCGGTGCAGACCTCTTGCATTTATACCGAACGAGAGCCCTACAG 420
    |||||
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 421 GAGAGCTTGGCCCGAGAGATTCTTCTGACAGTCTGAGAGGCCCTGGGGCATTTGCCAAC 480
    |||||
DB 141 GluAspLeuAlaArgGlyPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
QY 481 TCGGGGCTTCTCCACCGCAGCATCAAGAGAGAACATCTTATTCAGCTGAGCCCGCGC 540
    |||||
DB 161 CysGlyValLeuHisArgAspIleArgAspGlnAsnIleLeuIleAspLeuSerArgGly 180
QY 541 GAATCAAACTCATCGACTTCGGGTCGGGGCGCTCTCAAGGACACAGCTTACACGAGAC 600
    |||||

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Db 181 GluilelyleuileasphneglySerGlyAlaLeuLeuylasphThrValTyrThrAsp 200
 QY TTTGATGGAGCCCGAGTGTACAGTCTCCAGAGTGGATTGGCTACGCTACGACGAGC 660
 Db 201 PheaspGlyThrArgValTyrSerProProGlnTrrPleargYrHlsArgYrHlsGly 220
 QY AGGTGGCAGCTGTCTGGTCCCTTGGAGATCCGTCTATGACATGGTCTGGGAGATATT 720
 Db 221 ArgSerAlaIaValTrrPserLeuGlyIleLeuLeuYrHsPmetValCysGlyAspIle 240
 QY 721 CCGTTTGAAGACCAATGAAGATCATCAAGGCGCAAGTGTCTTCAGGCAACTGTCTCT 780
 Db 241 ProPheGlnHlsAspGlnGlnIleIlelySerGlyGlnValPhePheArgGlnThrValSer 260
 QY 781 TCAGAGTGTACAGCCTTAATTAATGGTGGCTGTCCCTGAGACCGTACGATCGGCGCTCC 840
 Db 261 SerGlnCysGlnHlsLeuIlelyTrpCysLeuSerLeuHlsProSerAspArgProSer 280
 QY 841 TTTGAAGAAATCCCGAACAATCCGTGGATGCAAGGATGACCTCTGCCGAGGAGCTTCT 900
 Db 281 PheGlnIuIleArgHlsAspHlsProTrrPmetGlnGlyAspLeuLeuProGlnAlaIaSer 300
 QY 901 GAGATCCATGTGCAAGTCTGTCTCAACCGGAAATCCAGCAAG 939
 Db 301 GluIleHlsLeuHlsSerLeuSerProGlySerSerIys 313
 RESULT 5
 ADR88371
 ID ADR88371 standard; protein; 313 AA.
 AC ADR88371;
 XX 18-NOV-2004 (first entry)
 DT Mus musculus PIM 1 protein.
 DE Mus musculus PIM 1 protein.
 XX Molecular scaffold; nuclear hormone receptor; TNF receptor;
 KM G-protein coupled receptor; methyl transferase; ligase; PIM; mouse.
 OS Mus musculus.
 XX US2004171062-A1.
 PN 02-SEP-2004.
 PD 28-FEB-2003; 2003US-00377268.
 PF 28-FEB-2002; 2002US-0360651P.
 PR 16-SEP-2002; 2002US-0411398P.
 PR 20-SEP-2002; 2002US-0412341P.
 PR 02-JAN-2003; 2003US-0437929P.
 XX (PLEX-) PLEXIXON INC.
 PA Hirth K, Milburn MV;
 PI WPI; 2004-642017/62.
 DR Designing a ligand binding to a target molecule, comprises identifying as
 XX PT molecular scaffold compounds binding to members of a molecular family,
 PT detecting orientation of scaffolds at a binding site of target, and
 PT synthesizing ligand.
 PS Disclosure; SEQ ID NO 10; 186BP; English.
 XX The present invention relates to a method of designing a ligand binding
 CC to a target molecule. The method involves identifying as molecular
 CC scaffolds compounds binding to members of a molecular family, detecting
 CC orientation of scaffolds at a binding site of target, and synthesizing
 CC ligand. The invention is useful for designing drug products and for
 CC designing ligand binding to target molecules such as nuclear hormone
 CC receptors, TNF receptors, G-protein coupled receptors, methyl
 CC transferases, ligases, etc. The present sequence is the Mus musculus PIM

CC 1 protein. This sequence is used to illustrate the method of invention.
 XX
 SQ Sequence 313 AA;
 Alignment Scores:
 Pred. No.: 5.03e-139 Length: 313
 Score: 1668.00 Matches: 313
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 95.37% Indels: 0
 DB: 8 Gaps: 0
 US-10-705-757-5 (1-942) x ADR88371 (1-313)
 QY 1 ATGCTCTGTCCAAAGTCAATCCCTGGCCCACTGGCGCCGCTCCGCAAGCACTG 60
 Db 1 MetLeuLeuSerIysHlsLeuSerLeuHlsAlaIleuValAlaArgProCysAsnAspLeu 20
 QY 61 CAGCCACCAAGCTGGCGCGCGGCAAGAGAGAGAGCCCTGGAGTGCAGTACAGTGT 120
 Db 21 HlsAlaThrIlyleuHlsAspProGlyIlyGlnIlyGlnProLeuIuSerGlnIlyrGlnVal 40
 QY 121 GGCCTCGTGTGGGCAAGCGGTGGCTTCGCTCGGTCTACTCTGGCATCCGCTCGCCGAC 180
 Db 41 GlyProLeuLeuGlySerGlyIlyPheGlySerValTyrSerGlyIleArgValAlaAsp 60
 QY 181 AACTTGGCCGATGGCCATTAAGCAGTGGAGAAAGACCGGATTTCCGATTGGGGAGAACTG 240
 Db 61 AsnLeuProValAlaIlelyHlsValGlnIlyAspArgIleSerAspTrrPglIyGlnLeu 80
 QY 241 CCCAATGGACCCCGAGGCGCCATGGAAGTGGCTCTGTGAAAGAGGAGCTCGGACTTC 300
 Db 81 ProAsnGlyThrArgValPProMetGlnValValLeuLeuIlySerValSerSerAspPhe 100
 QY 301 TCGGCGCTCATTAAGTCTTGAAGTGTTCGAGAGGCGCCGATAGTTCGTGATCTGT 360
 Db 101 SerGlyValIleArgLeuLeuAspTrrPheGlnIlyArgProAspSerPheValIleLeu 120
 QY 361 GAGAGGCCGGAACCGGTGCAAGACTCTTGAATTTATCCGGAAGAGAGGCCCTTACAG 420
 Db 121 GluArgProGlnProValGlnAspLeuPheAspPheIleThrGlnIlyrGlyAlaLeuGln 140
 QY 421 GAGACCTGGCCCGAGAGATTTCTTCTGGAGGTCTGAGGCGGTGGCGGACTTCCCAAC 480
 Db 141 GluAspLeuHlsArgGlyPhePheTrrPglValLeuGlnIlaValAlaArgHlsCysHlsAsn 160
 QY 481 TGCAGGATTTCTCCACCGCGCATCATCAAGACGAGAACTTTATCGACTGAGCCGCGGC 540
 Db 161 CysGlyValLeuHlsArgAspIlelyAspGlnAsnIleLeuIleAspLeuSerArgGly 180
 QY 541 GAATCAAACTCATGCACTTCGGGTGGGGGCGCTCTCAAGACACAGTCTTACGAGAC 600
 Db 181 GluIlelyleuIleAspPheGlySerGlyAlaLeuLeuIlyAspThrValTyrThrAsp 200
 QY 601 TTTGATGGAGCCCGAGTGTACAGTCTCCAGAGTGGATTGGCTACGCTACGACGAGC 660
 Db 201 PheaspGlyThrArgValTyrSerProProGlnTrrPleargYrHlsArgYrHlsGly 220
 QY 661 AGGTGGCAGCTGTCTGGTCCCTTGGAGATCCGTCTATGACATGGTCTGGGAGATATT 720
 Db 221 ArgSerAlaIaValTrrPserLeuGlyIleLeuLeuYrHsPmetValCysGlyAspIle 240
 QY 721 CCGTTTGAAGACCAATGAAGATCATCAAGGCGCAAGTGTCTTCAGGCAACTGTCTCT 780
 Db 241 ProPheGlnHlsAspGlnGlnIleIlelySerGlyGlnValPhePheArgGlnThrValSer 260
 QY 781 TCAGAGTGTACAGCCTTAATTAATGGTGGCTGTCCCTGAGACCGTACGATCGGCGCTCC 840
 Db 261 SerGlnCysGlnHlsLeuIlelyTrpCysLeuSerLeuHlsProSerAspArgProSer 280
 QY 841 TTTGAAGAAATCCCGAACAATCCGTGGATGCAAGGATGACCTCTGCCGAGGAGCTTCT 900
 Db 281 PheGlnIuIleArgHlsAspHlsProTrrPmetGlnGlyAspLeuLeuProGlnAlaIaSer 300

QY 901 GAGATCCATCTGCAGATCTGTCCACGGGATCCAGCAAG 939
 |||||
 Db 301 GIUILEHLEuHISerLeuSerProGlySerSerIys 313

RESULT 6
 ABG33016 standard; protein; 313 AA.

XX ABG33016;

XX 20-DEC-2002 (first entry)

XX Rat protein kinase phosphorylation site #2.

XX HKID-1; serine/threonine kinase; cellular proliferative disorder;
 XX differentiative disorder; cancer; haematopoietic neoplastic disorder;
 XX acute promyeloid leukaemia; APLM; Chronic myelogenous leukaemia; CML;
 XX Waldenstrom's macroglobulinaemia; WM; rat.

XX Rattus norvegicus.

XX US2002115120-A1.

XX 22-AUG-2002.

XX 04-OCT-2001; 2001US-00971791.

XX 26-JAN-1999; 99US-00237543.

XX 23-AUG-2000; 2000US-00644450.

XX (MILL-) MILLENNIUM PHARM INC.

XX Kapeller-Libermann R, Rudolph-Owen LA, Machbeth K;

XX WPI; 2002-712471/77.

XX Modulating levels or activity of HKID-1 polypeptides, a member of
 PT serine/threonine kinase superfamily, for treating cancer, by contacting
 PT cell expressing the polypeptide with a modulator of the polypeptide.

XX Example 3; Page 39-40; 48pp; English.

XX The invention describes a method of modulating the level or activity of
 CC human HKID-1 polypeptide, a member of serine/threonine kinase
 CC superfamily. The method involves contacting a cell expressing the
 CC polypeptide or nucleic acid with an agent to modulate the level or
 CC activity of polypeptide, or level of nucleic acid molecule. The method is
 CC useful for modulating the level or activity of HKID-1 polypeptide or
 CC polynucleotide in a subject having or predisposed to having a disorder
 CC involving cancer. Modulating HKID-1 expression or activity is useful for
 CC therapeutic purposes, for treating cellular proliferative and/or
 CC differentiative disorders including cancer or haematopoietic neoplastic
 CC disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
 CC leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
 CC amino acid sequence of a rat protein kinase phosphorylation site

XX Sequence 313 AA;

XX Alignment Scores:

Pred. No.: 1,45e-131 Length: 313
 Score: 1584.00 Matches: 295
 Percent Similarity: 96.81% Conservative: 8
 Best Local Similarity: 94.25% Mismatches: 10
 Query Match: 90.57% Indels: 0
 DB: 5 Gaps: 0

US-10-705-757-5 (1-942) x ABG33016 (1-313)

QY 1 ATGCTCCTGTCGAAGATCACTCCCTGGCCGACCTGGCCGCCCTTCGAAGCACTG 60
 |||||
 Db 1 MetLeuLeuSerIysIleAsnSerLeuAlaIleLeuAlaIleProCysAsnAspLeu 20

QY 61 CAGGCCACCAAGCTGGCCGCCGCAAGAAAGAGCCCTGGAGTCCAGTACCAAGTGG 120
 |||||
 Db 21 HIsAlaAnLysLeuAlaProGlyLysGlyLysProLeuGlnSerGlnTyrGlnVal 40
 QY 121 GGGCCCGCTGTTGGGAGCGGGTGGCTTGGCTGGCTACTCTGGCATCCGCCCGCAG 180
 |||||
 Db 41 GlyProLeuLeuGlySerGlyGlyIleGlySerValTyrSerGlyIleArgValAlaAsp 60
 QY 181 AACTGGCCGGTGGCCATTAAAGCAGCTGGAGAAAGACCGGATTTCCGATTGGGAGAACTG 240
 |||||
 Db 61 AsnLeuProValAlaIleIleHisValGlnLysAspArgIleSerAspTrpGlyGlnLeu 80
 QY 241 CCCAATGGACCCCGAGTGGCCCATGGAAAGTGGTCTGTTGAAGAGTGAAGTCCGACTTC 300
 |||||
 Db 81 ProAsnGlyThrArgValProMetGlnValValLeuLeuLysValSerSerGlyPhe 100
 QY 301 TGGGGCGTCATTAAKCTTCTGGACTGCTTCCAGAGAGCCCGAATGTTTGGTGTGATCCG 360
 |||||
 Db 101 SerGlyValIleArgLeuLeuAspTrpPheGlnArgProAspSerPheValLeuIleLeu 120
 QY 361 GAGAGCCCGAAGCCGGTGGCAAGACTCTTCGACTTTATCAACGAAAGAGAGCCCTACAG 420
 |||||
 Db 121 GlnArgProGlnProValGlnAspLeuPheAspPheIleThrGlnArgGlyAlaLeuGln 140
 QY 421 GAGGACTGGCCCGAGATTTCTTGGCAGAGTGTGAGAGCCGTGCGGACTTGCACAAAC 480
 |||||
 Db 141 GlnGlnLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
 QY 481 TGGCGGGTCTTCCACCGGACATCAAGAGACCGAAACATTTAATGACCTGAGCCGCGGC 540
 |||||
 Db 161 CysGlyValLeuHisArgAspIleLysAspGlnAsnIleLeuIleAspLeuAsnArgGly 180
 QY 541 GAAATCAAACTCATGCACTTCGGGTCGGGAGCGCTGCTCAAGAGACAGTCTTACAGGAGC 600
 |||||
 Db 181 GlnLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200
 QY 601 TTTGATGGAGCCCGAGTGTACAGTCTCCAGAGTGAATTCGCTACCATCGTACCAAGCGC 660
 |||||
 Db 201 PheAspGlyThrArgValTyrSerProProGlnTrpIleArgTyrHisArgTyrHisGly 220
 QY 661 AGCTGGGAGCTGTCTGTGCTCCCTTGGGATCCCTGCTATGACATGCTCGCGCAATATT 720
 |||||
 Db 221 ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
 QY 721 CCGTTTGAAGCAGATGAAGATCATCAAGAGGCGCAAGTGTCTTCAAGGCAACTGTCTCT 780
 |||||
 Db 241 ProPheGlnHisAspGlnGlnIleValLysGlyGlnValTyrPheArgGlnArgValSer 260
 QY 781 TCAGAGTGTCAAGCACCCTTAATGATGTGCTGTCTCCCTGAAGCCGTCAAGATCGCCCTCC 840
 |||||
 Db 261 SerGlnCysGlnHisLeuIleIleGlyTrpCysLeuSerLeuArgProSerAspArgProSer 280
 QY 841 TTTGAAGAAATCCGAAACCATTCGTGATGACAGGAGTGAACCTTCCGCCAGCAGCTTCT 900
 |||||
 Db 281 PheGlnGlnIleGlnHisAspTrpTrpMetGlnAspValLeuLeuProGlnAlaThrAla 300
 QY 901 GAGATCCATCTGCAGATCTGTCCACGGGATCCAGCAAG 939
 |||||
 Db 301 GIUILEHLEuHISerLeuSerProSerProSerIys 313

RESULT 7
 AA019789 standard; protein; 313 AA.
 ID AA019789;
 XX AA019789;
 AC AA019789;
 XX 11-AUG-2003 (first entry)
 XX Rat PIM kinase.
 DT Rat PIM kinase.
 XX Rat, PIM1 kinase; PIM3 kinase; pain; analgesic.
 KM Rat, PIM1 kinase; PIM3 kinase; pain; analgesic.
 XX Rattus sp.

XX MO200293173-A2.
 PN
 XX
 PD 21-NOV-2002.
 XX
 XX 13-MAY-2002; 2002WO-BP005234.
 XX
 XX 11-MAY-2001; 2001DE-01023055.
 XX
 PA (CHER) GRUBENTHAL GMBH.
 XX
 PI Wehne E, Schaefer MK;
 XX
 DR WPI; 2003-120715/11.
 DR N-PSDB; AB269187.
 XX
 PT Method for identifying analgesics, useful particularly for treating
 PT chronic pain, by screening compounds for interaction with PIM-1 or -3
 PT kinase, or related compounds.
 XX
 PS Claim 1; Fig 1D; 97pp; German.
 XX
 CC The present invention relates to a method of identifying pain-regulating
 CC compounds, involving screening candidate compounds for interaction with
 CC PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
 CC useful for treating chronic pain, particularly of neuropathic or
 CC inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
 CC neurodegenerative diseases). The present sequence is rat PIM1 kinase
 XX
 SQ Sequence 313 AA;

Alignment Scores:
 Pred. No.: 1,45e-131 Length: 313
 Score: 1594.00 Matches: 295
 Percent Similarity: 96.81% Conservative: 8
 Best Local Similarity: 94.25% Mismatches: 10
 Query Match: 90.57% Indels: 0
 DB: 6 Gaps: 0

US-10-705-757-5 (1-942) x AMO19789 (1-313)

QY 1 ATGCTCTGTCCAAAGATCAACTCCCTGCGCCACTGCGCGCCCGCTTCGAACAGCTG 60
 DB 1 MetLeuLeuSerIleIleAsnSerIleuAlaIleLeuArgIleAlaProCysAsnAspLeu 20
 QY 61 CACGCCCAACAGCTGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 DB 21 H1A1AAsnIleLeuAlaProGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 40
 QY 121 GGCCCGCTGTGGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 DB 41 GlyProLeuLeuGlySerIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 60
 QY 181 AACTGCGCGTGGGCGCTTAAGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 DB 61 AsnLeuProValAlaIleIleIleValIleGlyIleAspArgIleSerSerIleGlyIle 80
 QY 241 CCCAATGAGACCCGAGTCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 DB 81 ProAsnGlyThrArgValAlaProMetGlyValIleLeuLeuIleValSerSerGlyPhe 100
 QY 301 TGGCGGCTCATTAAGATTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 DB 101 SerGlyValIleIleArgLeuLeuAspIlePheGlyIleGlyIleGlyIleGlyIle 120
 QY 361 GAGAGCGCGAAGCCGAGTGAAGACTCTTCACTTATCAAGAGAGAGAGAGAGAGAGAG 420
 DB 121 GluArgProGluProValAlaIleAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 421 GAGAGCTGCGCGCGAGAGATTTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 DB 141 GluGluLeuAlaArgSerPhePheThrGlnValIleGluAlaValArgIleCysHisAsn 160

QY 481 TCGGGGTTCTCCACCGAGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 161 CysGlyValIleuH1A1ArgAspIleIleAspArgIleuAsnIleuIleAspLeuAsnArgGly 180
 QY 541 GAATCAAACTCATGACTTTCGGGTCGGGCGCGCTTCGAAGACACAGCTTACAGAGAC 600
 DB 181 GluLeuIleuIleAspPheGlySerGlyAlaIleLeuIleuIleAspPheValIleThrAsp 200
 QY 601 TTTGATGGGACCGGAGTGAACAGTCTCCAGAGTGGATTCGATCAATGCTACAGAGAG 660
 DB 201 PheAspGlyThrArgValIleSerProGluIlePheIleArgIleIleArgIleIleGly 220
 QY 661 AGTCCGAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 DB 221 ArgSerAlaAlaValIlePheSerIleuGlyIleLeuLeuIleuIleAspMetValCysGlyAspIle 240
 QY 721 CCGTTTGAACAGATGAAGATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 DB 241 ProPheGluH1A1AspGluIleValIleValIleValIleValIleValIleValIleValIle 260
 QY 781 TCAAGTGTCAACACTTATTAAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 DB 261 SerGluCysGlnH1A1IleuIleArgIlePheCysLeuSerIleuArgPheSerAspArgProSer 280
 QY 841 TTTGAAGAAATCCGGAACCATCCGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 DB 281 PheGluGluIleGlnH1A1IleuH1A1ProIlePheCysIleuAspValIleuProGlnAlaThrAla 300
 QY 901 GAGATCCATCTGACAGTCTGTCAACGGAGATCCAGCAAG 929
 DB 301 GluIleH1A1SerIleuSerProSerProSerIleIle 313

RESULT 8

ABR62938
 ID ABR62938 standard; protein; 313 AA.

AC ABR62938;

DT 04-DEC-2003 (first entry)

DE Rat serine/threonine protein kinase PIM-1.

KW Rat; PIM-1; protein kinase; enzyme.

OS Rattus norvegicus.

PN WO2003060130-A2.

PD 24-JUL-2003.

PF 20-JAN-2003; 2003WO-BP000492.

PR 19-JAN-2002; 2002EP-00001401.

PA (AVENTIS) AVENTIS PHARMA DEUT GMBH.

PI Korn M, Mueller G, Schneider R, Tschank G;

DR WPI; 2003-598536/56.

PT New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
 PT agent for identifying anti-type 2 diabetes mellitus drugs, or for
 PT treating insulin resistance or type 2 diabetes mellitus.

PS Example 2; Page 39; 40pp; English.

CC The present sequence is the protein sequence of the rat serine/threonine
 CC protein kinase and proto-oncogene, PIM-1. PIM-1 proteins are the
 CC paralogues of novel human and murine PIM-3 proteins (see ABR62932 and
 CC ABR62933) of the invention, which are therefore expected to be involved
 CC in cancer and cell growth regulation. PIM-3 is also involved in the
 CC development of insulin resistance and type 2 diabetes mellitus. The
 CC invention relates to the use of PIM-3 nucleic acids and proteins in:

CC screening assays for compounds that modulate insulin resistance or type 2
 CC diabetes mellitus; detection assays for detecting insulin resistance or
 CC type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
 CC forensic biology); predictive medicine (e.g. diagnostic or prognostic
 CC assays, monitoring clinical trials, pharmacogenomics); and for the
 CC preparing a medication for the treatment of insulin resistance or type 2
 CC diabetes mellitus
 CC
 XX
 SQ Sequence 313 AA;

Alignment Scores:

Pred. No.: 1,45e-131 Length: 313
 Score: 1584.00 Matches: 295
 Percent Similarity: 96.81% Conservative: 8
 Best Local Similarity: 94.25% Mismatches: 10
 Query Match: 90.57% Indels: 0
 DB: Gaps: 0

US-10-705-757-5 (1-942) x ABR62938 (1-313)

QY 1 AAGCTCTGTGCAAGATCAACTCCCTGGCCACCTTGCGGCGCCGCTGCAACGACCTG 60
 DB 1 MetLeuLeuSerIylLeuAsnSerIylLeuAlaHisLeuArgAlaIaProCysAsnAspLeu 20
 QY 61 CACGCCACCAAGCTGGCGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 DB 21 HisAlaAsnIylLeuAlaProGlyIylGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 40
 QY 121 GGGCGCGCTGTGGGCGAGCGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 180
 DB 41 GlyProLeuLeuIylSerGlyIylGlyGlySerValIylSerIylLeuArgValAlaAsp 60
 QY 181 AACTTGCCTGGTGGCATTAAAGCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 DB 61 AsnLeuProValAlaIleuHisIleuValGlyIylAspArgIleSerAspTrpGlyGlyLeu 80
 QY 241 CCCAATGGACCCGAGTGGCCATGAGAGAGTGTCTGTGTAAGAGAGAGAGAGAGAGAGAG 300
 DB 81 ProAsnGlyThrArgValIleProMetGlyValIleValIleuLeuIylValIleSerGlyPhe 100
 QY 301 TCGGGCGCTATTGACTTCTGCACTGGTTCAGAGAGCGGAGTGTCTGTCTGTCTGTCTG 360
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGlyIylArgProAspSerPheValIleuIleu 120
 QY 361 GAGAGGCCGGAACCGGAGCAAGACTCTTTCGACTTATACCGAAGAGAGAGAGAGAGAGAG 420
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGlyIylArgIylAlaLeuGln 140
 QY 421 GAGGACCTGGCCGAGAGATTCTTCTGGAGGTGCTGAGAGCGCTGCGGCAATGCCAAG 480
 DB 141 GluGlnIleuAlaIleArgSerPhePheTrpGlnValIleuGlnAlaValArgHisCysHisAsn 160
 QY 481 TCGGGGGTCTCCACCGGCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 161 CysGlyValIleuHisArgAspIleuIylAspGlnAsnIleuIleuAspLeuAsnArgGly 180
 QY 541 GAAATCAAACTCATGCACTTGGGCTGGGGGCGCTGCTCAAGAGAGAGAGAGAGAGAGAG 600
 DB 181 GlnIleuIleuLeuIleAspPheGlySerGlyAlaLeuLeuIylAspThrValIylTrnAsp 200
 QY 601 TTTGATGGAGCCGAGGTGATCACTCTCCAGAGTGTGCTACCATCGCTACCAAGAGAG 660
 DB 201 PheAspGlyThrArgValIylSerProProGluTrpIleArgGlyHisArgIylHisGly 220
 QY 661 AGGTGGGAGCTGTGTGGTCCCTTGGAGATCTGCTCTATGACATGGTCTGGCGAGATATT 720
 DB 221 ArgSerAlaIleValIylTrpSerIleuGlyIleLeuLeuIylAspMetValCysGlyAspIle 240
 QY 721 CGCTTGAAGAGATCAAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 DB 241 ProPheGlnIleHisArgGlyIylGlnValIylArgIylValIylTrnArgGlnArgValSer 260
 QY 781 TCAGAGTGTACAGCACTTATTAAATGAGTGCCTGTCCCTGAGACCGTCAAGATCGGCCCTCC 840

DB 261 SerGlnCysGlnHisLeuIleArgTrpCysLeuSerIleArgProSerAspArgProSer 280
 QY 841 TTTGAAGAAATCCGGAACCATCCGAGATGCAAGGATGACCTTCCCGCAGGACGCTTCT 900
 DB 281 PheGlnGlyIleGlnAsnHisIleProTrpMetGlnAspValIleuProGlnAlaThrAla 300
 QY 901 GAGATCCATCTGCACAGTCTGTCAACCGGAGATCCAGCAAG 939
 DB 301 GlnIleHisLeuHisSerIleuSerProSerProSerIyls 313

RESULT 9

ABP54943
 ID ABP54943 standard; protein; 313 AA.

AC ABP54943;

DT 13-JAN-2003 (first entry)

DE Human Pim1.

KW Pim1; tyrosine threonine kinase; TTK; protein kinase; enzyme;

KW mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;

KW human; gene therapy.

OS Homo sapiens.

PN WO200268444-A1.

PD 06-SEP-2002.

PF 21-FEB-2002; 2002WO-US005278.

PR 21-FEB-2001; 2001US-0271254P.

PA (CHIR) CHIRON CORP.

PI Reinhard C, Jefferson AB, Chan VW;

DR MPI: 2002-698650/75.

DR N-PsDB: ABV73989.

XX Reducing growth of cancer cells comprises reducing Tyrosine Threonine

XX Kinase (TTK) activity, useful in diagnosing and treating disorders with

XX abnormal expression levels and activity of TTK, such as lung, colon,

XX prostate and ovarian cancer.

XX disclosure; Page 80-81; 113pp; English.

XX The present sequence is the protein sequence of human Pim1, a protein

XX related to tyrosine threonine kinase (TTK, see ABP54938) . TTK

XX polynucleotides and polypeptides of the invention encompasses

XX polynucleotides and polypeptides having sequence similarity or sequence

XX identity to human TTK and other genes and gene products related to TTK,

XX such as Pim1. The invention is based on the finding that TTK is

XX CC differentially expressed in various forms of cancer. It provides methods

XX for the identification of cancerous cells, especially breast cancer and

XX CC colon cancer cells, by detection of expression levels of TTK, as well as

XX CC diagnostic, prognostic and therapeutic methods. These methods can be used

XX as the basis of rational therapy. Assays for identifying molecules that

XX CC modulate the activity of these genes in cancers, as well as methods of

XX CC inhibiting tumour growth by inhibiting the activity of TTK are also

XX provided

SQ Sequence 313 AA;

Alignment Scores:

Pred. No.: 2.18e-131 Length: 313
 Score: 1582.00 Matches: 294
 Percent Similarity: 97.12% Conservative: 10
 Best Local Similarity: 93.93% Mismatches: 9
 Query Match: 90.45% Indels: 0
 DB: Gaps: 0

```

US-10-705-757-5 (1-942) x ABP54943 (1-313)
QY 1 ATGCTCTGTTCGAAGATCAACTCCCTGGCCCACTGGCGCCGCCCTGCAAGCACTTG 60
DB 1 MetLeuLeuSerIysIleAsnSerIleuAlaHisLeuAlaProCyAsnAspLeu 20
QY 61 CAGCCCAACAAGCTGGCGCGGCAAGAGAAAGAGAGCCCTGGAGTCCAGTACCAAGTG 120
DB 1 HisAlaThrIlyeLysAlaProGlyLysGluLysGluProLeuGluSerGlnIlyVal 40
QY 121 GCGCCGCTGTGGCAGCGGTGGCTGGCTGGCTGACTTCTGGCATCCGCGTCCGAC 180
DB 41 GlyProLeuLeuGlySerGlyIlyPheGlySerAllyIlySerGlyIleArgValSerAsp 60
QY 181 AACTTCCCGGTGGCCATTTAAGCAGCTGGAGAAAGACCGGATTTCCGATTGGAGAACTG 240
DB 61 AsnLeuProValAlaIleIyValIyGlyLysAspArgIleSerAspArgIlyGluLeu 80
QY 241 CCCAATGGCAACCGGAGCGCCATGAAGTGGTCTGTTGAAGAGTGAAGTGGAGCTTC 300
DB 81 ProAsnIlyThrArgValProMetGlyValIleuLeuLysValSerSerGlyPhe 100
QY 301 TCGGCGCTCATTTAGACTTCTGCACTGGTTCGAGAGCCCGCATGTTCTGCTGATCTG 360
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGlyLysArgProAspSerPheValIleuLeu 120
QY 361 GAGAGCGCCCAACCGGTGCAAGACCTTCTGACTTTATCACCGAAGAGAGCCCTTAC 420
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGlnArgIlyAlaLeuGln 140
QY 421 GAGAGCTGGCCCGAGAGATTTCTTGGCAGGTGCTGGAGCCCGTGGCGCATTTGCACAAC 480
DB 141 GlnGluLeuLysAlaAspSerPhePheTrpGlnAlaLeuLysAlaValAlaGlnHisCyAsnAsn 160
QY 481 TGGCGGGTCTTCCACCGCCGACATCAAGAGACGAGAACTTTAATCGACTGAGCGCGGC 540
DB 161 CyGlyIlyAlaLeuHisArgAspIleLysAspGlyAsnIleLeuIleAspLeuAsnArgGly 180
QY 541 GAAATCAAACTCATGCACTTCGGGTCCGGGCGCGCTGCTCAAGACACAGTCTTACACGAC 600
DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValIlyThrAsp 200
QY 601 TTTGATGGGACCCGAGGTACAGTCTTCCAGAGTGGATTTGGCTTACCTGCTACACGCG 660
DB 201 PheAspIlyThrArgValIlySerProGluIlyPheArgIlyHisArgIlyHisGly 220
QY 661 AGGTCCGAGCTGCTGTGCTCCCTGGAGTCTGCTCATGACATGCTGGGAGATATT 720
DB 221 ArgSerAlaAlaValIlyPheSerLeuGlyIleLeuLeuLysAspMetValCyAsnLysAspIle 240
QY 721 CCGTTTGAGCAGCAGTGAAGAGATCATCAAGAGCGCAAGTGTCTTCAAGCAAACTGTCT 780
DB 241 ProPheGluIlyHisArgIlyGluIleIleArgIlyGlnAlaPhePheArgGlnArgValSer 260
QY 781 TCAAGAGTTCAGCACTTTAATTAATGATGCTGCTCCCTGAGACCGTCAAGTCCGCTCC 840
DB 261 SerGluLysGlnHisLeuIleArgTrpCyLeuAlaLeuArgProSerAspArgProThr 280
QY 841 TTTGAGAAGAAATCCGGAGACATTCGTTGATGAGAGGTACCTTCCGCCCCGAGCACTTC 900
DB 281 PheGluIlyIlyIleGlnAsnHisProTrpMetGlnAspValIleuLeuProGlnIlyThrAla 300
QY 901 GAGATCCATCTGCAAGTCTGTCAACCGGAGATCCAGCAAG 939
DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerIlys 313

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DT 20-DEC-2002 (first entry)
DB XX Human protein kinase phosphorylation site.
XX HKID-1; serine/threonine kinase; cellular proliferative disorder;
XX differentiative disorder; cancer; haematopoietic neoplastic disorder;
XX Acute promyeloid leukaemia; APL; Chronic myelogenous leukaemia; CML;
XX Waldenstrom's macroglobulinaemia; WM; human.
XX Homo sapiens.
XX US2002115120-A1.
XX PD 22-AUG-2002.
XX PF 04-OCT-2001; 2001US-00971791.
XX PR 26-JAN-1999; 99US-00237543.
XX PR 23-AUG-2000; 2000US-00644450.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Kapeller-Lidemann R, Rudolph-Owen JA, Macbeth K;
XX WPI; 2002-712471/77.
XX PT Modulating levels or activity of HKID-1 polypeptides, a member of
XX PT serine/threonine kinase superfamily, for treating cancer, by contacting
XX PT cell expressing the polypeptide with a modulator of the polypeptide.
XX PS Example 3; Page 40-41; 48pp; English.
XX CC The invention describes a method of modulating the level or activity of
XX CC human HKID-1 polypeptide, a member of serine/threonine kinase
XX CC superfamily. The method involves contacting a cell expressing the
XX CC polypeptide or nucleic acid with an agent to modulate the level or
XX CC activity of polypeptide, or level of nucleic acid molecule. The method is
XX CC useful for modulating the level or activity of HKID-1 polypeptide or
XX CC polynucleotide in a subject having or predisposed to having a disorder
XX CC involving cancer. Modulating HKID-1 expression or activity is useful for
XX CC therapeutic purposes, for treating cellular proliferative and/or
XX CC differentiative disorders including cancer or haematopoietic neoplastic
XX CC disorders e.g. Acute promyeloid leukaemia (APL), Chronic myelogenous
XX CC leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
XX CC amino acid sequence of a human protein kinase phosphorylation site
XX CC
SQ Sequence 313 AA:
Alignment Scores:
Pred. No.: 2,18e-131 Length: 313
Score: 1582.00 Matches: 294
Percent Similarity: 97.12% Conservative: 10
Best Local Similarity: 93.93% Mismatches: 9
Query Match: 90.45% Indels: 0
DB: 5 Gaps: 0
US-10-705-757-5 (1-942) x ABG33017 (1-313)
QY 1 ATGCTCTGTTCGAAGATCAACTCCCTGGCCCACTGGCGCCGCCCTGCAAGCACTTG 60
DB 1 MetLeuLeuSerIysIleAsnSerIleuAlaHisLeuAlaProCyAsnAspLeu 20
QY 61 CAGCCCAACAAGCTGGCGCGGCAAGAGAAAGAGAGCCCTGGAGTCCAGTACCAAGTG 120
DB 21 HisAlaThrIlyeLysAlaProGlyLysGluLysGluProLeuGluSerGlnIlyVal 40
QY 121 GCGCCGCTGTGGCAGCGGTGGCTGGCTGACTTCTGGCATCCGCGTCCGAC 180
DB 41 GlyProLeuLeuGlySerGlyIlyPheGlySerAllyIlySerGlyIleArgValSerAsp 60
QY 181 AACTTCCCGGTGGCCATTTAAGCAGCTGGAGAAAGACCGGATTTCCGATTGGAGAACTG 240
DB 61 AsnLeuProValAlaIleIyValIyGlyLysAspArgIleSerAspArgIlyGluLeu 80

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QY 241 CCAGATGGACCCGAGTGGCCATGGAAGTGTCTCTTGAAGAAGGTGAGCTCGACTTC 300
DB 81 ProbenGlyThrArgValProMetGluValLeuLeuLysValSerSerGlyPhe 100
QY 301 TCGGGCGTCATTAGACTTCTGACTGTGAGAGGCCGATAGTTCTGCTGATCTTG 360
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
QY 361 GAGAGGCCCGAACCAGTGGCAAGACCTTTGACTTATCAACGAGAGAGCCCTACAG 420
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 421 GAGAGCTGGACCCGAGGATTTCTTGGACAGTCTGAGAGCCGTGGCGCATTCACAAC 480
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn 160
QY 481 TGCGGGGTTCTCCACCGGACATCAAGAGAGAGAACATCTTAATCGACTGAGCCGGC 540
DB 161 CysGlyValLeuHisArgAspIleLeuAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY 541 GAATCAAACTCATTCGACTTCGGGGTGGGGCGCTGTCAAGACAGTCTACAGGAGC 600
DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyTrnAsp 200
QY 601 TTGATGGGACCCGAGTGTACAGTCTCTCAGAGTGGATTGCTACCATCGCTACACGGC 660
DB 201 PheAspGlyThrArgValTySerProProGluTrpIleArgTyHisArgTyHisGly 220
QY 661 AGGTGGAGCTGTCTGTGCTCTTGGAGTCTGTGCTCTATGACATGGTCTGCGAGATTT 720
DB 221 ArgSerAlaIaValTrpSerLeuGlyIleLeuLeuTyAspMetValCysGlyAspIle 240
QY 721 CCGTTGAGACAGATGAAGAGATCATCAAGGGCCAGTGTCTTCAAGCGCAACTGTCTCT 780
DB 241 ProPheGluHisAspGluGluIleLeuArgGlyGlnAlaPhePheArgGlnArgValSer 260
QY 781 TCAGAGTGTACAGACCTTATTAATGGTGTGCTGTGCTGAGACCGTCAAGTCCGCTCC 840
DB 261 SerGluCysGlnHisLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProTrn 280
QY 841 TTGGAAGAAATCCGAAACCATCCGTGTGATGACAGGGTGAACCTCTGCCCCAGGACCTTC 900
DB 281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGlnGluTrnAla 300
QY 901 GAGATCCATTCGACAGTCTGTCAACCGGGATTCACAGAG 939
DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313

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RESULT 11

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AAO19788
ID AAO19788 standard; protein; 313 AA.
AC AAO19788;
XX
XX 11-AUG-2003 (first entry)
XX
XX Human PIM1 kinase.
XX
XX Human; PIM1 kinase; PIM3 kinase; pain; analgesic.
XX
XX Homo sapiens.
XX
XX MO200293173-A2.
XX
XX 21-NOV-2002.
XX
XX 13-MAY-2002; 2002MO-BP005234.
XX
XX 11-MAY-2001; 2001DE-01023055.
XX
XX (CHEP ) GRUENENTHAL GMBH.
XX

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PI 1 Weihe E, Schaefer MK;
XX
XX WPI; 2003-120715/11.
DR N-PSDB; AB269186.
XX
XX Method for identifying analgesics, useful particularly for treating
PT chronic pain, by screening compounds for interaction with PIM-1 or -3
PT kinase, or related compounds.
XX
XX Claim 1; Fig 1B; 97p; German.
XX
XX The present invention relates to a method of identifying pain-regulating
CC compounds, involving screening candidate compounds for interaction with
CC PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC useful for treating chronic pain, particularly of neuropathic or
CC inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC neurodegenerative diseases). The present sequence is human PIM1 kinase
XX
XX Sequence 313 AA;
SQ
Alignment Scores:
Pred. No.: 2,18e-131 Length: 313
Score: 1582.00 Matches: 294
Percent Similarity: 97.12% Conservative: 10
Best Local Similarity: 93.93% Mismatches: 9
Query Match: 90.45% Indels: 0
DB: 6 Gaps: 0
US-10-705-757-5 (1-942) x AAO19788 (1-313)
QY 1 ATGCTCTGTCCAAAGTCAATCTCCCTGGCCACTGCGCGCCGCTTGCAACGACTTG 60
DB 1 MetLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20
QY 61 CACGCCACCAACTGGCGCGCGCGGCAAGAGAGAGCCCTGAGTCCGAGTACAGAGTG 120
DB 21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGlnSerGlnTyGlnVal 40
QY 121 GGCCTGCTGTGGGACGCGGTGAGTCTGAGTCACTTGGACTCCGCGTCCGCGAC 180
DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTySerGlyIleArgValSerAsp 60
QY 181 AACTTGGCGGTGGCCATTAAAGACGTGAGAAAGAGACCGGATTTCCGATTGGGGAGACTG 240
DB 61 AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyGluLeu 80
QY 241 CCAGATGGACCCGAGTGGCCATGGAAGTGTCTCTTGAAGAAGGTGAGCTCGACTTC 300
DB 81 ProbenGlyThrArgValProMetGluValLeuLeuLysValSerSerGlyPhe 100
QY 301 TCGGGCGTCATTAGACTTCTGACTGTGAGAGGCCGATAGTTCTGCTGATCTTG 360
DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
QY 361 GAGAGGCCCGAACCAGTGGCAAGACCTTTGACTTATCAACGAGAGAGCCCTACAG 420
DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
QY 421 GAGAGCTGGACCCGAGGATTTCTTGGACAGTCTGAGAGCCGTGGCGCATTCACAAC 480
DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn 160
QY 481 TGCGGGGTTCTCCACCGGACATCAAGAGAGAGAACATCTTAATCGACTGAGCCGGC 540
DB 161 CysGlyValLeuHisArgAspIleLeuAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY 541 GAATCAAACTCATTCGACTTCGGGGTGGGGCGCTGTCAAGACAGTCTACAGGAGC 600
DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyTrnAsp 200
QY 601 TTGATGGGACCCGAGTGTACAGTCTCTCAGAGTGGATTGCTACCATCGCTACACGGC 660
DB 201 PheAspGlyThrArgValTySerProProGluTrpIleArgTyHisArgTyHisGly 220

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QY 661 AGGTCGACAGCTGCTGCTGCTGAGATCCTGCTATGACAGATGCTGCGAGATATT 720
 |||||
 DB 221 ArgSerLeuAlaValITPserLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
 |||||
 QY 721 CGGTTGAGACGACGATGAAGATCATCAAGGCGCAAGTGTCTTTCAGCAAACTGCTCT 780
 |||||
 DB 241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
 |||||
 QY 781 TCAGAGTTCAGACCTTATTAAATGCTGCTGCTGCTGAGACCGTCAAGTCCGCTCC 840
 |||||
 DB 261 SerGlnCysGlnHisLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProThr 280
 |||||
 QY 841 TTGAAGAATCCGCAACATCCGTCGATGACGGGTGACCTCGCCGAGGAGAGCTTCT 900
 |||||
 DB 281 PheGluGluIleGlnHisMetIleProTyrMetGlnAspValLeuLeuProGlnGluThrAla 300
 |||||
 QY 901 GAGATCCATCTGCACAGCTGTGTCAACCGGATCCAGCAAG 939
 |||||
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerIys 313
 |||||
 RESULT 12
 ABU61613
 ID ABU61613 standard; protein; 313 AA.
 XX
 AC ABU61613;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Human PIM1 protein.
 XX
 KM Human; tyrosine threonine kinase; TTK; cancer; cytostatic;
 XX
 KM mitotic checkpoint gene; PIM1.
 OS Homo sapiens.
 PN US2003045491-A1.
 PD 06-MAR-2003.
 PF 21-FEB-2002; 2002US-00081119.
 PR 23-FEB-2001; 2001US-0289813P.
 PA (REIN/) REINHARD C.
 PA (JEFF/) JEFFERSON A B.
 PA (CHAN/) CHAN V W.
 PI Reinhard C, Jefferson AB, Chan VW;
 DR MPI: 2003-456566/43.
 DR N-PSDB; ACA62265.
 PT Detecting cancer in a subject, by comparing expression levels of tyrosine
 PT threonine kinase polypeptide or polynucleotide in a subject cell and a
 PT normal cell, where an increase in the expression level in the test cell
 PT is indicative of cancer.
 PS Disclosure; Page 34-35; 79pp; English.
 PS
 CC The invention relates to detecting cancer (other than ovarian cancer) in
 CC a subject, comprising comparing the expression levels of tyrosine
 CC threonine kinase (TTK, a mitotic checkpoint gene) polypeptide and/or
 CC polynucleotide in a test cell obtained from the subject and in a normal
 CC non-cancer cell, where an increase in the expression level of TTK protein
 CC or nucleic acid in the test cell compared to that in the normal cell,
 CC indicates the presence of cancer other than ovarian cancer. Also included
 CC are reducing growth of a cancerous cell (by contacting a cancerous cell
 CC with an amount of an agent effective to reduce TTK polypeptide activity
 CC in the cell), an assay for identifying a candidate agent that reduces
 CC growth of a cancerous cell (comprising: (i) detecting the activity of a
 CC TTK polypeptide in the presence of a candidate agent; and (ii) comparing
 CC the activity of TTK polypeptide in the presence of a candidate agent

CC relative to TTK polypeptide activity in the absence of the candidate
 CC agent), identifying an agent that reduces TTK activity (comprising: (i)
 CC contacting a cancerous cell displaying elevated expression of a TTK-
 CC encoding polynucleotide with a candidate agent; and (ii) determining the
 CC effect of the candidate agent on TTK polypeptide activity) and assessing
 CC the prognosis of a cancerous disease other than ovarian cancer in a
 CC subject (comprising: (i) detecting expression of TTK -encoding
 CC polynucleotide in a test cancer cell of a subject; and (ii) comparing a
 CC level of expression of TTK-encoding polynucleotide in the test cancer
 CC cell with a level of expression of the polynucleotide in a control non-
 CC cancer cell, where the level of expression of TTK in the test cancer cell
 CC is relative to the level of expression in the control non-cancer cell is
 CC indicative of the prognosis of the cancerous disease). The methods are
 CC useful for detecting cancer (other than ovarian cancer) in a subject,
 CC reducing growth of a cancerous cell, identifying an agent that reduces TTK
 CC activity and assessing the prognosis of a cancerous disease other than
 CC ovarian cancer. The methods are also useful for determining the ability
 CC of a subject to respond to a particular therapy e.g. as a basis of
 CC rational therapy. The present sequence represents a closely related
 CC protein to human TTK, in this case human PIM1 (not defined)
 XX
 SQ Sequence 313 AA;
 XX
 Alignment Scores:
 Pred. No.: 2,186-131 Length: 313
 Score: 1582.00 Matches: 294
 Percent Similarity: 97.12% Conservative: 10
 Best Local Similarity: 93.93% Mismatches: 9
 Query Match: 90.45% Indels: 0
 DB: 7 Gaps: 0
 US-10-705-757-5 (1-942) x ABU61613 (1-313)
 QY 1 ATGCTCTGTCCAAAGATCAACTCCCTGACCACCTGCGCGCCCTGCAAGCACTG 60
 |||||
 DB 1 MetLeuLeuSerIysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20
 |||||
 QY 61 CACGCCACCAAGCTGGCGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 |||||
 DB 21 HisAlaThrIysLeuAlaProGlyIysGlyGluProLeuGlnSerGlnVal 40
 |||||
 QY 121 GGGCGGCTGTGGGCGCGGCGGCTGCGGTACTGTCGATCCGCGCGCGGAG 180
 |||||
 DB 41 GlyProLeuLeuGlnSerIysGlyIysPheGlySerValIysSerGlyIleArgValSerAsp 60
 |||||
 QY 181 AACTGCGCGGTGCCATTAAAGACGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 |||||
 DB 61 AsnLeuProValAlaIleIysHisValGluIysAspArgIleSerAspTrpGlyGluLeu 80
 |||||
 QY 241 CCCAATGGCAACCGAGTCCCATGGAAGTGTCTGTTGAAGAGAGTTCGAGCTTC 300
 |||||
 DB 81 ProAsnGlyThrArgValProMetGluValIleuLeuIysValSerSerGlyPhe 100
 |||||
 QY 301 TGGGGGTCATTAAAGCTTGTGACGTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 |||||
 DB 101 SerGlyValIleIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleuLeu 120
 |||||
 QY 361 GAGAGGCCGGAACCGGTGCAAGACTCTTGCATTATGACGGAAGAGAGAGAGAGAG 420
 |||||
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 |||||
 QY 421 GAGAACCTGGCCGAGAGATTTCTTGGCAGGTGCTGAGAGAGAGAGAGAGAGAGAG 480
 |||||
 DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValIleuGluAlaValArgHisCysHisAsn 160
 |||||
 QY 481 TCGGGGGTTCACCGGAGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 |||||
 DB 161 CysGlyValIleHisIleArgAspIleIysAspGluAsnIleLeuIleAspLeuAsnArgGly 180
 |||||
 QY 541 GAATCAACTCATGCACTTCGGGTGCGGGGCGCTGCTCAAGAGAGAGAGAGAGAGAG 600
 |||||
 DB 181 GluLeuIysLeuIleAspPheIleSerGlyAlaLeuLeuIysAspThrValIyrThrAsp 200
 |||||

QY 601 TTGTATGGAGCCGAGTGTACAGTCTCTCCAGATGATTCGATACCATGCTACAGGCG 660
 |||||
 DB 201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
 |||||
 QY 661 AGGTGGCAGCTGTGTGTCCTTGGATCTGCTGTATGACATGGTCTGGCAGATATT 720
 |||||
 DB 221 ArgSerAlaIleValTyrPheLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
 |||||
 QY 721 CGCTTGGACGACATGAAGATCATCAAGGGCAAGTGTCTTACGGCAACTGTCTCT 780
 |||||
 DB 241 ProPheGluHisAspGluIleLeuArgGlyGlnValPhePheArgGlnArgValSer 260
 |||||
 QY 781 TCAGATGTACAGACCTTATTAATGATGCTGCTGCTGAGACCGTCAAGATCGAGCTCC 840
 |||||
 DB 261 SerGluCysGlnHisIleLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProThr 280
 |||||
 QY 841 TTGGAAGAAATCCGGAACCATCCGTGATGACAGGATGACCTCTGCCCAAGCACTTCT 900
 |||||
 DB 281 PheGluGluIleGlnHisAspIleLeuIleArgGlyGlnValPhePheArgGlnArgValSer 300
 |||||
 QY 901 GAGATTCATCTGACAGTCTGTACACGGGATCCAGCAAG 939
 |||||
 DB 301 GluIleHisIleLeuHisSerLeuSerProGlyProSerLys 313
 |||||
 RESULT 13
 ABR62939
 ID ABR62939 standard, protein; 313 AA.
 AC ABR62939;
 XX 04-DEC-2003 (first entry)
 XX Human serine/threonine protein kinase PIM-1.
 DE Human serine/threonine protein kinase PIM-1.
 XX Human; PIM-1; protein kinase; enzyme.
 KW Homo sapiens.
 OS MO2003060130-AA.
 XX 24-JUL-2003.
 PD 20-JAN-2003; 2003MO-BP000492.
 XX 19-JAN-2002; 2002EP-00001401.
 PR (AVET) AVENTIS PHARMA DEUT GMBH.
 XX PA Korn M, Mueller G, Schneider R, Techank G;
 XX PI WPI; 2003-598536/56.
 DR
 XX New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
 PT agent for identifying anti-type 2 diabetes mellitus drugs, or for
 PT treating insulin resistance or type 2 diabetes mellitus.
 XX
 PS Example 2; Page 40; 40pp; English.
 XX
 CC The present sequence is the protein sequence of the human
 CC serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins
 CC are the paralogues of novel human and murine PIM-3 proteins (see ABR62932
 CC and ABR62933) of the invention, which are therefore expected to be
 CC involved in cancer and cell growth regulation. PIM-3 is also involved in
 CC the development of insulin resistance and type 2 diabetes mellitus. The
 CC invention relates to the use of PIM-3 nucleic acids and proteins in:
 CC screening assays for compounds that modulate insulin resistance or type 2
 CC diabetes mellitus; detection assays for detecting insulin resistance or
 CC type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
 CC forensic biology); predictive medicine (e.g. diagnostic or prognostic
 CC assays, monitoring clinical trials, pharmacogenomics); and for the
 CC preparing a medicament for the treatment of insulin resistance or type 2
 CC diabetes mellitus

XX
 SQ Sequence 313 AA;
 Alignment Scores:
 Pred. No.: 2,186-131
 Score: 1582.00
 Percent Similarity: 97.12%
 Best Local Similarity: 93.93%
 Query Match: 90.45%
 DB: 7
 Gaps: 0
 US-10-705-757-5 (1-942) x ABR62939 (1-313)
 QY 1 ATGCTCTGTCTCCAGATCAACTCCCTGGCCCACTGCGCGCCGCCCTGCAACGACTG 60
 |||||
 DB 1 MetLeuLeuSerLysIleHisSerLeuAlaHisLeuArgAlaHisProCysHisAspLeu 20
 |||||
 QY 61 CACGCCACCAAGCTGCGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 |||||
 DB 21 HisAlaThrLysLeuAlaProGlyLysGlyLysProLeuGluSerGlnTyrGlnVal 40
 |||||
 QY 121 GGCCTGCTGTGGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 |||||
 DB 41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
 |||||
 QY 181 AACTGGCCGAGTGGCATTAAAGCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 |||||
 DB 61 AsnLeuProValAlaIleLysHisValGlnLysAspArgIleSerAspTrpGlyIleLeu 80
 |||||
 QY 241 CCCAATGGACCCGAGAGTCCCATGGAAGTGTCTCTGTTGAAGAAGAGTGGACTTCG 300
 |||||
 DB 81 ProAsnGlyThrArgValProMetGluValIleLeuLysValSerSerGlyPhe 100
 |||||
 QY 301 TCGGGGCGTATTAAGCTTGTGAGTGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 |||||
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluLysProAspSerPheValIleLeu 120
 |||||
 QY 361 GAGAGGCCGGAACCGAGTGCAGACCTCTTGAATTATGACCGAAGAGAGAGAGAGAGAG 420
 |||||
 DB 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 |||||
 QY 421 GAGACCTGCGCCGAGAGATCTTCTGCGCAGGTGTCTGAGAGCCGTGGGATTCGCCAAG 480
 |||||
 DB 141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
 |||||
 QY 481 TCGGGGGTCTCCACCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 |||||
 DB 161 CysGlyValLeuHisIleArgAspIleLysAspGluAsnIleLeuIleAspLeuHisArgGly 180
 |||||
 QY 541 GAATCAAACTCATGCACTTCCGGGTCCGGGGCGCTGCTCAAGAGACAGTCTTACAGGAG 600
 |||||
 DB 181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200
 |||||
 QY 601 TTGTATGGAGCCGAGTGTACAGTCTCTCCAGATGATTCGATACCATGCTACAGGCG 660
 |||||
 DB 201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220
 |||||
 QY 661 AGGTGGCAGCTGTGTGTCCTTGGATCTGCTGTATGACATGGTCTGGCAGATATT 720
 |||||
 DB 221 ArgSerAlaIleValTyrPheLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240
 |||||
 QY 721 CGCTTGGACGACATGAAGATCATCAAGGGCAAGTGTCTTACGGCAACTGTCTCT 780
 |||||
 DB 241 ProPheGluHisAspGluIleLeuArgGlyGlnValPhePheArgGlnArgValSer 260
 |||||
 QY 781 TCAGATGTACAGACCTTATTAATGATGCTGCTGCTGAGACCGTCAAGATCGAGCTCC 840
 |||||
 DB 261 SerGluCysGlnHisIleLeuIleArgTyrCysLeuAlaLeuArgProSerAspArgProThr 280
 |||||
 QY 841 TTGGAAGAAATCCGGAACCATCCGTGATGACAGGATGACCTCTGCCCAAGCACTTCT 900
 |||||
 DB 281 PheGluGluIleGlnHisAspIleLeuIleArgGlyGlnValPhePheArgGlnArgValSer 300
 |||||

QY 901 GAGATCCATCTGCACAGTCTGTCCAGCGGATCCAGCAAG 939
 DB 301 GIUIEHLIEUHLISERIEUSERPROGLYPROSERLYS 313

RESULT 14
 ADE55368
 ID ADE55368 standard; protein; 313 AA.

XX ADE55368;

DT 29-JAN-2004 (first entry)

DE Human Protein AAA60089, SEQ ID NO 1183.

XX Human pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

XX spared nerve injury; SNI; Chung.

OS Homo sapiens.

XX NO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GEHO) GEN HOSPITAL CORP.

XX (PARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; AAA60089.

PT New composition comprising two or more isolated polypeptides, useful for

PS preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017P; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 313 AA;

Alignment Scores:

Pred. No.: 2,18e-131 Length: 313
 Score: 1582.00 Matches: 294
 Percent Similarity: 97.12% Conservative: 10
 Best Local Similarity: 93.93% Mismatches: 9
 Query Match: 90.45% Indels: 0
 DB: 7 Gaps: 0

US-10-705-757-5 (1-942) x ADE55368 (1-313)

QY	1	ATGCTCCTGTCAAGATCAATCTCCCTGGCCACCTGGCGCCGCCCTTCGAACGACTG	60
DB	1	MetIeuLeuSerIylIeAsnSerIeAlaIhIeUaIrgIaIaIaProCyAsnAspIeu	20
QY	61	CAGGCCCAAGAGTGGCGCGCGGCAAGAGAGAGCCCTGAGTGGCAATGCAAGTG	120
DB	21	HieIaIaThryIeUaIaProGIyGluIyGluIaIProIeuGIuSerGIyGluIaI	40
QY	121	GGCCCGCTGTGGCGAGCGGTGGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	180
DB	41	GlyProIeuLeuIySerGIyGlyPneGIySerValIySerGIyIeArGValSerAsp	60
QY	181	AACCTGCGGTGGCCATTAAGACAGTGAAGAGACCGAGATTCCGATTGGGAGAACTG	240
DB	61	AsnIeuProValaIaIeIyShIeValGIuIyAspArgIleSerAspIrgIyGIuIeu	80
QY	241	CCCAATGGCAACCGAGTGGCCATGAAGATGGTCTGTGAAGAGTGGAGCTTC	300
DB	81	ProAsnGIyThryArGValIProMetGIuValIeUaIySerGIyPhe	100
QY	301	TGGGCGCTGATGACTTCCTGCACTGCTGCAAGGCGGCAAGTTCGCTGCTGCTG	360
DB	101	SerGIyValIeArGLeuEuaAspIrgIyPneGIyArGProAspSerPheValIeUaI	120
QY	361	GAGAGCCCGCAACCGGTGCAAGACTCTTCACTTATACCGCAAGAGAGGCTTACAG	420
DB	121	GIuArGProGIuProValGIuAspIeuPheAspPheIeThrGIuArGValIeUaI	140
QY	421	GAGAACCTGGCCGAGAGATTCTTGTGGCAAGTCTGAGGCGCTGGCGCAATTC	480
DB	141	GIuGIuIeUaIaIrgSerPhePheIrgIuValIeUaIaIaValIArgIhIeValI	160
QY	481	TGGGCGGTCTCCACCGCGCATCAAGAGAGCAATCTTATGACCTGACCTGGCGG	540
DB	161	CySGIyValIeUaIaIrgAspIleIyAspGIuAsnIleUaIeAspIeUaAsnArgIy	180
QY	541	GAATCAAACTCATCGACTTCGGGTGGCGGCGCTGCTCAAGAGACAGTCTACAGGAC	600
DB	181	GIuIeUaIeUaIeAspPheGIySerGIyAlaIeUaIeUaIyAspIhIeValIyThrAsp	200
QY	601	TTTGATGGGACCCGAGTGTACGTCTCCAGAGTGAATTCGTACCAATGCTTACAGG	660
DB	201	PheAspGIyThryArGValIySerProProGIuIrgIeArgIyThIeArgIyThIe	220
QY	661	AGGTGGGAGCTGTCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCTGTCCT	720
DB	221	ArgSerAlaIaIaIrgPheIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIe	240
QY	721	CCCTTGAAGACAGTGAAGAGATCATCAAGAGGCGCAAGTCTTCAAGCAACTGCTCT	780
DB	241	ProPheGIuIhIeAspIeUaIeUaIeIeIeArGGIyGluIaIaIeUaIeUaIeUaIe	260
QY	781	TCAAGTGTCAAGACCTTATTAATGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCT	840
DB	261	SerGIuGIyGIuIhIeUaIeUaIeArGTrCyIeUaIaIeUaIeUaIeUaIeUaIeUaIe	280
QY	841	TTTGAAGAATCCGGAACCATCCGTGAGAGGCGGTGACCTCCGCGCAAGAGCTTC	900
DB	281	PheGIuGIuIhIeIeUaIeUaIeIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIe	300
QY	901	GAGATCCATCTGCACAGTCTGTCCAGCGGATCCAGCAAG 939	
DB	301	GIUIEHLIEUHLISERIEUSERPROGLYPROSERLYS 313	

RESULT 15

ADP45083
ID ADP45083 standard; protein; 313 AA.

XX
AC ADP45083;

DT 12-FEB-2004 (first entry)

XX
DE Human kinase PIM1.

XX
KW Human; protein kinase; enzyme; inhibitor; PIM1.

OS Homo sapiens.

XX
PN MO2003081210-A2.

XX
PD 02-OCT-2003.

PF 20-MAR-2003; 2003MO-US008725.

XX
PR 21-MAR-2002; 2002US-0366892P.

XX
PA (SUNE-) SUNESIS PHARM INC.

XX
PI Prescott JC, Braisted A;

XX
DR WPI, 2003-865136/80.

XX
PT Identifying ligand binding to inactive conformation of target protein kinase (T) comprises contacting the conformation modified (T) which contains reactive group at binding site, with ligands and detecting kinase-ligand conjugate formation.

XX
PS Disclosure; SEQ ID NO 52; 260bp; English.

XX
CC The present invention relates to a method for identifying a ligand (L), which binds to an inactive conformation of target protein kinase (T). The method involves contacting inactive conformation of (T), which contains or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bonding to the reactive group thus forming a kinase- (L) conjugate (C). The method is useful for identifying protein kinase inhibitors that preferentially bind to inactive conformation of a target protein kinase. CC The present sequence is a protein kinase which may be modified via an amino acid substitution, for use in the method of the invention.

XX
SQ Sequence 313 AA;

Alignment Scores:

Pred. No.:	2,186-131	Length:	313
Score:	1582.00	Matches:	294
Percent Similarity:	97.12%	Conservative:	10
Best Local Similarity:	93.93%	Mismatches:	9
Query Match:	90.45%	Indels:	0
DB:	7	Gaps:	0

US-10-705-757-5 (1-942) x ADP45083 (1-313)

```

QY 1 ATGCTCTGTCCAGATCAATCCCTGCGCCGCGCCCTGCGAAGCACTG 60
   |||||
DB 1 MetLeuLeuSerIySleIeAnSerIeUAlIeISeuIrgAlaIaProCySaAnApLeu 20
QY 61 CAGGCCCAAGAGTGGGCGGCGGCAAGAGAGAGAGAGAGAGAGAGAGAG 120
   |||||
DB 21 HisAlaIThrIyISeuAlaProGIyIySglIySeIuProIeugIuSerGIyIyrgIInVal 40
QY 121 GGCCTGCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
   |||||
DB 41 GIyProIeugIuSerGIyIySglIySeIuIySerGIyIyIeAlIyIeAlIySerIy 60
QY 181 AACTTGGCGGTGGCATTAAGACGTGAGAGAGAGAGAGAGAGAGAGAGAG 240
   |||||

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DB 61 AenLeuProValAlaIleIyShtIeValGIuIySaAPArGIleSeArSpIrrpGIyIuLeu 80
QY 241 CCCAATGGACACCGGAGTGGCCCAATGGAAGTGCCTTGAAGAAGTGGCTCGGACTTC 300
   |||||
DB 81 ProAnGIyThIaIyValaIProMeIGluValIeLeuLeuIyIyValaIySeIeGIyIyIe 100
QY 301 TCGGCGGTCAATTAAGACTTGTGAGTGTTCGAGAGAGCGCCGATAGTTCGTGATCTTG 360
   |||||
DB 101 SerGIyValIleIaIySeuIeAnSpIrrpPheGIuArGIyProIaPSeIePheValIeIeLeu 120
QY 361 GAGAGCGCGGAACCGGTGCAAGACCTTTCGACTTATATACGGAACGAGAGAGAGAGAG 420
   |||||
DB 121 GluArGIyProGIyProValGIInAPSeuPheIleThIaIyGIyIyIeValaIyIeGIIn 140
QY 421 GAGAGCGTGGCGGAGATTCCTTGTGAGAGTGTTCGAGAGCGCGGTGCGGAGTTCGCAAC 480
   |||||
DB 141 GIuGIuLeuAlaIaIySeIePheIleThIaIyGIyIyIeValaIyIeGIInIeGIyIyIe 160
QY 481 TCGGCGGTTCCTCCACCGGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
   |||||
DB 161 CySglIyValIeUhiIaIyShtIeIySaAPGIuAnIleIeUhiIeAPSeuAnArGIy 180
QY 541 GAAATCAAACTATGACTTTCGGGTGCGGCGGCGCTGCTTACAGACACAGTCTTACAGAC 600
   |||||
DB 181 GIuLeuIyIeUhiIeAPSeuIySeIeGIyIyIeValaIeUhiIySaAPThIaIyThIaAP 200
QY 601 TTTGATGGAGCCGAGTGTACAGTCTTCGAGAGTGGATTCGCTACATGCTACGAGGAC 660
   |||||
DB 201 PheAPGIyThIaIyValaIySeIeProGIuIrrpIleArGIyIyIeArGIyIyIeGIy 220
QY 661 AGTGGCGAGTGTGTGCTGCTTGGAGTCTGCTTATGACATGCTTGGAGAGATAT 720
   |||||
DB 221 ArgSeIaIaIaIyIyIeIeIeIeIeIeIeIeIeIeIeIeIeIeIeIeIeIeIeIeIeIe 240
QY 721 CCGTTTGAAGACAGATGAAGATCATCAAGGCGCAAGTCTTTCAGGCAAACTGCTCT 780
   |||||
DB 241 ProPheGIuIhIaIyAPGIuIleIeIeIeIeIeIeIeIeIeIeIeIeIeIeIeIeIeIe 260
QY 781 TCAGAGTGCAGACCTTAAATGTGCTGTGCTGAGACCGTCAGATCGGCGCTCC 840
   |||||
DB 261 SerGIuCySglIyIeUhiIeArGIyIyIeUhiIeArGIyIyIeUhiIeArGIyIyIeUhi 280
QY 841 TTTGAAGAATCCGGAACCATCCGTGATGACAGGAGTGTGCTGCTGCGGAGAGAGTCT 900
   |||||
DB 281 PheGIuGIuIleGIuAnhiIeProIyPheIeGIuAnIyIeUhiIeUhiIeUhiIeUhiIe 300
QY 901 GAGATCATCTGCAAGTCTGTACCGGAGATCCAGCAAG 939
   |||||
DB 301 GIuIleIhIeUhiIeSerIeUhiIeSerProGIyProSerIyS 313

```

Search completed: September 22, 2005, 16:48:01
Job time : 130 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 16:17:56 ; Search time 30.871 Seconds
(without alignments)
5871.937 Million cell updates/sec

Title: US-10-705-757-5
Perfect score: 1749
Sequence: 1 atgcctcctgcacgaatcaaa.....caccggatccagcaagtag 942

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=cgnt_1/USPTO.epool_g/US10705757/runat_22092005_115015_22141/app_query.fasta_1.5333
-Db=PIR -QFMT=faetan -SUFPIX=n2p.rpr -MIMATCH=0.1 -LOOPCT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomum62 -TRANS=human40.cdf -LIST=45
-DOCALLGN=200 -THR SCORE=ppct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1668	95.4	313	1	TVMSPI
2	1584	90.6	313	1	S26298
3	1582	90.5	313	1	TVHUP1
4	861.5	49.3	370	1	S55333
5	628	35.9	363	2	T22255
6	504	28.8	409	2	T15435
7	391.5	22.4	481	2	I49072
8	379	21.7	504	2	T10449
9	379	21.7	1101	2	S6730
10	373	21.3	512	1	UC1446
11	373	21.3	1398	2	T13741
12	372	21.3	1358	2	S33653
13	370	21.2	511	1	A56009
14	367	21.0	512	2	T52633

15	361	20.6	513	1	S60304	serine/threonine-s
16	360.5	20.6	469	2	B84644	probable protein k
17	358.5	20.5	798	2	UC7500	dik protein - chic
18	357	20.4	512	2	T07788	probable serine/th
19	356	20.4	472	2	B90100	SNF-related kinase
20	355.5	20.3	651	2	S52244	p69Bg3 protein - A
21	353.5	20.2	887	2	T20941	hypothetical prote
22	351.5	20.1	504	2	T07415	probable serine/th
23	344.5	19.7	414	2	UN0323	Ca2+/calmodulin-de
24	344	19.7	726	2	T33998	hypothetical prote
25	342.5	19.6	445	2	T50802	serine/threonine p
26	342	19.6	502	2	T02306	probable protein k
27	342	19.6	513	1	S60303	serine/threonine-s
28	338	19.3	1518	2	S37928	probable purine nu
29	334	19.1	746	2	S62365	SNF1-related prote
30	333	19.0	435	2	E84707	probable protein k
31	332.5	19.0	442	2	T48203	hypothetical prote
32	330	18.9	461	2	T14822	probable serine/th
33	330	18.9	520	2	G86414	probable protein k
34	328.5	18.8	1246	2	G89287	protein H39E23.1 l
35	327.5	18.7	745	2	G01025	serine/threonine p
36	327	18.7	774	2	I48609	probable serine/th
37	326.5	18.7	489	2	T04862	serine/threonine-s
38	326	18.6	473	1	S59941	probable serine/th
39	326	18.6	1558	2	T29253	hypothetical prote
40	324	18.5	527	2	A53467	protein kinase SNF
41	323.5	18.5	1132	2	T18611	probable serine/th
42	323	18.5	713	2	S27966	probable serine/th
43	322	18.4	339	2	S56719	serine/threonine-s
44	322	18.4	622	1	S44859	serine/threonine-s
45	321	18.4	423	2	T40224	protein kinase - f

ALIGNMENTS

RESULT 1

TVMSPI
protein kinase (EC 2.7.1.37) pim-1 - mouse
N/Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prot.
C/Species: Mus musculus (house mouse)
C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C/Accession: A24169
R/Selien, G.; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen, J.;
Cell 46, 603-611, 1986
A/Title: The primary structure of the putative oncogene pim-1 shows extensive homology
A/Reference number: A24169; M0ID:86272109; PMID:3015420
A/Accession: A24169
A/Molecule type: DNA
A/Residues: 1-313 <SEL>
A/Cross-references: UNIPROT:P06803; GB:M13945; GB:M13946; NID:G200352; PIDN:AAA39930.1;
C/Comment: Pim-1 autophosphorylates at unknown sites.
A/Genetics:
A/Gene: pim-1
A/Introns: 26/1; 63/3; 80/3; 203/1; 262/1
C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine;
C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: ATP; autophosphorylation; phosphotransferase; proto-oncogene; serine/threonine
F/36-290/Domain: protein kinase homology <KIN>
F/44-52/Region: protein kinase ATP-binding motif
F/67/Active site: Lys #status predicted

Alignment Scores:

Pred. No.: 4.93e-72 Length: 313
Score: 1668.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.37% Indels: 0
DB: 1 Gaps: 0

US-10-705-757-5 (1-942) x TVMSPI (1-313)

QY 1 ANGCTCTGTCCAAAGTCAACTCCCTGGCCCACTGGCGGCCCTCGAACAGACGCTG 60

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Db      1 MetLeuLeuSerLyStIleAenSerLeuAlaHleuAArgLalArgProCyAsnAmpLeu 20
QY      61 CAGGCCCAAGACTGGCGCGCGGCAAGAGAGAGCCCTGGAGTGGCAAGTACAGGTTG 120
Db      21 HleAlaThrLyLeuAlaProGlyLyGlyGlyLysGlyLysGlyLysGlyLysGlyLys 40
QY      121 GGGCCGCTGTTGGCGAGCGGCTTGGCTCGGCTCGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db      41 GlyProLeuLeuGlySerGlyLyGlyPheGlySerValTySerGlyLysGlyAlaAla 60
QY      181 AACTTGGCGGTGGCCATTAAAGCACTGGAGAGAGAGCCGATTTCCGATTGGGAGAACTG 240
Db      61 AsnLeuProValAlaIleLyShleValGlnLysAAspArgLlLeseAspTrpGlyLys 80
QY      241 CCCAATGGCAACCGAGTGGCCCAATGGAAGTGGTCTGTTGAAGAAAGTGAAGCTTCA 300
Db      81 ProAsnGlyThrArgValAlProMetGluValValLeuLeuLysValSerSerAAspPhe 100
QY      301 TGGGGGCTCATTTAGACTTCTGCACTGGTGGAGAGCGCGGATGTTTGGTGGATCTTG 360
Db      101 SerGlyValIleLeuArgLeuLeuAAspTrpPheGlyLysArgProAAspSerPheVal 120
QY      361 GAGAGGCCCGAACCAGGTGCAAGACCTTCTGCACTTTATTCACCGAAGAGAGGCGCTTAC 420
Db      121 GlnArgProGluProValGlnAAspLeuPheAAspPheIleThrGlyLysGlyAlaLeu 140
QY      421 GAGGACTGGCCCGAGAGATTTCTTGGCAGGTGGTGGAGCGCGGATTTGGCCACAC 480
Db      141 GlnAAspLeuAlaArgGlyPhePheTrpGlnValLeuGlnAlaValArgHisCyShLys 160
QY      481 TGGGGGCTTCTCCACCGCGCATCAAGAGAGAACTTTATTCGACCTGAGCCGCGG 540
Db      161 CySeGlyValIleuHisArgAAspIleLyAAspGlnAsnIleLeuIleAAspLeuSerA 180
QY      541 GAAATCAAACTCATCACTTCGAGTCCGAGGCGCGCTGCTCAAGGACACAGTCTACAGGAC 600
Db      181 GlnIleLyLeuIleAAspPheGlySerGlyAlaLeuLeuLysAAspTrpValTyTrp 200
QY      601 TTGATGGAGAACCGAGTGTACAGTCTCTCAAGTGGATTCGCTACCATCCGCTACAGG 660
Db      201 PheAspGlyThrArgValTySerProProGluTrpIleArgTyHisArgTyHisGly 220
QY      661 AGGTGGGAGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db      221 ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyAAspMetValCySeGlyAAsp 240
QY      721 CCGTTTGAGACAGATGAAAGATCATCAAGGCGCGCAAGTGTCTTCAAGCAACTGTCT 780
Db      241 ProPheGlnHisAAspArgGlnGlnIleIleLyGlyGlnValAlaPheAAspArgIle 260
QY      781 TCAGAGTGTGACACCTTTATTAATAGTGGCTGTCTGCTGAGACCGGTACATCGGCTTC 840
Db      261 SerGlnCySeGlnHisLeuIleLyTrpCyLeuSerLeuAAspProSerAAspArgPro 280
QY      841 TTGGAAGAATTCGGGAGCAATCGGTGGATGAGAGGTTACCTTCGCGCCGAGGAGCTTC 900
Db      281 PheGlnIleuIleAAspAAsnHisProTrpMetGlnHisAAspLeuProGlnAlaAAsp 300
QY      901 GAGATTCATCTGCACAGTGTCTGCACCGGAGTCCAGCAAG 939
Db      301 GlnIleHisLeuHisSerLeuSerProGlySerSerTyS 313

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RESULT 2

S26298
 protein kinase (EC 2.7.1.37) p1m-1 - rat
 N:Alternate names: kinase-related transforming protein p1m-1; p1m-1 proto-oncogene prote
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
 C:Accession: S26298
 R:Winget, D.; Reeve, R.; Magnuson, N.S.
 Nucleic Acids Res. 20, 3183-3189, 1992
 A:Title: Characterization of the testes-specific p1m-1 transcript in rat.

```

A:Reference number: S26298; MUID:92319652; PMID:1620615
A:Accession: S26298
A:Molecule type: mRNA
A:Residues: 1-313 <MIN>
A:Cross-references: UNIPROT:P26794; EMBL:X63675; NID:g565902; PIDD:CAA45214.1; PID:g565903
A:Experimental source: testis
A:Note: testis-specific transcript is shorter and more stable than the somatic transcript
C:Comment: p1m-1 autophosphorylates at unknown sites.
C:Function:
A:Note: In testis may be involved in signal transduction events of normal germ cell matu
C:Key words: ATP; autophosphorylation; phosphoprotein; protein kinase homology
F:36-290/Domain: protein kinase homology <KIN>
F:44-52/Region: protein kinase ATP-binding motif
F:67/Active site: Lys #status predicted

Alignment Scores:
Pred. No.: 4,58e-68 Length: 313
Score: 1584.00 Matches: 295
Percent Similarity: 96.81% Conservative: 8
Best Local Similarity: 94.25% Mismatches: 10
Query Match: 90.57% Indels: 0
DB: 1 Gaps: 0

US-10-705-757-5 (1-942) x S26298 (1-313)

QY      1 ATGCTCTCTCCAAAGTCAATCTCTGCGGCCCACTGGCGCGCGCCCTTCGCAACGACTTG 60
Db      1 MetLeuLeuSerLyStIleAenSerLeuAlaHleuAArgLalArgProCyAsnAmpLeu 20
QY      61 CAGGCCCAAGACTGGCGCGCGGCAAGAGAGAGCCCTGGAGTGGCAAGTACAGGTTG 120
Db      21 HleAlaThrLyLeuAlaProGlyLyGlyGlyLysGlyLysGlyLysGlyLysGlyLys 40
QY      121 GGGCCGCTGTTGGCGAGCGGCTTGGCTCGGCTCGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db      41 GlyProLeuLeuGlySerGlyLyGlyPheGlySerValTySerGlyLysGlyAlaAla 60
QY      181 AACTTGGCGGTGGCCATTAAAGCACTGGAGAGAGAGCCGATTTCCGATTGGGAGAACTG 240
Db      61 AsnLeuProValAlaIleLyShleValGlnLysAAspArgLlLeseAspTrpGlyLys 80
QY      241 CCCAATGGCAACCGAGTGGCCCAATGGAAGTGGTCTGTTGAAGAAAGTGAAGCTTCA 300
Db      81 ProAsnGlyThrArgValAlProMetGluValValLeuLeuLysValSerSerAAspPhe 100
QY      301 TGGGGGCTCATTTAGACTTCTGCACTGGTGGAGAGCGCGGATGTTTGGTGGATCTTG 360
Db      101 SerGlyValIleLeuArgLeuLeuAAspTrpPheGlyLysArgProAAspSerPheVal 120
QY      361 GAGAGGCCCGAACCAGGTGCAAGACCTTCTGCACTTTATTCACCGAAGAGAGGCGCTTAC 420
Db      121 GlnArgProGluProValGlnAAspLeuPheAAspPheIleThrGlyLysGlyAlaLeu 140
QY      421 GAGGACTGGCCCGAGAGATTTCTTGGCAGGTGGTGGAGCGCGGATTTGGCCACAC 480
Db      141 GlnAAspLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCyShLys 160
QY      481 TGGGGGCTTCTCCACCGGACATCAAGAGAGAACTTTATTCGACCTGAGCCGCGG 540
Db      161 CySeGlyValIleuHisArgAAspIleLyAAspGlnAsnIleLeuIleAAspLeuSerA 180
QY      541 GAAATCAAACTCATCACTTCGAGTCCGAGGCGCGCTGCTCAAGGACACAGTCTACAGGAC 600
Db      181 GlnLeuLyLeuIleAAspPheGlySerGlyAlaLeuLeuLysAAspTrpValTyTrp 200
QY      601 TTGATGGAGAACCGAGTGTACAGTCTCTGAGAGTGGATTCGCTACCATCGCTACAGG 660
Db      201 PheAspGlyThrArgValTySerProProGluTrpIleArgTyHisArgTyHisGly 220
QY      661 AGGTGGGAGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720

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Db	221	argseralalalavaltripserleucilylretleuenutryraapmevalcyseglyasplle	240
Qy	721	ccgrrttgagcagcagtaagagatcatcmaagggccaaagtgttcttcagccaaactgtctct	780
Db	241	prophegglunhsaapsglunlilevallysglygnvaltryrphearglnarvalaser	260
Qy	781	tcagagstgcagacacttatpaaatrgtgcctgtccctcgaaacagtcagatcgagccctcc	840
Db	261	serglucybglnhlsbleuileargftrpcybleusertleuamgproserasphargproser	280
Qy	841	tttgaaagaaatcccggaacatccgtgatgcagsgstgaacttcctcccccagggcagcttct	900
Db	281	phegluglunlileglnasnhlsaprotfpmetglnaservalileuelproglnalathra1a	300
Qy	901	gagatccatctgcacagctctgcacccggagatccagcaag	939
Db	301	giullehlsbleuhlsaserleuserproserproserlyvs	313

RESULT 3

protein kinase EC 2.7.1.37) p1m-1 - human
N/Alternate names: kinase-related transforming protein p1m-1; p1m-1 proto-oncogene product
C/Species: Homo sapiens (man)
C/Idate: 31-Mar-1989 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C/Accession: J00327; A46554; A27476; I58412
R/Reever, R.; Spies, G.A.; Klefer, M.; Barr, P.J.; Power, M.
Gene 90, 303-307, 1990
A/Title: Primary structure of the putative human oncogene, p1m-1.
A/Reference numbers: J00327; MUID:90382681; PMID:2205533
A/Accession: J00327
A/Molecule type: DNA
A/Residues: 1-313 <RER>
A/Cross-references: UNIPROT:P11309; GB:M27903; NID:G189958; PIDN:AAA60090.1; PID:G3870222
R/Meeker, T.C.; Nagarajan, L.; ar-hushdi, A.; Croce, C.M.
J. Cell. Biochem. 35, 105-112, 1987
A/Title: Cloning and characterization of the human p1m-1 gene: a putative oncogene related to the src gene
A/Reference numbers: A46554; PMID:3429489
A/Accession: A46554
A/Molecule type: mRNA
A/Residues: 1-313 <MER>
A/Cross-references: GB:M4779; NID:G1066790; PIDN:AAA81553.1; PID:G1066791
R/Zakut-Houri, R.; Hazut, S.; Givol, D.; Teitelman, A.
Gene 54, 105-111, 1987
A/Title: The cDNA sequence and gene analysis of the human p1m oncogene.
A/Reference numbers: A27476; MUID:87277423; PMID:3475233
A/Accession: A27476
A/Molecule type: mRNA
A/Residues: 1-14, 'RA', 17-313 <ZAK>
A/Cross-references: GB:M6750; NID:G189956; PIDN:AAA60089.1; PID:G189957
R/Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.
Oncogene Reg. 1, 103-112, 1987
A/Title: Comparison of the human and mouse p1m-1 cDNAs: Nucleotide sequence and immunologic cross-reactivity
A/Reference numbers: I58412; MUID:88217305; PMID:3328709
A/Accession: I58412
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Structure: preliminary; translated from GB/EMBL/DBJ
A/Residues: 1-313 <DOM>
A/Molecule type: mRNA
C/Comment: p1m-1 autophosphorylates at unknown sites.
C/GeneticDB:
A/Gene: GDB:P1M1
A/Cross-references: GDB:I19495; OMIM:164960
A/Map position: 6p21.2-6p21.2
A/Intons: 28/2; 63/3; 80/3; 203/1; 262/1
C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate
C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
P.36-290/Domain: protein kinase homology <Kin>
P.44-52/Region: protein kinase ATP-binding motif
P.67/Active site: Lys #catalytic predicted

Alignment Scores:

Pred. No.:	5,7e-68	length:	313
Score:	1562.00	Matches:	294
Percent Similarity:	97.12%	Conservative:	10
Best Local Similarity:	93.93%	Mismatches:	9
Query Match:	90.45%	Indels:	0
DB:	1	Gaps:	0

	US-10-705-757-5 (1-942) x TVHUP1 (1-313)
QY	1 ATGCTCTGTCCAAAGTCAATCTCCGTGGCCCACTGGCGCCGCCGCCCTCGAAGACTG 60
Db	1 MetLeuLeuSerIyValIeAsnSerLeuLahIstLeuAgaIaIaIaProCYAsnAspLeu 20
QY	61 CAGGCCAACCAAGCTGGCGCGCGGCAAAAGAAAGAGAGCCCTCGAGTGGCACTACAGAGT 120
Db	21 HisIaIaThIyLeuLahIaProGlyIySgIySgIyProlGluSerGlnTyGlnVal 40
QY	121 GGCCTGCTGTGGGCAAGCGGTGGCTTCGCTCGCTCTACTCTGGCATCCGCGTGGCCGAC 180
Db	41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTySerGlyIyIeArgValSerAsp 60
QY	181 AACTGCGCGGTGGCCATTAGACACTGGAGAAAGACCCGATTTCCGATTGGGAGAACTG 240
Db	61 AsnLeuProValAaIaIeIyShIaValGluTyAspArgIleSerAspTrpGlyGluLeu 80
QY	241 CCCAATGGGCAACCCGAGTGGCCCATGGAGAGGTCCTGTGAAGAAAGTAGCTCCGCACTTC 300
Db	81 ProAsnGlyTyThrArgValaIaProMetGlnValaIleuLeuLysIyIaValSerSerGlyPhe 100
QY	301 TCGGGGCGCTATTAGACTTTCGACTGTTCGAGAGGCCCGCATAGTTTCGTCTGATCTCG 360
Db	101 SerGlyValIleIeArgLeuLeuAspTrpPheGluArgProAspSerPheValIleuLeu 120
QY	361 GAGAGGCCCGGAACCGGTGCAAGACTCTTCCACTTTATACCCGAACGAGAGCCCTACAG 420
Db	121 GluArgProGluProValaIaGlnAspLeuPheAspPheIleThrGluArgIyIaIeGln 140
QY	421 GAGGACCTGGCCCGAGAGATTCTTCGGCAGGCGTGGAGGCGCGGCGGCAATTGGCAAC 480
Db	141 GlnGlnLeuLahIaArgSerPhePheTrpGlnValaIeGlnIaValaIaArgIaCyHisAsn 160
QY	481 TGGCGGGGTTCTCCACCCGCGACATCAAGACGAAACATCTTAATGCACTGAGCCGCGGC 540
Db	161 CySgIyValIeLeuHisIaArgAspTrpIleTyAspGlnIaLeuLahIeAspLeuAsnArgGly 180
QY	541 GAAATCAAACTCATGCACTTCGGGTGGGGGCGCTGCTCAAGGACACAGTTTACCGGAC 600
Db	181 GluLeuLysLeuLahIeAspPheGlySerGlyIaIeLeuLysIyAspThrValTyThrAsp 200
QY	601 TTTGATGGGACCCGAGTGTACAGTCTCCAGAGTGGAATTCCGCTCAACATCGGTACACGCG 660
Db	201 PheAspGlyTyThrArgValaIySerProGlnTrpIleArgIyThrIaArgTyHisGly 220
QY	661 AGGTGGGCACTGTCTGATCCCTTGGGATCTGTCTATGACATGCTTCGAGGATATT 720
Db	221 ArgSerAlaIaIaTrpSerLeuGlyIleLeuLeuTyraAspMetValCySgIyAspIle 240
QY	721 CCGTTGAGCAGATGAAAGATCATCAAGGGCCCAAGTCTTTCAGGCAAACTGTCTCT 780
Db	241 ProPheGlnHisIaSpGlnGluIleIleArgGlyGlnValaIaPhePheArgGlnArgValSer 260
QY	781 TCAGAGTGCAGACCTTATTAAATGGGCGCTGCTCCGAGAACCGTGAATCGGCGCCCTCC 840
Db	261 SerGlnCySgIaHisIeLeuLahIeArgTrpCySgLeuLahIaAspGlnProSerAspArgProThr 280
QY	841 TTTGAAGAAATCGGAACCATCCGTGAATGCAAGGTGACCTCTGCCCCAGCAGCTTCT 900
Db	281 PheGlnGluIleIeGlnAsnHisProTrpMetGlnAspValIeLeuLeuProGlnGluThrAla 300
QY	901 GAGATGCATCTGCACAGTCTGTCACCGGGATCCAGCAAG 939
Db	301 GlnIleHisIeLeuHisSerLeuSerProGlyProSerIyS 913

Db 48 AlaValArgThrCysAapAenAlaLeuValAlaValLysPheIleGluArgSerAsnVal 67
 QY 223 TCCGATTTGGGAGAACTGCCAATGAGCCGAGTGCCTGAAAGTGCTCTTGAAG 282
 Db 68 LysGluTrpAlaArgIle---AsnGlyGluGlnValProMetGluIleCysMetLeuAla 86
 QY 283 AAGGTGAGCTCGACTTCTGGGCGTCATTAGACTTCCTGAGCTGTGAGAGGCCGAT 342
 Db 87 LysCysSerLys---ValArgGlyValIleArgLysLeuAspTrpIlyrSerIleProGlu 105
 QY 343 AGTTTCGTCTGATCTCGAAGAGCCGAAACCGGTGCAAGACTCTTCGACTTATGACC 402
 Db 106 GlyPheLeuIleValMetGluArgProIlyrProCysIleAspMetPheAspPheIleLys 125
 QY 403 GAACGAGAGCCCTACAGAGAGACTCGCCGAGGATTTCTGCGAGGTGCTGAGACC 462
 Db 126 GlyGlnGlyLysIleSerGluAspMetAlaArgPheLeuPheArgGlnIleAlaValThr 145
 QY 463 GTGCGGATTCGCAACTGCGGGTTCTCCACCGGCATCAGAGCAGAGAACTGTA 522
 Db 146 ValHisGluCysValGlnAsnArgValLeuHisArgAspLeuLysAspGluAsnIleVal 165
 QY 523 ATGCACTGAGCCCGCGCAATCAACTCATCGACTTCGGGTGCGGCGCTGCTGAC 582
 Db 166 IleAspLeuValThrGlySerThrLysLeuIleAspPheGlyAlaIleAlaThrValLeuArg 185
 QY 583 GACCACTTACAGCACTTGTATGAGACCCGAGTGTACACTCTTCCAGAGTGATTCGC 642
 Db 186 ArgSerIlyrSerAspPheGlnGlyThrArgLeuIlyrCysProProGluTrpPheLeu 205
 QY 643 TACATGCTACCAAGGAGGTGCGGAGTGTGCGCTTCGCTGAGTGTCTATGAC 702
 Db 206 HisSerLeuIlyrLeuGlyArgGluAlaValIlePheLeuGlyValLeuLeuIlyrAsn 225
 QY 703 ATGCTCGCGAGATATTCGTTGAGCAGCAGTAAAGATC-----ATCAAG 750
 Db 226 SerLeuAsnGlyArgLeuProPheArgAsnGluLysAspIleCysThrAlaHisLeuLeu 245
 QY 751 GGGCACTGTTCTTACGAGCAACTGTCTCTTCAAGGTGTCAGCACTTATTAATGTGC 810
 Db 246 GlyProLeuProPhePheValProValSerIleGluValIlyAspLeuIleSerLysCys 265
 QY 811 CTGTCCTGAGACCGTGCAGATCGGCGCTTCGTTGAGAAATCCGAGCACTCGTGATG 870
 Db 266 LeuThrPheAspProPheGlnArgCysSerLeuGlnAlaIleLeuAsnHisProTrpVal 285
 QY 871 CAGGTCACCTCTG 885
 Db 286 LysGlnGlnThrLeu 290

RESULT 6

T15435
 hypothetical protein C06B8.3 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C/Accession: T15435
 R/Favella, A.
 submitted to the EMBL Data Library, February 1994
 A/Description: The sequence of C. elegans cosmid C06B8.
 A/Reference number: 218350
 A/Accession: T15435
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Features: 1-409 <FAV>
 A/Cross-references: EMBL:U00043; NID:9458983; PID:9458986; PID:AAA5040.1; CESP:C06B8.3
 C/Genetic:
 A/Genes: C06B8.3
 A/Intons: 24/1; 76/3; 107/2; 145/3; 199/1; 307/1; 375/1
 Alignment Scores: 4.54e-17 Length: 409
 Pred. No.: 504.00 Matches: 109

Percent Similarity: 55.25% Conservative: 54
 Best Local Similarity: 36.95% Mismatches: 124
 Query Match: 28.82% Indels: 8
 DB: 2 Gaps: 5

US-10-705-757-5 (1-942) x T15435 (1-409)

QY 1 ATGCTCTGTCCAAAGATCACTCCCTGCGCCACCTGCGCCGCGCCCTGCAAGACTG 60
 Db 1 MetIleLysArgLysLeuGlnAspLeuAlaValCysCysSerIyrglnValAspPheLeu 20
 QY 61 CAGCCCAACAGCTGGCGCGGCAAGAGAGAGCCCTGAGGTGCGAGTACAGATG 120
 Db 21 HisGluLysLys-----HisSerValIleAspLeuPheLysArgGlySerGluVal 36
 QY 121 GCGCCGCTGTGTGGCAGCCGTGCTTCGCTCGATCTTCTGACATCCGCTGCCGAC 180
 Db 37 LeuAspGluIleGlyArgGlyGlyPheGlyIleValIyrglnAlaThrThrArgGlnAsp 56
 QY 181 ---AAGTCCCGGTGCGCATTAAGCAGTGAAGAGACCGGATTCGATTGGGAGAA 237
 Db 57 GlyGlnGlnProValAlaValLysPheValGlnHisLysHisValArgSerTrp---Thr 75
 QY 238 TGCGCCAATGAGCACCAGTGCAGTGAAGTGTCTGTTGAAGAGTGAAGTGCAGT 297
 Db 76 MetThrCysArgGlnLeuIleProSerGluValCysHisLeu---GluThrCysGluAsp 94
 QY 298 TTCTCGGCGCTCATTAAGACTTCTGACCTGTGTGAGAGGCCGATTAAGTTCGTGATC 357
 Db 95 IleProGlyValIleLysIleLeuAspTrpPheAlaAsnSerLysGlyPheLeuIleVal 114
 QY 358 CTGAGAGAGCCCAACCGGTGCAAGACTTCTTGACTTTATCAACCAAGAGAGCCCTA 417
 Db 115 MetGluArgProAlaAsnCysMetAspLeuPheAspMetValSerValHisGlyProLeu 134
 QY 418 CAGAGACTGCGCCGAGAGATTTCTTGGCAGAGTGTGAGGCCGCGGCGCATTCGAC 477
 Db 135 AsnGluAspMetGlyLysPheIlePheLysGlnValIleThrThrValPheAspMetIlyr 154
 QY 478 AAC---TGCGGGTTCTCCACCGCAGCATCAAGAGAGAGAACTTAAATGACTGAGC 534
 Db 155 SerLysHisGlyLeuLeuHisArgAspIleLysAspGluAsnLeuIleValAspMetAsn 174
 QY 535 CCGCGGAAATCAAACTCATGACTTCGCGGTGCGGCGCTGCTCAAGACACAGTTAC 594
 Db 175 ThrGlyGluValLysLeuValAspPheGlyAlaThrAlaIyrglnLysAlaThrLys 194
 QY 595 ACGGACTTGAATGGAGCCGAGGTACAGTCTCCAGAGTGTGAGTTCACATCGCTAC 654
 Db 195 LysGluPheGlnGlyThrArgSerIlyrCysProProGluTrpPheArgAspGlnLeuIlyr 214
 QY 655 CAGGAGGTGCGCAGCTGTCTGTGCTTCGCTGAGATCTGATGACATGATCTGCGGA 714
 Db 215 LeuProLeuGlnAlaThrSerTrpSerLeuGlyValLeuLeuPheIleLeuLeuThrGly 234
 QY 715 GATATTCGTTGAGACGATGAAGAGATCATCAAGGCGCAAGTGTCTTACGAGAACT 774
 Db 235 LysLeuProPheArgAsnGlnIleGlnIleCysLeuGlyAsnValIlyAspPheProAsp 254
 QY 775 GTCTCTTCAAGAGTGCAGCACTTAAATGATGCTGCGCTGAGACCGTGAAGTCCG 834
 Db 255 LeuSerLysGluValCysGlnLeuValIlySerCysLeuThrSerThrSerAlaArg 274
 QY 835 CCTCTCTTGAAGAAATCCGGAACATCCGTGATCAGAGTGCAG 879
 Db 275 AlaSerLeuAlaGlnIleAlaIleAspProTrpMetGluThrAsp 289

RESULT 7

T49072
 protein kinase - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
 C/Accession: I49072


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Db      122  CyenH1ArgAsnMetValIn1eArgAspLeuLeuProGluAsnLeuLeuLeuAsp--- 140
QY      532  AGCGCGCGCGAATCAATCATGACTTGGGTCGGGCGCGCTGCTCAAGACACAGTC 591
Db      141  SerLySCysAsnValLyS1eAlaSerPheGlyLeuSerAsn1LeuMetArgAspGlyIn1e 160
QY      592  TACACGAGATTTGAT---GGGACCGGAGTGTACAGCTCTGAGATGAGATGATGCTGATGAT 648
Db      161  PheLeuLeuTherSerCysGlySerProAsn1ValAlaProGluVal1LeuSerGlyLyS 180
QY      649  CGGTACACGCGACGAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 708
Db      181  LeuTyra1AglyProGluValAspVal1TrpSerCysGlyVal1LeuTyra1LeuLeu 200
QY      709  TGGGAGATTTTCCGTTTGAAGCAGCATGAAGATC-----ATCCAG 750
Db      201  CysGly1ThLeuProPheAsp---AspGluAsn1LeProAsnLeuPheLyS1LeLyS 219
QY      751  GGGCAAGTGTTC---TTACAGGCAAGCTGTCTTTCAGAGTGTGACGACCTTATTAAATG 807
Db      220  GlyGly1LeuTyThLeuProSerH1eLeuSerSerGlyAlaArgGluLeu1LeuProSer 239
QY      808  TGGCTGTCTGCTGACGAGCTGATGCGGCTCTCTTGAAGAAATCCGGAACCATCCGTCG 867
Db      240  MetLeuValValAspProMetLySArg1LeTh1LeProGlu1LeArgGln1LeProTrp 259
QY      868  ATGCAGGCTGACCTC 882
Db      260  PheGlnAlaH1eLeu 264

RESULT 9
866730
hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein O2034
C/Species: Saccharomyces cerevisiae
C/Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 16-Aug-2004
C/Accession: S66730
R/Annoter: W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; Wiemann, S.
submitted to the Protein Sequence Database, July 1996
A/Reference number: S66723
A/Molecule type: DNA
A/Residues: 1-1101 <ANS>
A/Cross-references: UNIPROT:Q08217; EMBL:Z74788; NID:g1419846; PIDN:CAA9051.1; PID:e251
A/Experimental source: strain S288C
C/Genetics:
A/Cross-references: SCD:S0005405
A/Map position: 15L
C/Superfamily: protein kinase homology
C/Keywords: ATP
F/839-1099/Domain: protein kinase homology <KIN>
F/847-855/Region: protein kinase ATP-binding motif

Alignment Scores:
Pred. No.: 2 95e-11 Length: 1101
Score: 379.00 Matches: 91
Percent Similarity: 55.51% Conservative: 60
Best Local Similarity: 33.46% Mismatches: 95
Query Match: 21.67% Indels: 26
Db: 2 Gaps: 8

US-10-705-757-5 (1-942) x S66730 (1-1101)
QY      106  TCGCAATACAGAGTGGCGCGCTGTGTGGCAGCGGTGCTTCGCTCGGTACTCTGTC 165
Db      839  SerAspPheThr1LeuGlnValMetGlyGluGlyAlaTyrGlyValAsnLeuCys 858
QY      166  ATTCGCGTGGCGACACTTGGCGGTGATTAAGACAGTGAAGAAGACCGGATT--- 222
Db      859  IleH1AsnArgGln1eArg1eTyra1Val1Leu1eMet1ePheLeuArg1eLeu 878
QY      223  ---TCCGATTGG-----GGAGAACTGCGCAATGACACCGAGTGGCC 261

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Db      879  ValAspThr1TrpValArgAspArgLySLeuGlyTh1LeProSerGlu1LeGln1le--- 897
QY      262  ATGGAATGATCTCTGTTAAAGAGTGAAGTCTGGAATCTTCCGGGCTCATTAAGATTTG 321
Db      898  -----MetAlaThrLeuAsnLySAsnSerGln1u-----Asn1LeuLySLeuLeu 913
QY      322  GACTGCGAGAGCGCCGATGATGTTTCGTGCTGATCTGAGAGGCGCCGAACCGGAGCA 381
Db      914  AspPhePheGluAspAspArg1eTyra1le-----GluThrProValH1e 929
QY      382  -----GACSTCTTGACTTATTCACGGAACGAGAGCGCTTACGAG 423
Db      930  GlyGly1ThGlySer1LeAspLeuPheAspVal1LeGluPheLySAspMetValGlu 949
QY      424  GACTGCGCGCGAGATTTCTGGCAGGTGCTGAGCGCGCTGCGGATCCCAACTGC 483
Db      950  H1SGluAlaLySLeuValPheLySVal1AlaSer1LeLyS1eH1eAspGln 969
QY      484  GGGGTCTCCACCGGACATCAAGACAGGAACATTTAATGACCTGACCGCGCGCA 543
Db      970  Gly1eValH1eArgAsp1LeLySAspGluAsnVal1LeValAsp---SerH1eGlyPhe 988
QY      544  ATCAAACTGATGACTTCCGGGTGCGGCGCTGCTCAAGACACAGTCTACACGACTTT 603
Db      989  ValLySLeu1LeAspPheGlySerAlaAlaTyr1LeLySerg1eProPheAspValPhe 1008
QY      604  GATGGACCCGAGGTACAGTCTCCAGAGTGGATTGGTACCATGCTACACGCGCAG 663
Db      1009  ValGly1ThMetAsp1eTyra1AlaProGluVal1eGly1eSerSerTyra1LyS1eLyS 1028
QY      664  TCGGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
Db      1029  ProGlnAsp1eTrpAlaLeuGlyVal1eLeuTyTh1Le1eTyra1LyS1eGluAsnPro 1048
QY      724  TTGAGCAGCATGAAGATCATCAAGCGCAAGTCTTCAAGCAACT-----GTC 777
Db      1049  TyrTyraH1eAspGlu1LeuGlnGlyGluLeuArgPheAspLySerg1eH1eVal 1068
QY      778  TTTTCAGAGTGTCAAGCACTTTAATGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
Db      1069  SerGluGluCysG1eSer1eLeu1eLySArg1eLeuTh1eArgGluValAspLySArgPro 1088
QY      838  TCCTTGAAGAAATCCGGAACCATCCGTGGAATGCAG 873
Db      1089  Thr1eAspGlu1LeuTyra1LySAsp1eTyra1leLyS 1100

RESULT 10
JCI446
serine/threonine-specific protein kinase (EC 2.7.1.1-) AK21 - Arabidopsis thaliana
N/Alternate names: protein kinase SNF1 homolog
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JCI446; S58266; S66334
R/LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Keels, M.
Gene 120, 249-254, 1992
A/Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein
A/Reference number: JCI446; MUID:93013041; PMID:3339373
A/Accession: JCI446
A/Molecule type: DNA
A/Residues: 1-512 <LEGS>
A/Cross-references: UNIPROT:Q08997; GB:M3023; NID:g166599; PIDN:AAA32736.1; PID:g16660
R/Thummler, F.; Kirchner, M.; Teuber, R.; Dietrich, P.
submitted to the EMBL Data Library, May 1995
A/Description: Differential accumulation of the transcripts of 22 novel protein kinase
A/Reference number: S58266
A/Accession: S58266
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 144-198 <THU>
A/Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
R/Thummler, F.; Kirchner, M.; Teuber, R.; Dietrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A/Title: Differential accumulation of the transcripts of 22 novel protein kinase genes

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A:Reference number: S66314; MUID:96123233; PMID:8534852
A:Accession: S66334
A:Molecule type: DNA
A:Residues: 144-198 <THR2>
A:Cross-references: EMBL:X86966; NID:9928909; PIDN:CA60529.1; PID:9928910
C:Comment: This enzyme plays an important role in a signal transduction cascade regulating
C:Genetics:
A:Gene: AKI10; AK21
A:Intons: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C:Function:
A:Description: catalyzes the formation of peptidyl-L-serine-phosphate or peptidyl-L-threonine
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinases
F:17-271/Domain: protein kinase homology <KIN>
F:25-33/Region: protein kinase ATP-binding motif
F:48,67,142,144/Active site: Lys, Glu, Asp, Lys #acetate predicted
F:147,151/Binding site: magnesium (Asn, Asp) #acetate predicted

[illegible]

US-10-705-757-5 (1-942) x JC1446 (1-512)

```

OY      94  GAGGCCCTGAGAGTCGCAAGTACAGAGTGGGCGCGCTGTTGGGAGAGCGAGTGGCTGGCTGG  153
           |||      |||      |||      |||      |||      |||      |||      |||
Db      13  GUSERTILEUPROAMTYRILYUENGLYARGTHIRLEUGLYLLEGLYSERFHEGLYARG  32
OY      154  GTCTACTCGGATCGCGCTGCGCGCAACTTGGCCGCTGGCCGTCATTAGACACGTGGAGAA  213
           |||      |||      |||      |||      |||      |||      |||      |||
Db      33  VALLYSILEAGLISHALALEUTHIRGLYHLSYGLVALALALLEYSILEUEANARG  52
OY      214  GACCGGATTTCCGATTTGGGAGAACTGCCCAATGGACCCCGAGTGGCCATGGAAGTGTC  273
           |||      |||      |||      |||      |||      |||      |||      |||
Db      53  ARGLYSILEYASN-----MetGluMetGluGluValAlaArgGluIleYs  69
OY      274  CTGTGAAGAAAGTGAGCTCGGACTTCTCGGGGCGTCAATTAGATTTCTGCACTGGTTCGAG  333
           |||      |||      |||      |||      |||      |||      |||      |||
Db      70  ILELEAAARGLEUPHEMETHISPROHS-----IleIleArgLeuYrGluValIleGlu  87
OY      334  AGGCCCGATAGTTGCTGCTGATCTCGAGAGGCGCGAAACGGGTAGAGACCTTTTCGAC  393
           |||      |||      |||      |||      |||      |||      |||      |||
Db      88  THIPROTHIRAPILETYRILEUVALMETGLUTYRVALASNSEK---GluGluLeuPheAsp  106
OY      394  TTTATCCAGCAAGAGAGCCCTCAACGAGAGACCTGGCCCGAGAGATTCTTGGCGAGTGG  453
           |||      |||      |||      |||      |||      |||      |||      |||
Db      107  TYRILEVALGILYSEGLYARGLEUGINGLUBERGLUALARGYASNPHIEPHEGLINGLITLE  126
OY      454  CTGAGAGGCGCGTGGCGGATTCGACCAACTCGCGGGTTCCTCCACCGGACATCAAGAGAG  513
           |||      |||      |||      |||      |||      |||      |||      |||
Db      127  ILESERGLYVALGILUTYRCYSNHSARGASMEVALVALNHSARGAPRLEUYSIPROGLN  146
OY      514  AACATCTTATGAGCTCTGAGCGCGCGCGGAATAACTCATGACTTCGGGTGGGGCGG  573
           |||      |||      |||      |||      |||      |||      |||      |||
Db      147  ASNLEULEULEUASNP---SerYrsCyAsnValLysIleLeuAspPheGluLeuSerAsn  165
OY      574  CTGCTCAAGAGACAGATGTACACGAGACTTGAT---GGGACCGGAGGTACAGTCTCCCA  630
           |||      |||      |||      |||      |||      |||      |||      |||
Db      166  ILEMETARGASRGLYHISERHEUYSYRHSERCYSGLYSERPROAMNTYRILALALPRO  185
OY      631  GAGTGGATTCGCTAACCATGCTATCCACGCGGAGGTGGGACGTGTCTGGTCCCTTGGAGAT  690
           |||      |||      |||      |||      |||      |||      |||      |||
Db      186  GILUVALIIESERGLYUYSERLYRAGLYPROGLUVALASPRVALTPRSEYCYGLYVAL  2050
OY      691  CTGCTCTATGACATGCTCGCGGAGADATTCGTTTGAGAGACATGAAGAGATC-----  7448
           |||      |||      |||      |||      |||      |||      |||      |||
Db      206  ILELEUYRALALEUENUCYSGLYTHIRLEUPHIEPHEP---AspGluAsnIleProAsn  224
OY      745  -----ATCAAGGCGCCAAAGTGTTC---TTCAAGGCAAACTGTCTTCAGAGTGT  7899

```

Db 225 leuphelyalylaleysbilylleyrthleuproserrhlsleusereproglYla 244

Qy 790 CAGCACCTTATTAATGATGCTCTGTCCTCGAGACCGTCAGATCGACCCCTCTTGAAAGA 849

Db 245 ArgaspleuileproargmetleuvalValaspprometlysarGValthrlleProglu 264

Qy 850 ATCCGGAACCATCCGCGATGACGAGGTACCTC 882

Db 265 lilearglnhisprotrpheidlnahlsleu 275

RESULT 11

hypothetical protein 22E5.8 - fruit fly (*Drosophila melanogaster*)

C:\species: Dirosophina melanogaster
C:\Date: 13-Aug-1999 #sequence revision 13-Aug-1999 #text change 09-Jul-2004

C/ACCESSION: 113/71
R:Murphy, L.; Harris, D.; Barrell, B.

A:Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.
Submitted to the EMBL Data Library, April 1999

A;Reference number: 2176688
A;Accession: T13741

A:Status: preliminary; translated from GB/EMBL/DBJ

A;Residues: 1-1398 <MOR>
A:Cross-references: INIT

C;Genetics:
A:Cross-references: F]vBase:FBcm0000667

A; Introns: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3

21

Pred. No.:

Percent Similarity

Query Match:

3.

(C)
 (C)
 (C)
 (C)
 (C)
 (C)
 (C)
 (C)

[illegible]

DB 131 LYE

142 630
 07

DB 151 ASI

QY	199	AAC
		1111

Db 170 LYE

QY 259 CCC

Db 186 Ty1

QY 319 CTC

Db 204 Ty1

QY 379 CAJ

Db 223 G1j

QY 439 TTC

Db 243 Ly8

QY 499 GAO

Db 263 Asp

QY 559 TTCGGG---TCGGGGGGCGCTGCTCAAGACACAGCTTACAGCACTTGTGAGACCCGA 615
 ||||| |||
 Db 282 PheGlyPheSerHisnHLePheLysProGlyGluLeuAlaThrTrpCysGlySerPro 301
 QY 616 GTGTACAGTCTCCAGACAGTGGATTTCCTACCATCTACACAGCAGAGTGGAGCTGTG 675
 ||||| |||||
 Db 302 ProTyrAlaAlaLeuProGluValPheGluGlyLysGlnTrpThrGlyProGluIleAspIle 321
 QY 676 TGGTCCCTTGGGATCTGCTCTATGACATGGTCTGCGAGATATTCGCTTTGAGCAGAT 735
 ||||| |||||
 Db 322 TrpSerLeuGlyValValLeuTyrValLeuValCysGlyLysAlaLeuProPheAspGlySer 341
 QY 736 -----GAAAGATCATCAAGGGCGCAAGTGTCTTACAGCAAACTGTC 777
 ||||| |||||
 Db 342 ThrLeuGlnSerLeuThrArgPheArgValLeuSerGlyLysPheArgIleProPhePheMet 361
 QY 778 TCTTCAGAGTGTGACGACCTTATTAATGATGGCTGTCTCTGAGACCGCTGAGATCGGCC 837
 ||||| |||||
 Db 362 SerSerGluCysGlyLysIleLeuIleArgGlyMetLeuValLeuGluProThrArgArgTyr 381
 QY 838 TCCTTTGAGAAATCCGAAACATCCGTGATGACAGGCTGACTCTGTG 885
 ||||| |||||
 Db 382 ThrIleAspGlnIleLeuArgHisArgGlyTrpMetCysProGluLeuLeu 397
 ||||| |||||
 RESULT 12
 S33653
 Probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
 N/A/Alternate names: protein YAL002; protein YAL017w; secretory protein SSP138
 C/Species: Saccharomyces cerevisiae
 C/Date: 30-Sep-1993 #sequence revision 02-Aug-1994 #text_change 16-Aug-2004
 C/Accession: S33653; S36717; S36732; JH0486
 R/Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton, A.; Kabac
 Yeast 9, 543-549, 1993
 A/Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae enc
 A/Reference number: S33653; MUID:93311122; PMID:8322517
 A/Accession: S33653
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-1358 <CL>
 A/Cross-references: UNIPROT:P31374; EMBL:L05146
 R/Ouellette, B.F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; D
 submitted to the EMBL Data Library, January 1993
 A/Description: Sequencing of Chromosome I from Saccharomyces cerevisiae: analysis of a 3
 A/Reference number: S36711
 A/Accession: S36717
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-864,867-1358 <OUB>
 A/Cross-references: EMBL:L05146; NID:G171851; PIDN:AAC04940.1; PID:G171858; MIPS:YAL017w
 R/Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Buseey, H.
 Yeast 8, 133-145, 1992
 A/Title: Identification of a Saccharomyces cerevisiae homolog of the SNF2 transcriptions
 A/Reference number: S22266; MUID:92221690; PMID:1561836
 A/Accession: S36732
 A/Status: translation not shown
 A/Molecule type: DNA
 A/Residues: 1-72,'E',74-154 <SID>
 A/Status: translation not shown
 C/Genetic: SCD:FUN31; SSP138
 A/Cross-references: SGD:S0000015; MIPS:YAL017w
 A/Map position: 1L
 C/Superfamily: protein kinase homology
 C/Keywords: ATP; glycoprotein; phosphotransferase; serine/threonine-specific protein kin
 P/1096-1356/Domain: protein kinase homology <KIN>
 F/1104-1112/Region: protein kinase ATP-binding motif
 F/6,128/Binding site: carbohydrate (asn) (covalent) #status predicted

F/1232/Active site: Asp #status predicted
 Alignment Scores:
 Pred. No.: 6,03e-11 Length: 1358
 Score: 372.00 Matches: 88
 Percent Similarity: 55.04% Conservative: 54
 Best Local Similarity: 34.11% Mismatches: 100
 Query Match: 21.27% Indels: 16
 DB: 2 Gaps: 6
 US-10-705-757-5 (1-942) x S33653 (1-1358)
 QY 130 TTGGGAGGGGGTGGCTTGGCTGCTGCTTACTGTGATCCGGCTCCGCAAACTGCCG 189
 ||||| |||||
 Db 1104 MetGlyGluGlyAlaTyrGlyLysValAsnLeuCysIleIleLysValAsnArgTyrIle 1123
 QY 190 GTGGCACTTAAGACAGCTGGAGAAAGACCGGAT-----TCCGATTGGGAGAACTGCC 243
 ||||| |||||
 Db 1124 ValValIleLysMetIlePheLysGluArgIleLeuValAspThrTrpValaLysArg 1143
 QY 244 AATGCAACCCGAGTCCCATGAAAGTGTCTGTGTAAGAAGGTGAGC--TCGACTTC 300
 ||||| |||||
 Db 1144 LysLeuGlyThrIleProSerGluIleGlnIleMetAlaThrLeuAsnLysProHis 1163
 QY 301 TCGGGGTCATTAAGTCTTGTGATCTGATCTGATCGAGAGCCGATAGTTCTGCTGATCTG 360
 ||||| |||||
 Db 1164 GluAsnIleLeuArgLeuLeuAspPhePheGluAspAspArgTyrTyrIle----- 1181
 QY 361 GAGAGCGCCGAAACCGGTGCA-----GACCTTTCGACTTATCAC 402
 ||||| |||||
 Db 1182 -----GluThrProValHisGlyLysGlnGlyCysIleAspLeuPheAspLeuIleGlu 1199
 QY 403 GAACGAGAGCCCTACAGAGACCTGCGCCGAGATTTCTTGAGAGTGTGAGAGCC 462
 ||||| |||||
 Db 1200 PheLysThrAsnMetThrGluPheGluIleValLysLeuIlePheLysGlnValaLysGly 1219
 QY 463 GTGGGCACTTGGCAACATCGCGGGTTCCTCCACCGGACATCAAGACGAAACATCTTA 522
 ||||| |||||
 Db 1220 IleLysIleLeuHisAspGlnGlyIleValHisArgAspIleLysAspGluValaLys 1239
 QY 523 ATGCAGCTGACCGCCGCAAAATCAATCATCATGATCTTGGGGTGGGGGCGTGTCAAG 582
 ||||| |||||
 Db 1240 ValAsp---SerLysGlyPheValLysIleIleAspPheIleSerAlaIleTyrValLys 1258
 QY 583 GACACAGTCTACACGCACTTGTGATGAGACCGGAGTGTACAGTCTCCAGATGTATCCG 642
 ||||| |||||
 Db 1259 SerGlyProPheAspValPheValGlyThrIleAspTyrAlaAlaProGluValaLysGly 1278
 QY 643 TACCATCGCTACACGCGAGTGTGCGAGCTGTCTGCTGCTGGATCTGCTTATGAC 702
 ||||| |||||
 Db 1279 GlyAsnProTyrGluIleGlnProGluAspIleTyrAlaIleGlyLysLeuLeuTyrThr 1298
 QY 703 ATGGTCTGCGAGATATTCGTTGAGCAGATGAAGATCATCAAGGCGCAAGGTTC 762
 ||||| |||||
 Db 1299 ValValaPheLysGluAsnProPheTyrAsnIleAspGluIleLeuGluLysLeuLys 1318
 QY 763 TTCAGG-----CAACTGTCTTTCAGAGTGTACAGCTTATTAATGATGCTGCC 816
 ||||| |||||
 Db 1319 PheAsnAlaGluGluValaSerGluAspCysIleGluLeuIleLysSerIleLeuAsn 1338
 QY 817 CTGAGACCTCAGATGTGGCTCTTGAAGAAATCCGAAACCATCCGATG 870
 ||||| |||||
 Db 1339 ArgCysValaProLysArgProThrIleAspIleAsnAsnAspLysThrLeu 1356
 ||||| |||||
 RESULT 13
 A56009
 Probable serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco
 C/Species: Nicotiana tabacum (common tobacco)
 C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 09-Jul-2004
 C/Accession: A56009
 R/Muranaka, T.; Banno, H.; Machida, Y.
 Mol. Cell. Biol. 14, 2958-2965, 1994
 A/Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces cer

base of Saccharomyces cerevisiae.

A:Reference number: A56009; MUID:94217693; PMID:8164654

A:Accession: A56009

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-511 <MUR>

A:Cross-references: UNIPROT:Q40544; GB:D26602; NID:g496384; PIDN:BA05649.1; PID:g496385

C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

C:Superfamily: AMP-activated protein kinase; protein kinase homology

C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase

F:17-271/Domain: protein kinase homology <KIN>

F:25-33/Region: protein kinase ATP-binding motif

F:48-67/142,144/Active site: Lys, Glu, Asp, Lys #status predicted

F:147,151/Binding site: magnesium (asn, asp) #status predicted

Alignment Scores:

Pred. No.: 9,266-11 Length: 511

Score: 370.00 Matches: 93

Percent Similarity: 51.64% Conservative: 49

Best Local Similarity: 33.82% Mismatches: 117

Query Match: 21.15% Indels: 16

DB: 1 Gaps: 8

US-10-705-757-5 (1-942) x A56009 (1-511)

QY 82 GCGAAGAAAGAGCCCTGAGTGCAGTACAGTGGCCCGCTGTGGCAGCGGT 141

DB 9 GlycerSerValGluSerPheLeuArgAsnTyrLysLeuGlyThrLeuGlyIleGly 28

QY 142 GGGCTTGGCTGGCTGACTCTGGCATCCGCGTCCGAGCAACTGGCCGGTGGCATTAG 201

DB 29 SerPheGlyLysValLysIleAlaGluHisThrLeuThrGlyHisLysValAlaValLys 48

QY 202 CAGGTGAGAGAGCCGAGATTCCGATTGGGAGAACTGCCCAATGACCCGAGTCCC 261

DB 49 IleLeuAsnArgLysIleLysAsn-----MetGluMetGluLysValArg 65

QY 262 ATGCAAGTGGTCTGTGTAAGAGAGTGGAGTCTCTCGGCGCTCATTTGACTTCG 321

DB 66 ArgGluIleLysIleLeuLysIlePheMetHisProHis-----IleIleArgLeuTyr 83

QY 322 GACTGTTGAGAGCGCCGATGATTTCGCTGATCTGAGTGGAGGCGCCCAACCGAGTCA 381

DB 84 GluValValGluThrProSerArgIleTyrValValMetGluTyrValLysSer---Gly 102

QY 382 GACCTTTGACTTTATTCACCGAAGAGACCTTACAGAGAGACTGGCCGAGGATTC 441

DB 103 GluLeuPheAspTyrLysIleValGluLysArgLeuGluLysArgLysPhe 122

QY 442 TTCTGGCAGGTGCTGGAGCGCGGCAATTGCCCAACTGGCGGTTCTCCACCGGAC 501

DB 123 PheGluGluIleIleSerGlyValGluTyrCysHisArgPheMetValAlaHisArgAsp 142

QY 502 ATTCAGAGAGAGAACTTTAATGACCTGAGCGCGGAGAACTCAACTCATGCTTC 561

DB 143 LeuLysProGluLysMetLeuLeuAsp---SerLysTyrAsnValLysIleAlaPhe 161

QY 562 GGGTGGGGGCGCTGCTCAAGACACAGTCTACAGAGACTTTGAT---GGAGCCGAGTG 618

DB 162 GlyLeuSerAsnIleMetArgAspGlyHisPheLeuLysThrSerCysGlySerProAsn 181

QY 619 TACAGTCTCCAGAGTGGAGTGGTACATCGTACACGAGCGAGTGGAGTGTCTGG 678

DB 182 TyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyr 201

QY 679 TCCCTTGGAGTCTGCTGTATGACATGATCTGGCGAGATATTCGTTTGGCAGATGA 738

DB 202 SerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAsp---AspGlu 220

QY 739 GAGATC-----ATCAG--GGCCAGTGTCTTCAAGCAACTGTC 777

DB 221 AsnIleProAsnLeuPheLysIleLysIleGlyGlyMetIleSerLeuProSerHisLeu 240

QY 778 TCTTCAGAGTGCAGACCTTATTAAATGGTCCCTGTCGAGACCGTACAGATGGCCC 837

DB 241 SerAlaGlyAlaArgAspLeuIleProArgMetLysIleValAspProMetLysArgMet 260

QY 838 TCCCTTGAAGAAATCCGAGACCATCGGTGATGACAGGTTGACTTC 882

DB 261 ThrIleProGluIleArgMetHisProTyrPheGluAlaHisLeu 275

RESULT 14

T52633

serine/threonine-specific protein kinase (EC 2.7.1.-) AKIN1 [validated] - Arabidopsis t

N:Alternate names: SNF1 protein kinase omolog AKIN1

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004

C:Accession: T52633

R:Bhalero, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machid

Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999

A:title: Regulatory interaction of PRL1 WD protein with Arabidopsis SNF1-like protein ki

A:Reference number: 225116; MUID:99238528; PMID:10220464

A:Accession: T52633

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-512 <BHA>

A:Cross-references: UNIPROT:P29598; EMBL:X99279; PIDN:CAA67671.1

A:Experimental source: cultivar Columbia

C:Genetics:

A:Gene: AKIN1

C:Function:

A:Description: EC 2.7.1.-; serine/threonine-specific protein kinase AKIN1 [validated,]

complements SNF1 mutations in yeast

C:Superfamily: AMP-activated protein kinase; protein kinase homology

C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Alignment Scores:

Pred. No.: 1,286-10 Length: 512

Score: 367.00 Matches: 95

Percent Similarity: 52.40% Conservative: 47

Best Local Similarity: 35.06% Mismatches: 113

Query Match: 20.98% Indels: 16

DB: 2 Gaps: 8

US-10-705-757-5 (1-942) x T52633 (1-512)

QY 94 GAGCCCTGAGAGTGCAGTACAGTGGGCGCGCTGTGGAGCGTGGCTTCGCTCG 153

DB 14 GluSerIleLeuProAsnTyrLysLeuGlyLysThrLeuGlyIleGlySerPheGlyLys 33

QY 154 GTTACTCTGGCATCCGCGTCCGCAAACTTGGCGGTGGCCATTAAAGCAGTGAAG 213

DB 34 ValLysIleAlaGluHisIleValAlaThrGlyHisLysValAlaIleLysIleLeuAsnArg 53

QY 214 GACCGGATTTCCGATTGGGGAGAACTGCCCAATGGCACCCGAGTCCCATGAGTGTCT 273

DB 54 ArgLysIleLysAsn-----MetGluMetGluGluLysValArgArgLysIleLys 70

QY 274 CTGTGAAGAAGTGAAGTCTCGGACTTTCGCGCTCATTTGACTTCTGAGTGTCTGAC 333

DB 71 IleLeuArgLeuPheMetHisProHis-----IleIleArgGluTyrGluValIleGlu 88

QY 334 AGCGCCGATGTTGTGTGATCTGTGAGAGAGCGCCGAACCGGTGCAAGACTTTTGAC 393

DB 89 ThrThrSerAspIleTyrValValMetGluTyrValLysSer---GlyLysLeuPheAsp 107

QY 394 TTTATTCACGAACGAGAGACCTTACAGAGAGACCTTGGCCGAGATTTCTTGGCAGGTG 453

DB 108 TyrIleValGluLysGlyArgLeuGluGluLysArgLysValAlaArgAspPheGluGluIle 127

QY 454 CTGAGAGCGCGTGGCATTTGGCAACAACGCGGGTTCTCACCGGACATCAAGACGAG 513

DB 128 IleSerGlyValGluTyrCysHisArgPheMetValAlaHisArgPheLeuLysProGlu 147

QY 514 AACATCTTAATGACCTGAGCGCGCGGCAAACTCATGACTTTCGGTTCGGGGCGG 573

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Db      148 AsnLeuLeuLeuSer---SerArgCysAsnIleValIleAlaAspPheGlyLeuSerAsn 166
      574 CTGCTCAAGAGACACAGCTTACACGAGCTTTGAT---GGAGCCGAGTGTACAGTCTCTCA 630
      167 ValMetArgAspGlyAsnLeuLeuValThreSerCysGlySerProAsnTyrAlaAlaPro 186
      631 GAGTGGATTCGCTACCACTGCTACACGAGGAGGAGCTGCTGCTGCTTGGATC 650
      187 GluValIleSerGlyLeuValLeuTyrAlaGlyProGluValAlaValTyrSerCysGlyVal 206
      691 CTGCTCTATGACATGGCTGCTGAGGATATATCCGTTTGAGCAGCAGTGAAGATC----- 744
      207 IleLeuTyrAlaLeuLeuValCysGlyThrLeuProPheAsp---AspGluAsnIleProAsn 225
      745 -----ATCAAGGGCCAGAGTGTTC---TTCAAGCAACCTGCTCTTCAAGATGT 789
      226 LeuPheLeuValIleValGlyGlyIleTyrThrLeuProSerHisLeuSerSerGluAla 245
      790 CAGCAGCTTATTAATGAGTCCCTGCTGCTGAGACCGTCAAGATGGCCCTCTTGAAGA 849
      246 ArgAspLeuLeuProArgMetLeuIleValAspProValIlyAspGlyIleThrIleProGlu 265
      850 ATCCGGAACCACTCCGTGATGACGAGGTC 882
      266 IleArgGlnHisArgTyrPheGlnThrHisLeu 276

RESULT 15
S60304
serine/threonine-specific protein kinase (BC 2.7.1.-) BKIN12 (version 2) - barley
C1.Date: 19-Mar-1997 #sequence_rev: 15-Aug-1997 #text_change 09-Jul-2004
C1.Accession: S60304; S24579
R1.Halford, N.G.; Vicente-CarboJose, J.; Sabelli, P.A.; Shewry, P.R.; Hamppel, U.; Krezl
Plant J. 2, 791-797, 1992
A1.Title: Molecular analyses of a barley multigene family homologous to the yeast protein
A1.Reference number: S60303; PMID:93258420; PMID:1302632
A1.Accession: S60304
A1.Status: preliminary
A1.Molecule type: mRNA
A1.Cross-references: UNIPROT:Q40030; EMBL:X65604
R1.Halford, N.G.
submitted to the EMBL Data Library, April 1992
A1.Reference number: S24578
A1.Accession: S24579
A1.Status: preliminary
A1.Molecule type: mRNA
A1.Residues: 1-61, 'A', 63-513 <HA2>
A1.Cross-references: EMBL:X65604; NID:gi18933; P1DN:CAA46554.1; P1D:gi18934
C1.Function:
A1.Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C1.Superfamily: AMP-activated protein kinase; protein kinase homology
C1.Keyword: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F1.5-772/Domain: protein kinase homology <KIN>
F1.23-31/Region: protein kinase ATP-binding motif
F1.46,65,143,145/Active site: Lys, Glu, Asp, Lys #status predicted
F1.48,152/Binding site: magnesium (Asn, Asp) #status predicted

Alignment Scores:
Pred. No.: 2 46e-10 Length: 513
Score: 361.00 Matches: 94
Percent Similarity: 50.72% Conservative: 46
Best Local Similarity: 34.06% Mismatches: 120
Query Match: 20.64% Indels: 16
DB: 1 Gaps: 8

US-10-705-757-5 (1-942) x S60304 (1-513)
QY      82 GCGAAGAGAGAGCCGCTGAGTGCACAGTACAGAGTGGCCGCGTGTGGCAGCGGT 141
      8 GlyGlyHisSerGlyValLeuValAsn---TyrAsnLeuGlyLysThrLeuGlyLeuGly 26

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QY      142 GCGTTCGCTCGGTCTACTCTGGACATCCGCGTCCGAGACAACTTCCGCTGGCATTAAG 201
      27 ThrPheGlyAspValIlyValAlaGluArgAsnValThrGlyGlnArgValAlaIleLys 46
      202 CAGGTGAAGAGAGCCGATTTCCGATTTGGGAGAACTGCCAAATGGACCCGAGTGGCC 261
      47 IleLeuAsnArgGlySerMetGlyThrMetGluMetGluGlyLysAsnArg----- 64
      262 ATGAAGAGTGCCTGTGAAGAGGTGAGCTCGACTTC-----TCGGAGCTCATTAAG 315
      65 -----GluIleValMetArgLeuPheIleAspPheIleHisProHisIleIleArg 82
      316 CTTCGAGATGCTGTCAGAGCCCGCATTTCTGCTGATCTGCTGAGAGGCCGGAACCG 375
      83 ValTyrGluValIleGluThrProLysAspIlePheValAlaMetGluTyrCysAsnAsn 102
      376 GTGCAAGACCTCTTCAGCTTTATCACAGCAAGAGAGCCCTCAGAGAGAGTGGCCGGA 435
      103 ---GlyGluLeuLeuAspTyrIleIleGluAsnGlyArgLeuGlnGluAspGluAlaArg 121
      436 GGAATCTTGGAGGTGCTGAGAGCCGCTGAGGATGCTGCACAACTGGCGGTTCTCAC 495
      122 ArgIlePheGlnGlnIleLeuAlaGlyIleGlyTyrCysHisArgIleMetValHis 141
      496 CCGGACATCAAGAGAGCAATCTTAATGCACTGAGCCGCGGCAATCAATCAATCATC 555
      142 ArgAspLeuLysProGluAsnLeuLeuAsp---SerArgTyrAsnValIlyLeuAla 160
      556 GACTTCGGTTCGGGGCGCTGCTCAAGACAGTGTTCAGGCACTTTGAT---GGAGCC 612
      161 AspPheGlyLeuSerAsnValMetArgAspGlyHisPheLeuLysThrSerCysGlySer 180
      613 CGAGTGTACAGTCTTCAGAGTGGATTCGCTACATCGCTACACGAGGAGTCCGAGCT 672
      181 LeuAsnTyrAlaAlaProGluIleIleSerSerLysLeuTyrAlaGlyProGluValAsp 200
      673 GTCTGCTCCCTGGATCTGCTGTATGACATGCTGCGGAGATATTCGTTTGACAC 732
      201 ValTyrSerCysGlyValValLeuTyrAlaLeuLeuValSerValProPheAsp 220
      733 GATGA-----GAGATCATCAAGGCGCAAGTGTCTTCAAGGCAACT--- 774
      221 AspAsnIleProSerLeuPheArgLysIleValGlyGlyThrTyrIleLeuProSerTyr 240
      775 GTCTCTTCAAGTGTCAAGCACTTAAATGATGCTGCTCCCTGAGACCGTCAAGTCCG 834
      241 LeuSerAspSerAlaArgAspLeuLeuProLysLeuLeuAsnIleAspProMetLysArg 260
      835 CCTCTCTTGAAGAAATCCGGAACCATCGTGGATGACAGGAGCTC 882
      261 IleThrPheHisGluIleArgValHisProTyrPheLysAsnHisLeu 276

Search completed: September 22, 2005, 17:20:41
Job time : 40.871 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 15:59:25 ; Search time 155.516 Seconds
(without alignments)
6203.583 Million cell updates/sec

Title: US-10-705-757-5

Perfect score: 1749
Sequence: 1 atgcctctctgcacagatcaaa.....caccgggacccagcaagtag 942

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+n2p.model -DEV=x1p
-Q/cgnt2.1/USPTO.spool_p/US10705757/runat.22092005.115015.22129/app.query.fasta.1.5333
-DB=uniprot -QFMT=faetan -SUFIX=n2p.rup -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdd -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NOR=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10705757 @CGNT_1.1.980 @runat.22092005.115015.22129 -NCP=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEY TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -YGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: uniprot_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1668	95.4	313	1	PIM1_MOUSE
2	1662	95.0	313	2	O8CFN8
3	1584	90.6	313	1	PIM1_FELCA
4	1582	90.6	313	1	PIM1_RAT
5	1582	90.5	313	1	PIM1_HUMAN
6	1574	90.0	313	1	PIM1_BOVIN
7	1131	64.7	323	1	PIM3_MOUSE
8	1123.5	64.2	326	1	PIM3_MOUSE
9	1122.5	64.2	326	1	PIM3_MOUSE
10	1119	64.0	326	1	PIM3_MOUSE
11	1113	63.6	325	1	PIM3_HUMAN
12	1110	63.5	325	2	PIM3_XENLA
13	1087	49.3	311	2	O8R2P0
14	861.5	49.3	311	2	O8R2P0
15	861.5	49.3	311	2	O8R2P0
16	856	48.9	311	1	PIM2_MOUSE

17	849	48.5	310	2	Q7ZVU5	Q7ZVU5 brachydanio
18	846	48.4	310	2	O8JFM9	O8JFM9 brachydanio
19	841	48.1	310	1	PIM1_BRARE	O9yfs5 brachydanio
20	839	48.0	310	2	O6DI52	O6DI52 brachydanio
21	697.5	39.9	221	2	O8RI20	O8RI20 mus musculus
22	628	35.9	441	2	O20443	O20443 caenorhabdi
23	504	28.8	378	2	O8T3F1	O8T3F1 caenorhabdi
24	504	28.8	566	2	O17737	O17737 caenorhabdi
25	415.5	23.8	134	2	O6P2U9	O6P2U9 homo sapien
26	399	22.5	1383	1	PASK_MOUSE	O8ce6 mus musculus
27	394	22.5	125	2	O6Q2K5	O6Q2K5 canis famli
28	388	22.2	658	2	O641K5	O641K5 mus musculus
29	385	22.0	1206	2	O6FUT1	O6fui1 candida gla
30	382.5	21.9	432	2	O7OXR8	O7oxr8 giardia lam
31	379	21.7	504	2	P931I3	P931I3 cucumis sat
32	379	21.7	1101	1	KOE5_YEAST	O08217 saccharomyc
33	379	21.7	1336	2	O6FRS7	O6frs7 candida gla
34	378.5	21.6	661	1	ARK5_HUMAN	O60285 homo sapien
35	378.5	21.6	779	1	SNIL_MOUSE	O60670 mus musculus
36	378	21.6	1107	2	O6CJ10	O6c310 yarrowia li
37	377.5	21.6	776	1	SNIL_RAT	O9rius rattus norv
38	375.5	21.5	643	2	O7R0B9	O7r0b9 giardia lam
39	374.5	21.4	292	2	O7QD91	O7qd91 anopheles g
40	374.5	21.4	518	2	O7PR39	O7pr39 anopheles g
41	374.5	21.4	1229	2	O6CKW4	O6ckw4 kluyveromyc
42	373	21.3	535	1	KI10_ARATH	O38937 arabidopsis
43	373	21.3	794	1	KI11_HUMAN	O8cd3 homo sapien
44	373	21.3	1398	2	O77268	O77268 drosophila
45	373	21.3	1398	2	O9W532	O9w532 drosophila

ALIGNMENTS

RESULT 1
PIM1_MOUSE
ID PIM1_MOUSE STANDARD; PRT; 313 AA.
AC P06803;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Proto-oncogene serine/threonine-protein kinase Pim-1 (BC 2.7.1.37).
GN Name=Pim1; Synonyms=Pim-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
RA Seiten G., Cuypers H.T., Boelens W., Robanus-Maandag E., Verbeek J.,
RA Domen J., van Beveren C., Berns A.;
RT "The primary structure of the putative oncogene pim-1 shows extensive
RT homology with protein kinases.";
RL Cell 46:603-611 (1986).
RN [2]
RP INTERACTION WITH RP9.
RX MEDLINE=20389540; PubMed=10931201;
RA Maiz H., Harada Y., Nagakubo D., Kitaara H., Ikeda M., Tamai K.,
RA Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
RT "PAP-1, a novel target protein of phosphorylation by Pim-1 kinase.";
RL Eur. J. Biochem. 267:516-5178 (2000).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Binds to RP9.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -1- PTM: Autophosphorylated (By similarity).
CC -1- DISEASE: Frequently activated by provirus insertion in murine
CC leukemia virus-induced T-cell lymphomas.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).

CC EMBL; M13945; AAA39930.1; -.
 DR PIR; A24169; TVMSPL.
 DR HSSP; O63450; 1A06.
 DR MGD; MG1:97584; P1m1.
 DR InterPro; IPR011009; Kinase_1like.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR008271; Ser_cyt_pkin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
 KW Serine/threonine-protein kinase; Phosphatase.
 FT DOMAIN 38 290
 FT NP BIND 44 52 ATP (By similarity).
 FT BINDING 67 67 ATP (By similarity).
 FT ACT_SITE 167 167 Proton acceptor (By similarity).
 FT ACT_SITE 167 167 Proton acceptor (By similarity).
 SQ SEQUENCE 313 AA; 35536 MW; 79F479B9DCBDC16 CRC64;

Alignment Scores:

Pred. No.:	2,25e-111	Length:	313
Score:	1668.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.37%	Indels:	0
DB:	1	Gaps:	0

US-10-705-757-5 (1-942) x PIM1_MOUSE (1-313)

QY 1 ATGCTCTGTGCAAGATCACTCCCTGGCCCGCCGCTGCAAGACTTG 60
 DB 1 MetLeuLeuSerLysIleAsnSerLeuAlaIleLeuArgIlaArgProCyAsnAspLeu 20
 QY 61 CAGGCCACCAAGTGGCGCGCGGCAAGAGAGCCCTGGAGTCCGACTCCAGG 120
 DB 21 HisAlaThrIleLeuAlaProGlyIleGlyIleGlyIleProLeuIleSerGlnIleVal 40
 QY 121 GGGCCGCTGTGGCAGCGGCTGCTCGGCTCTACTCTGCAATCCGCTGCGCGAC 180
 DB 41 GlyProLeuLeuIleSerGlyIleGlyIleSerValIleSerIleAlaGlyAlaAsp 60
 QY 181 AACTGGCCGCTGCCATTAAAGACGTGAGAGAGACCGGATTTCCGATTGGGAGAACTG 240
 DB 61 AsnLeuProValAlaIleIleValIleValIleValIleValIleValIleValIleVal 80
 QY 241 CCGAATGGGACCGGAGGCGGCAAGAGTCTCTGTTGAAGAGAGTGGGACTTC 300
 DB 81 ProAsnGlyThrIleArgValIleProMetGlyValIleValIleValIleValIleValIleVal 100
 QY 301 TCGGCGCTGATTAAGACTTCTGACTGCTGAGAGGCGGATAGTTCTGCTGATCTTG 360
 DB 101 SerGlyValIleIleArgLeuLeuAspIleArgIleArgProAspSerPheValIleIleLeu 120
 QY 361 GAGAGGCGGACCGGCTGCAAGACTTCTGACTTTATCCAGGAGGAGGCGCTTACG 420
 DB 121 GluArgProGlyIleProValIleGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
 QY 421 GAGAGCTGGCCCGGAGGATCTTCTGCAAGTCTGAGAGGCGGCTGGGCACTTC 480
 DB 141 GluAspLeuAlaArgGlyIlePheIleThrGlnValIleValIleValIleValIleValIleVal 160
 QY 481 TGGCGGCTTCTCCACCGGACATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 DB 161 CysGlyValIleLeuIleAspGlyIleValIleValIleValIleValIleValIleValIleVal 180
 QY 541 GAAATCAACTCATCGACTTCGGGCTGGGCGGCTGCTCAAGGACAGTCTACACGAGAC 600

DB 181 GluIleValIleLeuAspPheGlySerGlyAlaLeuLeuValAspThrValIleThrAsp 200
 QY 601 TTTGATGGACCCGAGTGAAGTCAAGTCTCCAGAGTGAATTCGATACCATGCTACCAAGC 660
 DB 201 PheAspGlyThrArgValIleSerProProGluIleAlaGlyIleArgGlyIleArgGly 220
 QY 661 AGGTGGGACGCTGTGCTGCTCCCTGGGATCCGCTCTATGACATGGTCCGAGATATT 720
 DB 221 ArgSerAlaIleValIleThrSerLeuGlyIleLeuLeuValIleValIleValIleValIleVal 240
 QY 721 CCGTTGAGCAGCAGATGAGAGATCATCAAGGCGCAAGTCTTTCAGGAGAACTGCTTC 780
 DB 241 ProPheGluIleAspGluIleIleIleValIleValIleValIleValIleValIleValIleVal 260
 QY 781 TCAGAGTGCAGACCTTATTAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 DB 261 SerGluIleValIleValIleValIleValIleValIleValIleValIleValIleValIleVal 280
 QY 841 TTTGAGAAATCCGAGACCATCCGTGATGACAGGCTGACCTTCGCCAGGACCTTCT 900
 DB 281 PheGluGluIleAlaArgAsnIleProIleProIleProIleProIleProIleProIleProIle 300
 QY 901 GAGATTCATTCGACAGTCTGTCACCGGATCCAGCAG 939
 DB 301 GluIleAlaLeuIleSerIleSerProGlySerSerLys 313

RESULT 2
 OBCFN8 PRELIMINARY; PRT; 313 AA.
 AC OBCFN8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Proviral integration site 1.
 GN Name=Pim1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain, and Eye;
 RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McKernan K.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettlemen M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalske U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RN [4]
 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strauberg R.;
 CC Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC042885; AAH42885.1; -
 DR EMBL; BC053019; AAH53019.1; -
 DR EMBL; BC055316; AAH55316.1; -
 DR MGD; MGI:97584; Pim1.
 DR GO; GO:000524; F1ATP binding; IEA.
 DR GO; GO:0004674; F1protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F1transferase activity; IEA.
 DR GO; GO:0006468; F1protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR007219; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR008271; Ser_thr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 313 AA; 35451 MW; 1294F16A03B7C7D7 CRC64;

Alignment Scores:

Pred. No.: 6,066-111 Length: 313
 Score: 1662.00 Matches: 312
 Percent Similarity: 99.68% Conservative: 0
 Best Local Similarity: 99.68% Mismatches: 1
 Query Match: 95.03% Indels: 0
 DB: 2 Gaps: 0

US-10-705-757-5 (1-942) x Q8CFN8 (1-313)

QY 1 ATGCTCTGTCCAAAGTCAACTCCCTGCGCCCGCCGCTTCGACGACTTG 60
 DB 1 MetLeuLeuSerIysIleAsnSerLeuAlaHisLeuAlaIleProCysAsnAspLeu 20
 QY 61 CACGCCACCAAGCTGGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 DB 21 HisAlaThrIleLeuAlaProGlyIleGlyIleGlyIleProLeuIleSerGlyIleVal 40
 QY 121 GGGCCGCTGTGGGAGCGGCTGCTTCCGCTCGCTTACTTGACATCCGCTGCGCGAC 180
 DB 41 GlyProLeuLeuGlySerGlyIleGlyIleSerValIleSerGlyIleArgValAlaAsp 60
 QY 181 AACTTCGCGGTGGCCATTAGACGCTGGAGAGAGAGAGAGAGAGAGAGAGAG 240
 DB 61 AsnLeuProValAlaIleIleValIleValIleValIleValIleValIleValIleVal 80
 QY 241 CCCAATGGGACCCGAGTCCCATGGAAGTGTCTGTGAAAGAGAGAGAGAGAGAG 300
 DB 81 ProAsnGlyThrArgValIleProMetGluValIleLeuLeuIleValIleSerSerAspPhe 100
 QY 301 TCGGGGCTGATTAGACTTCTGAGCTGGTGGAGAGCGCGATGTTCTGCTGATCTTG 360
 DB 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
 QY 361 GAGAGGCCGACCCGCTGCAAGACTCTTTCATTCACGAGAGAGAGAGAGAGAG 420
 DB 121 GluArgProGluProValIleAspLeuPheAspPheIleThrGluArgIleAlaLeuGln 140
 QY 421 GAGAGCTGGCGCGAGAGATCTTCTGGAGAGTCTGAGAGCGTGGGAGAGAGAG 480
 DB 141 GluAspLeuAlaArgIlePhePheTrpGlnValIleGluAlaValIleArgHisCysHisAsn 160
 QY 481 TGGGGGGTCTCCACCGCGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 161 CysGlyValLeuLeuHisArgAspIleIleValAspGluAsnIleLeuIleAspLeuSerArgGly 180

QY 541 GAAATCAACTCATCGACTTCGGGATCGGGGCGCTGCTCAAGAGACAGTCTACACGAG 600
 DB 181 GluIleIleLeuLeuIleAspPheGlySerGlyAlaLeuLeuIleAspThrValIleThrAsp 200
 QY 601 TTTGATGGAGACCCGAGTGTACAGTCTCTCAAGTGGATTCTGATCATGCTACACGCG 660
 DB 201 PheAspGlyThrArgValIleSerProGluTrpIleArgIleHisArgIleHisGly 220
 QY 661 AGGTGGGACGCTGTGTCGTCCTTGGGATCCGCTCTAAGACATGGCTCGGAGATATT 720
 DB 221 ArgSerAlaIleValIlePheSerLeuGlyIleLeuLeuIleValIleAspValIleGlyAspIle 240
 QY 721 CCGTTGACACGATGATGAAGATCATCAAGAGCGCAAGTGTCTTCAAGAGAACTGTCT 780
 DB 241 ProPheGluHisAspIleGluIleIleIleIleGlySerGlyIleValIlePheArgGlnThrValSer 260
 QY 781 TCAGAGTGTACGACCTTATTAAGTGTCTGTCTCCCTGAGACCGTCAAGTGGCGCTTC 840
 DB 261 SerGluCysGlnHisIleLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIle 280
 QY 841 TTTGAGAGAAATCCGAGACCATCTCGTGGATGACGAGTGTACCTCTGCGCCAGAGACTTCT 900
 DB 281 PheGluGluIleArgAsnHisProTrpMetGlnGlyAspLeuLeuProGlnAlaIleSer 300
 QY 901 GAGATCCATCTGCACAGTCTGTACCGGATCCAGCAG 939
 DB 301 GluIleHisLeuHisSerLeuSerProGlySerSerIys 313

RESULT 3

PIM1_FELCA STANDARD; PRT; 313 AA.
 ID PIM1_FELCA

AC Q95LTD; 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).

GN Name=PIM1;

OS Felis silvestris catus (cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI_TaxID=9685;

RN [1]

RP SOURCE FROM N.A.

RA Fujino Y., Satoh H., Hisasue M., Masuda K., Ohno K., Tsujimoto H.;

RT "The cDNA sequence of the feline pim-1 oncogene.";

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC -1- SUBUNIT: Binds to Rps (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).

CC -1- PTM: Autophosphorylated (By similarity).

CC -1- Similarity: Belongs to the Ser/Thr protein kinase family. PIM subfamily.

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CC EMBL; AB073748; BAB71752.1; -
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 38 290 Protein kinase.

FT NP BIND 44 52 ATP (By similarity).
 FT BINDING 67 67 ATP (By similarity).
 FT ACT SITE 167 167 Proton acceptor (By similarity).
 SQ SEQUENCE 313 AA; 35685 MW; C0B8268D638E867 CRC64;

Alignment Scores:

Pred. No.: 2,43e-105 Length: 313
 Score: 1584.00 Matches: 295
 Percent Similarity: 96.81% Conservative: 8
 Best Local Similarity: 94.25% Mismatches: 10
 Query Match: 90.57% Indels: 0
 DB: 1 Gaps: 0

US-10-705-757-5 (1-942) x PIM1_PELCA (1-313)

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QY 1  AAGCTCTGCTGCAAGATCAACTCCCTGGCCCACTGGCGCCGCCCTTCGAACGACCTG 60
DB 1  MetLeuLeuSerIysLeuSerLeuAlaHisLeuAlaArgThrAlaProCysAsnAspLeu 20
QY 61  CACGCCACCAAGCTGGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 21  HisAlaThrIleuLeuAlaProGlyIleGluIleGluProLeuGlnSerGlnIleVal 40
QY 121  GGGCCGCTGTGGGAGCGGCTTCGCGCTCTACTTGGCATCCGCGTCCGCGAC 180
DB 41  GlyProLeuLeuGlySerGlyIlePheGlySerValIleSerGlyIleArgValAlaAsp 60
QY 181  AACTTCGCGCGTGGCCATTAAGCAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 61  AsnLeuProValAlaIleIleValHisValGluIleAspArgIleSerAspTrpGlyIleLeu 80
QY 241  CCCAATGGACCGCGAGTGGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTTC 300
DB 81  ProAsnGlyThrArgValProMetGluValValLeuLeuIleValSerSerGlyPhe 100
QY 301  TCGGCGCTGATTAGACTTCTGAGCTGCTGAGAGAGCGCCAGATTCGCTGATCTTG 360
DB 101  SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleLeu 120
QY 361  GAAAGCGCCGAGACCGGTGGCAAGACTCTTGAATTCATCCGAGAGAGAGAGAGAGAGAGAG 420
DB 121  GluArgProGluProValGlnAspLeuPheAspPheIleThrIleValGlyAlaLeuGln 140
QY 421  GAGAGACTGGCGCGAGATTCCTTCTGGCAGAGTCTGGAGCGCGTGGCGCATTCGCAAC 480
DB 141  GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValArgHisCysHisAsn 160
QY 481  TGGCGGCTTCTCCAGCGGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCG 540
DB 161  CysGlyValLeuHisArgAspIleIleValAspGluAsnIleLeuIleAspLeuAsnArgGly 180
QY 541  GAAATCAAACTCATCGACTTCGGGTCGGGGCGCTGTCAAGAGACAGCTTCACAGGAG 600
DB 181  GluLeuIleuLeuLeuAspPheGlySerGlyIleLeuLeuIleAspThrValIleTrpAsp 200
QY 601  TTGATGAGAGCGGAGGTACAGTCTCCAGAGAGTGGATTCGCTACCATCTCCGCTCCAG 660
DB 201  PheAspGlyThrArgValIleTrpSerProGluIleTrpIleArgIleHisArgIleHisGly 220
QY 661  AGGTCCGAGCTGTCTGCTCTTGGAGATCTGCTCTATGACATGCTTCGCGAGATATT 720
DB 221  ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuIleAspMetValCysGlyAspIle 240
QY 721  CCGTTTGAAGACATGAGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 241  ProPheGluHisAspGluGlnIleIleArgGlyIleValAlaPhePheArgGlnAspValSer 260
QY 781  TCAGAGTGCAGACCTTATTAATGCTGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 261  SerGluCysGlnHisLeuIleArgIleTrpCysLeuAlaIleuArgProSerAspArgProSer 280
QY 841  TTGGAAGAAATCCGGAACATCCGTGATGCAAGGAGTCACTCTGCGCCGAGGAGACTTCT 900
DB 1  MetLeuLeuSerIysLeuSerLeuAlaHisLeuAlaArgThrAlaProCysAsnAspLeu 20

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DB 281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGlnIleThrAla 300
 QY 901 GAGATTCATCTGCAAGATCAACTCCCTGGCCCACTGGCGCCGCCCTTCGAACGACCTG 939
 DB 301 GluIleHisLeuHisSerLeuSerProGlyProSerIleVal 313

RESULT 4

ID PIM1_RAT STANDARD; PRT; 313 AA.
 AC P26784;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
 GN Name=Pim1; Synonyms=Pim-1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=92319652; PubMed=1620615;
 RA Winget D.; Reeves R.; Magnuson N.S.;
 RT "Characterization of the testes-specific pim-1 transcript in rat";
 RL Nucleic Acids Res. 20:3183-3189(1992).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBUNIT: Binds to Rps9 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -1- PTM: Autophosphorylated (By similarity).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM subfamily.

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 CC -----

CC EMBL: X63675; CAA45214.1; -
 DR PIR: S26298; S26298.
 DR RGD: 3330; Pim1.
 DR InterPro: IPR011009; Kinase like.
 DR InterPro: IPR000719; Prot kinase.
 DR InterPro: IPR008271; Ser_Thr_pkin_AS.
 DR Pfam: PF00069; PKinase; 1.
 DR ProDom: PD000001; Prot Kinase; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
 KW Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 38 290
 FT NP BIND 44 52 ATP (By similarity).
 FT BINDING 67 67 ATP (By similarity).
 FT ACT SITE 167 167 Proton acceptor (By similarity).
 SQ SEQUENCE 313 AA; 35630 MW; D5757DA9F1821BF9 CRC64;

Alignment Scores:

Pred. No.: 2,43e-105 Length: 313
 Score: 1584.00 Matches: 295
 Percent Similarity: 96.81% Conservative: 8
 Best Local Similarity: 94.25% Mismatches: 10
 Query Match: 90.57% Indels: 0
 DB: 1 Gaps: 0

US-10-705-757-5 (1-942) x PIM1_RAT (1-313)

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QY 1  AAGCTCTGCTGCAAGATCAACTCCCTGGCCCACTGGCGCCGCCCTTCGAACGACCTG 60
DB 1  MetLeuLeuSerIysLeuSerLeuAlaHisLeuAlaArgThrAlaProCysAsnAspLeu 20

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[illegible]

NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=90382681; PubMed=2205533; DOI=10.1016/0378-1119(90)90195-W;
 Reeves R., Spies G.A., Klefer M., Barr P.J., Power M.;
 "Primary structure of the putative human oncogene, p1m-1.";
 RL Gene 90:303-307(1990).
 [2]
 SEQUENCE FROM N.A.
 MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
 Zakut-Houri R., Hazum S., Givol D., Teleman A.;
 "The cDNA sequence and gene analysis of the human p1m oncogene.";
 RL Gene 54:105-111(1987).
 [3]
 SEQUENCE FROM N.A.
 MEDLINE=88217305; PubMed=3329709;
 Domen J., von Lindern M., Hermans A., Breuer M., Grosveld G.,
 Berns A.;
 "Comparison of the human and mouse p1m-1 cDNAs: nucleotide sequence
 and immunological identification of the in vitro synthesized p1m-1
 protein.";
 RL Oncogene Res. 1:103-112(1987).
 [4]
 SEQUENCE FROM N.A.
 MEDLINE=88115604; PubMed=3429489;
 Wecker T.C., Nagarajan L., Ar-Rushdi A., Croce C.M.;
 "Cloning and characterization of the human p1m-1 gene: a putative
 oncogene related to the protein kinases.";
 RL J. Cell. Biochem. 35:105-112(1987).
 [5]
 SEQUENCE FROM N.A.
 TISSUE=Kidney;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhac N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Umed T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McEwan P.J., McEwan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
 Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 Whitling M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Buttefield J.S.N., Krzywinski M.I., Skalska V., Smallos D.E.,
 Scheraga A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 SEQUENCE OF 1-202 FROM N.A.
 MEDLINE=21354098; PubMed=11460166; DOI=10.1038/35085588;
 Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,
 Chaganti R.S.K., Kumpers R., Dalla-Favera R.;
 "Hypermethylation of multiple proto-oncogenes in B-cell diffuse large-
 cell lymphomas.";
 RL Nature 412:341-346(2001).
 [7]
 CHARACTERIZATION.
 MEDLINE=88246418; PubMed=2837645;
 Teleman A., Amson R., Zakut-Houri R., Givol D.;
 "Identification of the human p1m-1 gene product as a 33-kilodalton
 cytoplasmic protein with tyrosine kinase activity.";
 RL Mol. Cell. Biol. 8:1498-1503(1988).
 [8]
 FUNCTION.
 MEDLINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4;
 Koike N., Maizumi H., Taira T., Ariga H., Iguchi-Ariga S.M.M.;
 "Identification of heterochromatin protein 1 (HP1) as a


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DE  Proco-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN  Name=PIML;
OS  Bos taurus (Bovine) .
OC  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovinae; Bos .
OX  NCBI_TaxId=9913;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21109090; PubMed=11182156; DOI=10.1016/S0165-2427(00)00259-2;
RA  Wang Z., Petersen K., Weaver M.S., Magnuson N.S.;
RT  "CDNA cloning, sequencing and characterization of bovine pim-1.";
RL  Ver. Immunol. Immunopathol. 78:117-135(2001) .
CC  -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC  -1- SUBUNIT: Binds to Rb9 (By similarity) .
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity) .
CC  -1- PTM: Autophosphorylated (By similarity) .
CC  -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC  subfamily.
CC  -----
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CC  -----
DR  EMBL, AF259078; AAF67200.1; -
DR  HSSP; O63450; 1A06.
DR  InterPro; IPR011009; Kinase_1like.
DR  InterPro; IPR000719; Prot_Kinase.
DR  InterPro; IPR008271; Ser_thr_pkin_AS.
DR  Pfam; PF00069; Kinasee; 1.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW  ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
KW  Serine/threonine-protein kinase; Transferase.
FT  DOMAIN 38 290
FT  NP BIND 44 52 ATP (By similarity) .
FT  BINDING 67 67 ATP (By similarity) .
FT  ACT_SITE 167 167 Proton acceptor (By similarity) .
SQ  SEQUENCE 313 aa; 35629 MW; 9EF40229A847AD47 CRC64;

Alignment Scores:
Pred. No.: 1,276-104 Length: 313
Score: 1574.00 Matches: 292
Percent Similarity: 97.12% Conservative: 12
Best Local Similarity: 93.29% Mismatches: 9
Query Match: 89.99% Indels: 0
Gaps: 0

US-10-705-757-5 (1-942) * PIM1_BOVIN (1-313)

1  ATGCTCTGTCCAGATCAACTCCCTGGCCCACTGCGCGCCGCTCGAAGACCTG 60
Db  1  MetLeuLeuSerIylLehAenSerLeuAlaHleuAlaAlaProCySerAhpLeu 20
Oy  61  CAGCGCCACCAAGCTGGCGCGGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db  21  HlsAlaTrnIlylBleuAlaProGlyIylGlsIlylGluProLeuGlnSerGlnTylVal 40
Oy  121  GAGCGCGTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db  41  GllProLeuLeuGlySerGlyGlyIylGlySerValIylSerGlyIylLeuValAlaAsp 60
Oy  181  AACTTGGCGGTGGCCATTNAGACCTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db  61  AenLeuProValAlaAlaIleIylGlyHleValGluIylAspAArgIleSerAhpTyrGlnLeu 80
Oy  241  CCCAATGGACCCCGAGTCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

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[illegible]

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DR EMBL: AJ130845; CAB62386.1; -
 DR HSSP: Q63450; 1A06; Kinase like.
 DR InterPro: IPR011009; Kinase like.
 DR InterPro: IPR00719; Prot Kinase.
 DR InterPro: IPR002290; Ser Thr kinase.
 DR InterPro: IPR008271; Ser Thr_kin_AS.
 DR Pfam: PF00069; Kinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE DM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 DR ATP-binding: Phosphorylation; Serine/threonine-protein kinase;
 KM Transferase.
 FT DOMAIN 40 291 Protein kinase.
 FT NP_BIND 46 54 ATP (By similarity).
 FT BINDING 69 69 ATP (By similarity).
 FT ACT_SITE 168 168 Proton acceptor (By similarity).
 SQ SEQUENCE 323 AA; 36597 MW; E2A4FA20B6F6396C CRC64;

Alignment Scores:
 Pred. No.: 8.6e-73 Length: 323
 Score: 1131.00 Matches: 208
 Percent Similarity: 81.61% Conservative: 45
 Best Local Similarity: 67.10% Mismatches: 53
 Query Match: 64.67% Indels: 4
 DB: 1 Gaps: 3

US-10-705-757-5 (1-942) x PIM3_COTUA (1-323)

QY 1 ATGCTCTGCTGCAAGATCACTCCCTGGCCGACCTGGCCGCGCCGCTGCAAGACAGCTG 60
 DB 1 MetLeuLeuSerIysPheGlySerLeuAlaHisIleCysSerProAlaSerMetCysHis 20
 QY 61 CACGCCACCAAGCTGGCGCGG-----GGCAAGAGAAGAGCGCCCTGGAGTCGACGTAC 114
 DB 21 LeuProValIleSerIleuProProValIleValGluIleuIleuProPheAspIleValTyr 40
 QY 115 CAGGTGGGCGCGCTGTTGGGACAGCGGTGCTGCTCGCTCACTCTGGCATCCGCGTC 174
 DB 41 GluValGlySerValIleuGlySerGlyGlyPheGlyThrValTyrIleGlySerArgThr 60
 QY 175 GCGCAACAATGGCGGTGCGCTTAAAGACAGTGGAGAAGAGCGGATTCGCGTGGGGA 234
 DB 61 AlaAspGlyLeuProValAlaValIleValIleValIleValIleValIleValIleValIle 80
 QY 235 GAATGCCCAATGACCCGAGTGGCCATGAGTGGTCTGTTGAAGAAGAGTGAAGCTGC 294
 DB 81 ThrIle---GlyGlyValMetValProLeuGluIleValIleuLeuIleValIleGlySer 99
 QY 295 GACTTCTCGGCGCTCATTAAGCTTGGAGCTGTGGAGAGCGCCGATGACTTTCGTCG 354
 DB 100 GlyPheArgGlyValIleValIleValLeuLeuAspIleTyrIleValIleValIleValIle 119
 QY 355 ATCTGTGAAGAGCGCGCAAGCGGTGCAAGACCTCTGCACTTATACCGCAAGAGAGGCC 414
 DB 120 ValMetGluIleArgProGluLeuValIleValAspLeuPheAspPheIleThrGluIleVal 139
 QY 415 CTACAGAGGAGACCTGGCGCGAGATCTTCTGGCAGGTGCTGGAGGCGCTGCGGCAATGC 474
 DB 140 LeuAspGluAspThrAlaArgGlyPhePheArgGlyValIleuGluAlaValAlaArgHisCys 159
 QY 475 CACAACTGCGGGGTCTCCACCGGACATCAAGAGAGAGAACTTTAATCGACTGAGC 534
 DB 160 TyrGlyCysGlyValValIleHisArgAspIleValAspGluAsnLeuValIleAspLeuArg 179

QY 535 CCGCGCAATCAAACTCATGCACTTCGCGTGGCGGCGCTGCTCAAGACACAGCTTAC 594
 DB 180 ThrGlyIleuLeuValIleuLeuIleAspPheGlySerGlyAlaIleuLeuValAspThrValTyr 199
 QY 595 ACGAATTTGATGGAGCCCGAGTGAACGCTCTCCAGAGTGGATTCCTCAACATGGCTTC 654
 DB 200 ThrAspPheAspGlyThrArgValIleSerProProGluTyrIleArgTyrHisArgTyr 219
 QY 655 CACGCGAGTGGCGGCGCTGCTGCTGCTGGGATCTGCTTAAAGACATGGTGGCGGA 714
 DB 220 HisGlyArgSerAlaThrValIlePheSerLeuGlyValIleuLeuTyrAspMetValCysGly 239
 QY 715 GATATTCGCTTGAAGACAGTGAAGATCAATCAAGAGCGCAAGTCTTTCACGCAAACT 774
 DB 240 AspIleProPheGluGluAspGluIleuLeuArgGlyArgLeuTyrPheArgArgArg 259
 QY 775 GTCTCTTCAAGATGTCAGACACTTATTAATGTGCTGCTCCTTGAAGACCTGCAAGTCCG 834
 DB 260 IleSerProGluCysGluGluIleuLeuIleuIleuIleuIleuIleuIleuIleuIleuIleu 279
 QY 835 CCTCTCTTGAAGAAATCCGAAACATCCGATGAGT---CAGGAGACCTCCTGCGCCAG 891
 DB 280 ProThrLeuGluGluIlePheAspHisGluIleuValIleValIleValIleValIleVal 299
 QY 892 GCAGCTTCAAGATCAATCTGCACAGCTCG 921
 DB 300 GluAspCysAspIleArgLeuArgThrLeu 309

RESULT 8
 ID PIM3_MOUSE STANDARD, PRT, 326 AA.
 AC P58750;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
 GN Name=Pim3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon, and Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Scheffen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant P.L., Scheetz T.E.,
 RA Brownstein M.T., Uebin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriques S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield J.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
 CC subfamily.

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517 ATCTTAATCGACCTGAGCCGGCGGAATCAACTCATCGACTTCGGTCCGGGGCGCTG 576

Db	176	LeuLeuValAlaPheLeuAArgSerGIYgluLeuLysLeuLleAspPheGlySerGIYAlaVal	195
Qy	577	CTCAAGACACACAGCTCACAGCAAGATTGTGATGGGACCCGAGNGTACAGTCCCTCCGAGNGG	636
Db	196	LeuLysAspThrValTYrrThrPheAspGlyThrArgValTYrSerProProGluITrr	215
Qy	637	ATTGCTACCATCGCTACCAACGCGAGGTGGCGACGTGTGTCCTTGGGATCTCTCTC	696
Db	216	ILeArgTYrHisArgTYrHisGlyArgSerAlaThrValTrpSerLeuGlyValLeuLeu	235
Qy	697	TATGACATGGCTTCGCGAGATATTTCGTTTGAGCACATGAAGATCATCAAGGCCAA	756
Db	236	TYrAspMetValCysGlyAspIleProPheGluGlnAspGluGluLeuArgGlyArg	255
Qy	757	GTGTTCTTCAGGCAAACTGCTCTCTTCAGAGNGTCAGACCTTTAATAGTGCTGTCC	816
Db	256	LeuPhePheArgArgArgValIserProGluCysGlnIleuLleGluITrrCysLeuSer	275
Qy	817	CTGAGACCGTCAGATCGCGCCCTCTTGAAGAAATCCGGAACCATCCGTGGATGACAGGT	876
Db	276	LeuArgProSerGluArgProSerLeuAspGlnIleLeuAlaHisProITrrMetLeuGly	295

RESULT 9			
PIM3_RAT			
ID	PIM3_RAT	STANDARD;	PRT; 326 AA.
AC	070444;		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	28-FEB-2003 (Rel. 44, Last annotation update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Protein kinase		
DE	Kid-1) (Kinase induced by depolarization).		
OS	Name=Pim3; Synonyms=Kid1;		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Sprague-Dawley;		
RA	Konietzko U., Kuhl D.		
RT	"Pim-3 is a member of the pim kinase family."		
RL	Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.		
RL	[2]		
RP	SEQUENCE FROM N.A. AND CHARACTERIZATION.		
RP	MEDLINE=98288176; PubMed=9637272; DOI=10.1074/jbc.273.26.16535;		
RX	Reidman J.D., Viclan L., Crispino M., Tocco G., Marcheselli V.L.,		
RA	Bazan N.G., Baudry M., Herschman H.R.;		
RT	"KID-1, a protein kinase induced by depolarization in brain.";		
RL	J. Biol. Chem. 273:16535-16543(1998).		
CC	-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.		
CC	-1- TISSUE SPECIFICITY: Present in a number of unstimulated tissues,		
CC	including brain.		
CC	-1- INDUCTION: By membrane depolarization or forskolin.		
CC	-1- PTM: Autophosphorylated.		
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM		
CC	subfamily.		

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DR	EMBL; AF086624; AAC68900.1; ALT_INIT.
DR	EMBL; AF057026; AAC36065.1; --
DR	HSSP; 003656; IHOM.
DR	RGD; 620462; Pim3.
DR	InterPro; IPR011009; Kinase_like.
DR	InterPro; IPR000719; Prot_Kinase.
DR	InterPro; IPR008271; Ser_Thr_pkin_AS.
DR	

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DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
KW transferase.
FT DOMAIN 40 293 Protein kinase.
FT NP_BIND 46 54 ATP (by similarity).
FT BINDING 69 69 ATP (by similarity).
FT ACT_SITE 170 170 Proton acceptor (by similarity).
SQ SEQUENCE 326 AA; 36002 MW; DD6C9BF4635F851E CRC64;

Alignment Scores:
Pred. No.: 3,52e-72 Length: 326
Score: 1122.50 Matches: 213
Percent Similarity: 81.33% Conservative: 31
Best Local Similarity: 71.00% Mismatches: 43
Query Match: 64.18% Indels: 13
DB: 1 Gaps: 5

US-10-705-757-5 (1-942) x PIM3_RAT (1-326)
QY 1 ATGCTCTGTCGAAGATCACTCCCTGGCCCGCCCGCCCTGC----- 51
DB 1 MetLeuLeuSerYspheglYserLeuAlaHisLeu-----CysglYProglY 16
QY 52 -----AACGACCTGCACGCCACCAAGCTGGCCCGGCGA--GAGAGAGAGCCCTG 102
DB 17 GlyValAspHisLeuProValYsIlleLeuGlnProAlaYsAlaAspYsgLuserPhe 36
QY 103 GAGTCGACGATCAACAGGTGGCCCGCTGTTGGGAGCGGTGGCTTCGCTGCTACTCT 162
DB 37 GluIleValYrgIleValGlyAlaValIleuGlySerGlyYpheglYThrValYrAla 56
QY 163 GGCATCCGCGCTCCGCCGACACTGCGGTGGCCATTAAGACGTCGAGAGAGCGGAT 222
DB 57 GlySerYrgIleAlaAspGlyLeuProValAlaValYsHisValYValYsGluArgVal 76
QY 223 TCGCATGGGAGAGAACTGCGCAATGGCACCCGAGTGGCCATGAGAGTGTCTGTTGA 282
DB 77 ThrGluTrpGlySerLeu---GlyGlyMetAlaValProIleuGluValIleuLeuArg 95
QY 283 AAGGTG-----AGCTCGACTTCTCGGGCTCATTAAGACTTTCGACTGCTGAGAG 336
DB 96 LysValGlyAlaIleAlaGlyAlaIleArgGlyValIleArgLeuLeuAspTrpPheGluArg 115
QY 337 CCGGATAGTTCGTCGATCTCGAGAGAGCGCGAACCAGTGGCAAGCTTCGACTTC 396
DB 116 ProAspGlyPheLeuLeuValIleuGluArgProGluProAlaGlnAspLeuPheAspPhe 135
QY 397 ATCAGCAGAGAGAGAGCTTACAGAGAGAGCTGGCCCGAGATTCCTTGGCAGTGTG 456
DB 136 IleThrGluArgGlyAlaLeuAspGlnProLeuAlaArgYrgPhePheAlaGlnValIleu 155
QY 457 GAGGCGGTGGCGCTTCCCACTGCGGGGTCTCCACCGCGCATCAAGAGAGAGAG 516
DB 156 AlaAlaValArgHisCysHisAsnCyAGlyValAlaHisArgAspIleIleAspGluAsn 175
QY 517 ATCTATATGACGTCGAGCGCGGGAATCAATCACTGACTTCGGGTGGGGGCGCTG 576
DB 176 LeuLeuValAspLeuArgSerGlyIleuLeuYsLeuIleAspPheGlySerGlyAlaVal 195
QY 577 CTCAGAGACACAGCTTACACAGACTTTCATGAGAGCCGAGTGTACAGTCTCCAGAGTGG 636
DB 196 LeuIleAspThrValYrThrAspPheAspGlyThrYrgValYrSerProProGluTrp 215
QY 637 ATTCGTAACATGCTACACAGAGAGTGGCAGAGCTGTGGTCCCTGGAGATTCGCTC 696
DB 216 IleArgYrHisArgYrHisGlyArgSerAlaThrValTrpSerLeuGlyValIleuLeu 235

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QY 697 TATGACATGCTGTCCGAGAGATATTCCTTTGAGCAGATGAGAGATCATGAGGCCAA 756
DB 236 TyrAspMetValCysGlyAspIleProPheGluGlnAspGluGlnIleLeuArgGlyArg 255
QY 757 GTGTTCTTGAGCAAACTGTCTCTTCAAGAGTGCAGACCTTATTAATGTGGCTGTCC 816
DB 256 LeuPhePheArgArgArgValSerProGluCysGlnGlnIleuIleGluTrpCysLeuSer 275
QY 817 CTGAGACCGTCAGAGCGCCCTTCCTTGAAGAAATCCGGAAACCATCCGTGATGCGAGGT 876
DB 276 LeuArgProSerGluArgProSerLeuAspGlnIleAlaIleAspProTrpMetLeuGly 295

RESULT 10
PIM3_HUMAN STANDARD; PRT; 326 AA.
ID PIM3_HUMAN
AC O86V86;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN Name=PIM3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.C.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Blat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uedyn T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.B.,
RA Scherch A., Schein J.E., Jones S.J.M., Mera M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RS IDENTIFICATION FROM ESTS.
RX MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6;
RA Chichester C., Nikitin F., Raverint J.-C., Lisacek F.;
RT "Consistency checks for characterizing protein forms."
RL Comput. Biol. Chem. 27:29-35 (2003).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY:.. Belongs to the Ser/Thr protein kinase family. PIM
CC subfamily.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: BC052239; AAH52239.1; ALT INT.
CC InterPro: IPR011009; Kinase like.
CC InterPro: IPR000719; Kinase like.
CC InterPro: IPR008271; Ser_thr_pkin_AS.
CC Pfam: PF00069; Pkinase; 1.
CC ProDom: PD000001; Prot_kinase; 1.

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DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
 FT TRANSFERASE. 40 293 Protein kinase.
 FT NP BIND 46 54 ATP (By similarity).
 FT BINDING 69 69 ATP (By similarity).
 FT ACT SITE 170 170 Proton acceptor (By similarity).
 SQ SEQUENCE 326 AA; 35863 MW; 41FDP9DD2467A162 CRC64;

Alignment Scores:

Pred. No.:	6.27e-72	Length:	326
Score:	1119.00	Matches:	216
Percent Similarity:	78.93%	Conservative:	35
Beet Local Similarity:	67.92%	Mismatches:	53
Query Match:	63.98%	Indels:	14
DB:	1	Gaps:	6

US-10-705-757-5 (1-942) x PIM3_HUMAN (1-326)

```

QY 1 ATGCTCTGTTCAGATCACTCCGTCGCGCCGCGCCGCGCCCTGC----- 51
Db 1 MetLeuSerLysPheGlySerLeuAlaHisLeu-----CysGlyProGly 16
QY 52 -----AACGACCTGCACGCCACCAAGCTGCGCGCGCGCAA---GAGAAAGACCCCTG 102
Db 17 GlyValaAlaHisLeuProValaValaLeuGlnProAlaValaAspLysGlySerPhe 36
QY 103 GAGTCGACGACGACGAGTGGCGCGCGCTGTGGGACGCGGTGGCTCGGCTGCTACTCT 152
Db 37 GlnLysAlaLysGlnValaGlyAlaValaLeuGlySerGlyLysGlyThrValaVala 56
QY 163 GGCATCCGCTCGCGCAACCTGCGGTGCGCATTAAGACCTGAGAAAGACCGGATT 222
Db 57 GlySerArgLysAlaAspGlyLeuProValaAlaValaHisValaValaLysGlyVala 76
QY 223 TCCGATTGGGAGAACGCCCAATGGACCCGAGTCCCATGAGAGTGTCTGTGAAG 282
Db 77 ThrGlnTrpLysLeuLeu---GlyGlyAlaThrValaProLeuGlnValaValaLeuLys 95
QY 283 AAGGTG-----AGCTCGACTTCTCGGGGCTCATTAAGCTTGTGAGTGTGAGAG 336
Db 96 LysValaGlyAlaAlaGlyGlyAlaArgGlyValaLysLeuLeuAspTrpPheGlnLys 115
QY 337 CCGGATGATTCTGCTGATCTGAGAGAGCCGGAACCGGTGCAAGACTTCTGACTTT 396
Db 116 ProAspLysLeuLeuValaLeuGlnArgProGlnProAlaGlnAspLeuPheAspPhe 135
QY 397 ATCAGCGAAGAGAGAGCCCTTACAGAGAGACCTGCGCGAGATTCTTGGCAGGTGCTG 456
Db 136 IleThrGlnLysArgGlyAlaLeuAspGlnProLeuAlaArgTrpPheAlaGlnValaLeu 155
QY 457 GAGGCGGTGGGAGTGGCAACAAGTGGGGTCTTCCAGCGGCAATCAAGAGAGAGAGAAC 516
Db 156 AlaAlaValaArgHisCysHisSerCysGlyValaValaHisArgAspIleLysAspGlnLys 175
QY 517 ATCTTAATCAGACCTGAGCCCGCGGGAATCAACTCATGACTTCGGGTGGGGGCGCTG 576
Db 176 LeuLeuValaAspLeuArgSerGlyGlnLeuLysLeuLeuLeuAspPheGlySerGlyAlaLeu 195
QY 577 CTCAAGAGACAGTCTTACAGAGACTTTGATGGAGCCGAGGTGACAGTCTTCCAGAGTGG 636
Db 196 LeuLysAspThrValaLysThrAspPheAspGlyThrArgValaLysSerProGlnLys 215
QY 637 ATTCGACCATGCTGCTACAGAGAGGTGCGAGCTGTGCGCTTGGAGCTGCTGCTGCTG 696
Db 216 IleArgTrpHisArgGlyTrpHisArgSerAlaThrValaLysSerLeuGlyValaLeuLys 235
QY 697 TATGACATGCTGCTGCGAGATATTCGTTGACAGCAGATAGAGATCATCAAGGCGCA 756
Db 236 TyrAspMetValaCysGlyAspIleProPheGlnGlnAspGlnLysLeuAspGlyArg 255

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QY 757 GTGTTCTTGAGCAACGTCTCTTCAGAGTGCAGACCTTATTAATGAGCTGTGCC 816
Db 256 LeuLeuPheArgTrpArgValaSerProGlnCysGlnGlnLeuLysArgTrpCysLeuSer 275
QY 817 CTGAGACCGTTCAGATCGGCGCGCTCTTGAAGAAATCCGGAACCATCGGTGAGAGGCT 876
Db 276 LeuArgProSerGlnArgProSerLeuAspGlnIleAlaHisProTrpMetLeuGly 295
QY 877 ---GACCTCTGCGCCAGGAGCTTGTGAGATCATGCTGACAGTGTGACCG 927
Db 296 AlaAspGlyGlyAlaProGlnLysCysAspLeuArgLeuCysThrLeuAspPro 313

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RESULT 11

PIM3_XENLA STANDARD; PRT; 323 AA.
 ID PIM3_XENLA
 AC Q91822;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Pim-1).
 GN Name=PIM3; Synonyms=PIM1;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION SITES.
 RX MEDLINE=97256766; PubMed=909695; DOI=10.1074/jbc.272.16.10514;
 RA Palaty C.K., Kaimar G., Tai G., Oh S., Amankwa L., Affolter M.,
 RA Abersold R., Peluch S.L.;
 RT Identification of the autophosphorylation sites of the Xenopus laevis
 RT Pim-1 proto-oncogene-encoded protein kinase.";
 RL J. Biol. Chem. 272:10514-10521 (1997).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- PTM: Autophosphorylated.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
 CC subfamily.
 CC -1- CAUTION: Was originally (Ref.1) called Pim-1 but seems to
 CC represent the pim-3 isoform.

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 CC or send an email to license@isb-sib.ch).

```

CC -----
CC EMBL; L29495; AAA85389.1; -.
CC InterPro; IPR011009; Kinase_1like.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC Pfam; PF00069; Pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP, FALSE_NEG.
CC PROSITE; PS0011; PROTEIN KINASE DOM; 1.
CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
CC Transferase.
CC KW DOMAIN 40 291 Protein kinase.
CC FT NP_BIND 46 54 ATP (By similarity).
CC FT BINDING 69 69 ATP (By similarity).
CC FT ACT_SITE 168 168 Proton acceptor (By similarity).
CC FT MOD_RES 4 4 Phosphoserine (by autocatalysis)
CC FT MOD_RES 190 190 Phosphoserine (by autocatalysis)
CC FT MOD_RES 205 205 Phosphothreonine (by autocatalysis)
CC FT PARTIAL
CC SQ SEQUENCE 323 AA; 36964 MW; AB4DD61E799A38F CRC64;
CC Pred. No.: 1.69e-71 Length: 323

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Score: 1113.00 Matches: 208
 Percent Similarity: 80.38% Conservative: 46
 Best Local Similarity: 85.82% Mismatches: 56
 Query Match: 63.64% Indels: 6
 DB: 1 Gaps: 5

US-10-705-757-5 (1-942) x PIM3_XENIA (1-323)

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QY 1 ATGCTCTGTCGAAGATCAACTGCCCTGGCCCGCCGCGCCCTGCAACGACTG 60
DB 1 MetLeuLeuSerLysPheGlySerLeuAlaHisLe---CysAsnProSerAsnMetGlu 19
QY 61 CAC-----GCCACCAAGCTGGCGCGCGCAAA---GAGAAGGAGCCCTGAGTGCAG 111
DB 20 HisLeuProValLysIleLeuGlnProValLysValAspLysGlnProPheGluVal 39
QY 112 TACCAAGTGGGCGCGCTGTGGCAGCGGTGGCTTGGCTGCTTACTCTGCAATCCG 171
DB 40 TyrGlnValGlySerValValAlaSerGlyGlyPheGlyThrValTyrSerAspSerArg 59
QY 172 GTGCGCGCAACTGTGGCGGCTTAAAGCACTGGAAGAGACCGGATTCGATTCG 231
DB 60 IleAlaSerGlyGlnProValAlaValAlaValAlaValAlaValGlnValTrpGluTrp 79
QY 232 GGAAGACTGCCCAATGGCAGCCGAGTGCCTGGAAGTGGCTCTGTTGAAGAAGTGCAG 291
DB 80 GlyThrLeu---AsnGlyValMetValProLeuGlnIleValLeuLeuLysValPro 98
QY 292 TCGGACTTCTGGCGGCTCATTAAGCTTGTGAGCTGTTGAGAGCGCCGATCTTCG 351
DB 99 ThrAlaPheArgIleValIleAsnLeuLeuAspTrpTyrGlnArgProAspAlaPheLeu 118
QY 352 CTGATCTGTGAGAGGCGCGCAACCGGTGACCTTGTGACCTTATTCACCGAAGAGG 411
DB 119 IleValMetGlnArgProGlnProValLysAspLeuPheAspTrpIleTrpGluLysGly 138
QY 412 GCCCTACAGAGGAGCTGGCGCGAGATCTTGTGAGAGTGTGAGAGCGCTGCGGCA 471
DB 139 ProLeuAspGlnAspTrpAlaArgIleAspPheArgIleValLeuGlnAlaValAlaGlnHis 158
QY 472 TGGCAACAATGGCGGGCTTTCACCGGACATCAAGAGCAGAACTTTAATGCACCTG 531
DB 159 CysTyrAsnGlySerGlyValAlaHisArgAspIleLysAspIleAsnLeuValAlaSerTrp 178
QY 532 AGCGCGCGGCAATCAACTGCATGCATTCGCGGCGCGGCGCTGCTCAAGGACAGAC 591
DB 179 ArgAsnGlyGlnLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspTrpVal 198
QY 592 TACACGCACTTGTATGGGAGCCGAGTGTACAGTCTTCAGAGTGTGATTCGCTACATCC 651
DB 199 TyrThrAspPheAspGlyThrArgValTyrSerProProGlnTrpValAlaArgTyrHisArg 218
QY 652 TACACGCGAGGTGGCGAGCTGTGTGCTCCCTTGGGATCTGCTCTATGACATGTCTGC 711
DB 219 TyrHisGlyArgSerAlaTrpValTrpSerLeuGlyValLeuLeuTyrAspMetValTyr 238
QY 712 GGAATATTCGCTTGAAGCAGCATGAAAGATCATCAAGGCGCAAGTGTTCCTACAGCA 771
DB 239 GlyAspIleProPheGlnGlnAspGlnGlnIleValAlaArgValAlaArgLysCysPheArgGag 258
QY 772 ACTGCTCTTCAGAGTGTACGACACTTATTAATGTGTGCTGCTGCTGAGACGCTGAGAT 831
DB 259 ArgIleSerThrGlnCysGlnGlnIleLeuIleTyrCysLeuSerLeuAspGlnProSerAsp 278
QY 832 CGGCGCTCTTTGAAGAAATCCGAAACATCCGTCGATG---CAGGATGACTTCCTGCCC 888
DB 279 ArgProThrLeuGlnGlnIlePheAspHisProTrpMetCysArgCysAspLeuValLys 298
QY 889 CAGGACGCTTCAGATCCATCCATGCAGACAGTCTGTCAACCGGATCCAGC 936
DB 299 SerGlnAspCysAspLeuArgLeuArgThrIleAspAsnAspSerSer 314

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RESULT 12

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Q0811X8
ID Q0811X8 PRELIMINARY; PRT: 325 AA.
AC Q0811X8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KIDL.
GN Name=Pim3; Synonyms=Kidl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT:Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu L.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL: AY026239; AKK16606.1; -.
DR HSSP; Q03656; 1099.
DR MGD; MGI:1355297; Pim3.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 325 AA; 35931 MW; 77DBF8E2041B3F4 CRC64;

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Alignment Scores:

Pred. No.: 2,786-71 Length: 325
 Score: 1110.00 Matches: 212
 Percent Similarity: 81.33% Conservative: 32
 Best Local Similarity: 70.67% Mismatches: 42
 Query Match: 63.46% Indels: 14
 DB: 2 Gaps: 6

US-10-705-757-5 (1-942) x Q0811X8 (1-325)

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QY 1 ATGCTCTGTCGAAGATCAACTGCCCTGGCCCGCCGCGCCCTGCG----- 51
DB 1 MetLeuLeuSerLysPheGlySerLeuAlaHisLeu-----CysGlyProGly 16
QY 52 -----AACGACCTGCAGCGCCACCAAGCTGGCGCGCGCAAA---GAGAAGGAGCCGCTG 102
DB 17 GlyValAspHisLeuProValLysIleLeuGlnProAlaLysValAspLysSerPhe 36
QY 103 GAGTCGACATACAGATGGGCGCGCTGTGGCAGCGGTGAGCTCGCTCGCTTACTCT 162
DB 37 GluLysValTyrGlnValGlyValAlaValLeuGlnSerGlyGlyPheGlyThrValTyrAla 56
QY 163 GGCATCCGCGTGGCGGCAACTTGGCGGTCATTAAGCACTGAGAGAACCGGAT 222
DB 57 GlySerArgIleAlaAspGlyLeuProValAlaValAlaValAlaValLysGlnArgVal 76
QY 223 TCCGATTGGGAGGAAGCTGCCAATGAGCAGCGGCGCATTAAGTGTGCTGTTGAG 282
DB 77 ThrGlnTrpGlySerLeu---GlyIleValAlaValProLeuGlnValValLeuLeuArg 95
QY 283 AAGGTG-----AGCTCGGACTTTCGCGCGCTCATTAAGCTTGTGAGTGTTCGAGAG 336
DB 96 LysValGlyAlaAlaGlyGlyValAlaArgGlyValIleArgLeuLeuAspTrpPheGlnArg 115
QY 337 CCCGATGTTTGTGCTGATCTCGAGAGAGCCCGGAAACGAGTGCAGACCTTTCGACTTT 396
DB 116 ProAspGlyPheLeuLeuValLeuGlnArgProGlnProAlaGlnAspLeuPheAspPhe 135

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QY 397 ATCCAGCAAGAGAGAGCCCTACAGAGAGACCTGGCCCGAGATTTCTTGCGAGGTCTG 456
    |||||
Db 136 ILeThciunrgrglYalaleuAepgluProleuAlArgrphnealaglValleu 155
    |||||
QY 457 GAGGCCGTGGCGCATTCGCAACATGCGGGGTTCTCACCGGACATCAAGAGAGAGAC 516
    |||||
Db 156 AlAlaValArgrhlsCyshlsAenCGeGlYalValAlhlsArgrphlelYleAepgluAen 175
    |||||
QY 517 ATCTTAATCGACCTGAGAGCCCGCGGAAATCAACTATCTGACTTCGGGTGGGGCGCTG 576
    |||||
Db 176 LeuLeuValArgrhlsAenArgrhlsGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 195
    |||||
QY 577 CTCAGAGACACAGCTCTACAGAGACTTGTATGAGAGCCGAGGTACAGTCTCTCCAGAGTGG 636
    |||||
Db 196 LeuLeuAepArhThrValYlThrArphneAepglYlThrArgrValYlYserProProgluTIP 215
    |||||
QY 637 ATTGCTTACCATGCTTACACAGCGAGGTGGAGCTGTGCTCCCTTGAGATCTGCTC 696
    |||||
Db 216 ILeArgrYlArgrYlArgrYlArgrYlArgrYlArgrYlArgrYlArgrYlArgrYl 235
    |||||
QY 697 TATGACATGCTGCTCGGAGATATTCCTTTGAGACACATGAAGATCATCAAGAGCGCA 756
    |||||
Db 236 TyArspMetValCyseGlYArpIleProPhelGluLeuAepgluLeuArgrGlYArgr 255
    |||||
QY 757 GTGTTCTTACGAGCAACTGTCTCTTACAGAGTTCAGACCTTATTAATGTCGCTGTC 816
    |||||
Db 256 LeuPhneArgrArgrArgrValSerProgluCyseGluLeuLeuLeuLeuLeuLeuLeu 275
    |||||
QY 817 CTGAGACCGTCAAGATCGGCGCTCTTGAAGAAATCCGAGAACCTCCGTGAGATGACAGGT 876
    |||||
Db 276 LeuArgrProSerArgrArgrArgrProSerLeuAepgluLeuLeuLeuLeuLeuLeuLeu 294
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RESULT 13

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ID 066111 PRELIMINARY; PRT; 318 AA.
AC 066111;
DT 25-OCT-2004 (TEMBLrel. 28, Created)
DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Reinhold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pehey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;

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RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC081340; AA081340.1; -.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR000719; Prot Kinase.
DR InterPro: IPR002290; Ser Thr Kinase.
DR InterPro: IPR008271; Ser Thr Kin AS.
DR InterPro: IPR001245; Tyr Kinase.
DR Pfam: Pf00069; Kinase; 1.
DR ProDom: PD000001; Prot Kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein.
SQ
SEQUENCE 318 AA; 36547 MW; 48CCFF12797F01FDC CRC64;

Alignment Scores:
Pred. No. 1,24e-69 Length: 318
Score: 1087.00 Matches: 198
Percent Similarity: 81.36% Conservative: 42
Best Local Similarity: 67.12% Mismatches: 47
Query Match: 62.15% Indels: 8
DB: 2 Gaps: 3

US-10-705-757-5 (1-942) x Q66111 (1-318)
QY 7 CTGTCCAGATCAACTCTCGTGGCCACTGCGCGCCGCCCTTCAGACAGCTGACGCC 66
    |||||
Db 1 MetSerSerValGlnValIleYlThrs-----GlnYlserIlehsanYlThrsleu 17
    |||||
QY 67 ACCAAGCTGCGCGCGGCAAGAG-----AAGAGCCCTGAGATGCGAGTAC 114
    |||||
Db 18 AsnSerValPheProlyAspAspAspLeuProAlaValYlGluProPhelGluLeuAsnCyYlY 37
    |||||
QY 115 CAGGTGGGCGCGGTGTGGGAGCGGCGGCTTGGCTTCTGCTTACTCTGAGATCGCGCTG 174
    |||||
Db 38 GlnValGlyProValIleGlyThrsYlGlyPheGlyThrsValYlYserGlyAlaIleGly 57
    |||||
QY 175 GCGCAACTTGGCGGTGCGCATTAAGACGTGAGAGAGACCGGATTTCCGATTGGGGA 234
    |||||
Db 58 SerAspYlLeuProValAlaIleYlThrsIleValSerArgrAspArgrIleGlyGluMetCys 77
    |||||
QY 235 GAACTGCCAATGGGACCGGAGTGGCCATGAGAGAGTGTCTGTGAAGAGAGTGAAGTCTG 294
    |||||
Db 78 HlsMet---AsnGlyThrsLeuValProLeuGluIleYlThrsLeuYlYserValSerAsn 96
    |||||
QY 295 GACTTCTCGGCGTCACTTGAAGTCTGAGCTGGTGAAGAGCGCGATGTTGCGTGTG 354
    |||||
Db 97 GlyCyArgrGlyValIleArgrLeuLeuAepTrpYlGluArgrProAepglYlPheIleIle 116
    |||||
QY 355 ATCTTGAGAGAGCGCCGAGACCGGTGACAGACTCTTGAAGTATTAACCGAGAGAGAGCC 414
    |||||
Db 117 IleMetGluArgrProIleuProValGlnAepLeuPheIleThrsGluArgrGlyAla 136
    |||||
QY 415 CTACAGAGAGACTGCGCGGAGAGATTTCTTGGCAGGTCTGAGAGCGCGCTGGCACTTGC 474
    |||||
Db 137 LeuGlyGluGluLeuAlaThrsArphneArgrGlnValGlnAlaValArgrhlsCyS 156
    |||||
QY 475 CACCAATGCGGGGTTCTTCACCGCGGACATCAAGAGAGAGAAATCTTAATGACCGAGAGC 534
    |||||
Db 157 HlsSerCyAspArpValAlaIleArgrAepIleYlAspGluAenIleLeuValAspLeuArgr 176
    |||||
QY 535 CCGCGGAAATCAAACTCATGCACTTGGGAGTGGGGCGCTGCTCAAGAGACAGTCTAC 594
    |||||
Db 177 ThrAlaGluLeuLeuLeuIleAspPheGlySerGlyAlaLeuLeuArgrAspAlaValYlY 196
    |||||
QY 595 ACGAGATTGATGGAGACCGGAGGTGACGTCTCCAGAGTGAATTCCTACCATCGCTAC 654
    |||||
Db 197 ThrAspPheAspGlYlThrsArgrValYlYserProProgluTIPAlArgrPhehlsYlY 216
    |||||
QY 655 CACGAGAGTGGGAGCGCTGTGTCCTTGGAGATCGCTGATGAGACAGTGTGCGGGA 714
    |||||

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Db	21	HISGLYARGSERGLATHRVALTRPSERILEUGLYILEULEUETLYRASPMEVALCYGLY	236
Qy	715	GATPPTCCGTTTGAGACGATGAGATCATCAAGAGCCCAAGTGTCTTCAGGCAAACT	774
Db	237	ASPILEPROHEGLIHTIASHAPBPGIUILEULEUGLYSLYLSILEGLNTYRCAARG	256
Qy	775	GTCCTCTTCAAGAGTGTCAGACCCCTTATTAATGSGTCCGTGTCGAGACGCTCAGACGG	834
Db	257	VALSERARGIUNCYSGIHTIASHLEUILEGILUTRPGYLSERISERVAARGPROSERASPARG	276
Db	835	CCCTCTTGAAGAAATCCGGAACCATCCGTGAGTGCAGGCTGAC	879
Qy	277	PROSERILEUGIUNGIHTIASHLEUILEUIHSPROTPTMETSERGIINAP	291
RESULT 14			
Q8R2P0			
ID	08R2P0	PRELIMINARY;	PRT; 311 AA.
AC	08R2P0;		
DT	01-JUN-2002 (TrEMBLrel. 21, Created)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	P121 protein.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=FVB/N. TISSUE=Mammary tumor. C3;		
RX	MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Bietow K.H., Schaefer C.F., Bat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Mac S.I., Wang J., Hsieh F.,		
RA	Datchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein W.J., Udell T.B., Tohilyuk S., Carninci P., Frange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,		
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fatey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,		
RA	Kryzhanek M.I., Skalka U., Smallus D.E., Scherch A., Schein J.R.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=FVB/N. TISSUE=Mammary tumor. C3;		
RA	Strauberg R.;		
RL	Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.		
DR	EMBL; BC027376; AAH27376.1; -		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0044674; F:protein serine/threonine kinase activity; IEA.		
DR	GO; GO:0016740; F:transferase activity; IEA.		
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.		
DR	InterPro; IPR011009; Kinase_1like.		
DR	InterPro; IPR000719; Prot kinase.		
DR	InterPro; IPR002290; Ser_Thr_pkinase.		
DR	InterPro; IPR008271; Ser_Thr_pkin_AS.		
DR	Pfam; PF00069; PKinase1.1.		
DR	ProDom; PD000001; Prot kinase; 1.		
DR	SMART; SMO0220; S_TKc; 1.		
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.		
DR	PROSITE; PS00011; PROTEIN KINASE_DOM; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_SF; 1.		
DR	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.		
SO	SEQUENCE 311 AA; 34486 MW; F7B770908D23A710 CRC64;		

[illegible]

ID	PIM2_MOUSE	STANDARD:	PRT:	370 AA.
AC	Q62070, Q62071, Q62072;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Serine/threonine-protein kinase Pim-2 (EC 2.7.1.37).			
GN	Name:Pim2; Synonyms=Pim-2;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95300786; PubMed=7781606;			
RA	van der Lugt N.M., Domen J., Verhoeven E., Linders K.,			
RA	van der Gulden H., Allen J., Berns A.;			
RT	"Proviral tagging in E mu-myc transgenic mice lacking the Pim-1 proto-oncogene leads to compensatory activation of Pim-2."			
RL	EMO J. 14:2536-2544(1995).			
CC	-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.			
CC	-1- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative initiation;			
CC	Comment=3 isoforms, 1 (shown here), 2 and 3, are produced by			
CC	alternative initiation. Isoform 1 and isoform 2 initiate from			
CC	CTG codons;			
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM			
CC	subfamily.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; L41495; AAA98922.1; -.			
DR	EMBL; L41495; AAA98923.1; -.			
DR	EMBL; L41495; AAA98924.1; -.			
DR	PIR; S55333; S55333.			
DR	HSSP; O63450; 1A06.			
DR	MCD; MGI:97587; Pim2.			
DR	GO; GO:0005515; F:protein binding; IDI.			
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.			
DR	GO; GO:0006936; P:anti-apoptosis; IDA.			
DR	GO; GO:0008637; P:apoptotic mitochondrial changes; IDA.			
DR	InterPro; IPR011009; Kinase like.			
DR	InterPro; IPR000719; Prot. Kinase.			
DR	InterPro; IPR008271; Ser_Thr_Pkin_AS.			
DR	InterPro; IPR002290; Ser_Thr_Pkinase.			
DR	Pfam; PF00069; Pkinase; 1.			
DR	ProDom; PD000001; Prot_Kinase; 1.			
DR	SMART; SM00220; S_TKc; 1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
KW	Alternative initiation; ATP-binding; Phosphorylation;			
KW	Serine/threonine-protein kinase; Transferase.			
FT	CHAIN	1	370	Serine/threonine-protein kinase Pim-2,
FT				isoform 1.
FT	CHAIN	26	370	Serine/threonine-protein kinase Pim-2,
FT				isoform 2.
FT	CHAIN	60	370	Serine/threonine-protein kinase Pim-2,
FT				isoform 3.
FT	INIT_MET	26	26	For isoform 2.
FT	INIT_MET	60	60	For isoform 3.
FT	DOMAIN	91	345	Protein kinase.
FT	NP_BIND	97	105	ATP (By similarity).
FT	BINDING	120	120	ATP (By similarity).
FT	ACT_SITE	222	222	Proton acceptor (By similarity).
SO	SEQUENCE	370 AA;	40059 MW;	12BB70BFDD4DBE8A CRC64;

Alignment Scores:

[illegible]

Search completed: September 22, 2005, 17:14:55
Job time : 162.516 secs

Alignment Scores:

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 22, 2005, 16:26:26 ; Search time 127.935 Seconds

(without alignments)
5993.731 Million cell updates/sec

Title: US-10-705-757-5

Perfect score: 1749

Sequence: 1 agctctctgtccagatca.....caccggatccagcaagtag 942

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 3653042

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1668	95.4	313	9 US-09-971-791-7	Sequence 7, Appl
2	1668	95.4	313	15 US-10-348-081-14	Sequence 14, Appl
3	1668	95.4	313	16 US-10-664-421-2	Sequence 2, Appl
4	1668	95.4	313	16 US-10-377-266-10	Sequence 10, Appl
5	1668	95.4	313	18 US-10-705-757-6	Sequence 6, Appl
6	1668	95.4	313	18 US-10-941-635-2	Sequence 2, Appl
7	1584	90.6	313	9 US-09-971-791-8	Sequence 8, Appl
8	1584	90.6	313	15 US-10-348-081-12	Sequence 12, Appl
9	1584	90.6	313	18 US-10-705-757-4	Sequence 4, Appl
10	1582	90.5	313	9 US-09-971-791-9	Sequence 9, Appl
11	1582	90.5	313	14 US-10-081-119-18	Sequence 18, Appl
12	1582	90.5	313	15 US-10-394-322A-52	Sequence 52, Appl
13	1582	90.5	313	15 US-10-348-081-13	Sequence 13, Appl
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16	1582	90.5	313	16 US-10-377-266-9	Sequence 9, Appl
17	1582	90.5	313	17 US-10-951-389-18	Sequence 18, Appl
18	1582	90.5	313	17 US-10-951-406-18	Sequence 18, Appl
19	1582	90.5	313	17 US-10-951-477-18	Sequence 18, Appl
20	1582	90.5	313	18 US-10-977-087-18	Sequence 18, Appl
21	1582	90.5	313	18 US-10-705-757-2	Sequence 2, Appl
22	1582	90.5	313	18 US-10-941-635-1	Sequence 1, Appl
23	1582	90.5	313	18 US-10-941-635-152	Sequence 152, App
24	1580	90.3	313	16 US-10-620-052A-22	Sequence 22, Appl
25	1315	75.2	253	16 US-10-620-052A-71	Sequence 71, Appl
26	1131	64.7	323	16 US-10-664-421-7	Sequence 7, Appl
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37	1119	64.0	326	15 US-10-348-081-2	Sequence 2, Appl
38	1119	64.0	326	16 US-10-664-421-166	Sequence 166, App
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41	1119	64.0	374	15 US-10-425-114-54275	Sequence 54275, A
42	1113	63.6	323	15 US-09-971-791-6	Sequence 6, Appl
43	1113	63.6	323	15 US-10-348-081-11	Sequence 11, Appl
44	1113	63.6	323	16 US-10-664-421-8	Sequence 8, Appl
45	1113	63.6	323	16 US-10-377-266-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-971-791-7
; Sequence 7, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971, 791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644, 450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237, 543
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 313

TYPE: PRT
ORGANISM: Mus musculus
US-09-971-791-7

Alignment Scores:

Pred. No.:	2,676-117	Length:	313
Score:	1668.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.37%	Indels:	0
		Gaps:	0

US-10-705-757-5 (1-942) x US-09-971-791-7 (1-313)

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DB 21 Hisalathrluysleuialaroglylrglulysglulproleugluserglnlyrglnval 40
QY 121 GGCCTGCTGTGGGAGCGGCTTGGCTCGGCTACTCTGGCATCCGCGTCCGAC 180
DB 41 Glyproleuenuylserglylphneglylservaltyserglylleargvalalaar 60
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DB 81 Proaennglytharvalprometglulvalleuenuylserglnlyseraserpne 100
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RESULT 2

US-10-348-081-14
Sequence 14, Application US/10348081
Publication No. US20040038246A1
GENERAL INFORMATION:
APPLICANT: KORN, Marcus
APPLICANT: MUELLER, Guenter
APPLICANT: SCHNEIDER, Rudolf
APPLICANT: TSCHAN, Georg
TITLE OF INVENTION: P1W-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DE4V2002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.2
SEQ ID NO 14
LENGTH: 313

TYPE: PRT
ORGANISM: Mus musculus
US-10-348-081-14

Alignment Scores:

Pred. No.:	2,676-117	Length:	313
Score:	1668.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
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US-10-705-757-5 (1-942) x US-10-348-081-14 (1-313)

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DB 121 Gluhargproglulprovalgluharbleueneapneillethrglnuargllyalaleu 140
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Db	221	ArgSerAlaIleValITrpSerLeuGlyIleLeuLeuTYrAspMetValCysGlyAspIle	240
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Qy	781	TCAAGATGTCAAGACCTTATTAAATGATGCTCTCCCTAGACCGTTCAGATGGACCTCC	840
Db	261	SerGluCysGlnHisIleuLeuIleuTYrCysIleuSerLeuArgProSerAspArgProSer	280
Qy	841	TTTGAAGAAATCCGGAACCATCCGTGGATGACAGGGGTGACTCTCTGGCCCCAGGACGTTCT	900
Db	281	PheGluGluIleArgHisHisProITrpMetGlnGlyAspIleuLeuProGlnIleAlaIleSer	300
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/ Sequence 2, Application US/10664421
/ Publication No. US2004012864A1
/ GENERAL INFORMATION:
/ APPLICANT: BREMER, RABHA
/ APPLICANT: IBRAHIM, ABINAV
/ APPLICANT: KUMAR, ABHINAV
/ APPLICANT: MANDIVAN, VASLAN
/ APPLICANT: MILBURN, MICHAEL V.
/ TITLE OF INVENTION: CRYSTAL STRUCTURE OF P1M-1 KINASE
/ FILE REFERENCE: 039363/0703
/ CURRENT APPLICATION NUMBER: US/10/664,421
/ CURRENT FILING DATE: 2003-09-16
/ PRIOR APPLICATION NUMBER: 60/412,341
/ PRIOR FILING DATE: 2002-09-20
/ PRIOR APPLICATION NUMBER: 60/411,398
/ PRIOR FILING DATE: 2002-09-16
/ NUMBER OF SEQ ID NOS: 169
/ SOFTWARE: Patent In Ver. 3.2
/ SEQ ID NO 2
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-664-421-2

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Alignment Scores:	
Pred. No.:	2.67e-117
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Best Local Similarity:	100.00%
Query Match:	95.37%
DB:	16
	Gaps: 0
	Indels: 0
	Mismatches: 0
	Conservative: 0
	Matches: 311
	Length: 311

US-10-705-757-5 (1-942) x US-10-664-421-2 (1-313)

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Db 21 HisIleThrIysLeuAlaProGlyIysGlnIuProLeuGlnSerGlnTyrGlnVal 40
QY 121 GGCCCGCTGTGGCAGCGGTGGCTTCGCGTGGTCTACTGCGCATCCGCGTGGCCAC 180

Dd	41	GlYpRdLeuLeuGlYSerGlyrPheGlySerValTYrSerGlyIleArgValAlaAsp	60
QY	181	AACTGGCCGGTGGCCATTAAAGACAGTGGAGAAAGACCCGGAATTTCCGATTTGGGAGAACTG	240
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QY	241	CCCAATGGACCCCGAGTGGCCCATGGAAAGTGTCTCTGTGGAGAAAGAGTGAAGCTTCGACTTC	300
Dd	81	ProAenGIYThrArgValProMetGIuValIleuLeuYalYValSerSerAspPhe	100
QY	301	TCGGGCGGTCAATTAGCTTTGGACCTGGTTCAGAGAGCCCGAATAGTTTGCTGTGATCTCG	360
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QY	361	GAGAGGGCCCGAACCCGGTGCAGACCTCTTCGACTTATACCCGAACGAGAGGCCCTACAG	420
Dd	121	GIuArgProGIuProValGIuInAspLeuPheAspPheIlethGIuArgIYAlaLeuGIu	140
QY	421	GAGGACCTGGCCCGGAGATTTCTTCGGAGAGTGTGGAGACCCGTGCGGCAATTCGCAAAAC	480
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QY	481	TGCGGGGTTCTCCACCGGACATCAAGACGAAACATTATATGACCTTGACCGCGGC	540
Dd	161	CysGIYValIeuhIAsArgAspIleYuaAspGIuAenIleuIleAspLeuSerArgIY	180
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Dd	201	PheAspGIYThrArgValTYrSerProGIuTrpIleArgTYrshIaArgTYrshIY	220
QY	661	AGATGCGAGAGTGTGTGGTCTCTGGAGATCTGCTGTGACATAGTCTGCGGAAATATT	720
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QY	721	CCGTTTGGACGATGAAGAGATCATCAAGGGCCAAAGTGTCTTTCAGGCAAACTGTCTCT	780
Dd	241	ProPheGIuuhIAsArgGIuIleIleIeYsGIYAlValPhePheArgGIuThrAlaSer	260
QY	781	TCAGAGTGCAGACTTATTAATATGAGTGCCTGTCTCTGAGACCGTCAAGTGGCGCTTC	840
Dd	261	SerGIuCYsGIuuhIAsLeuIleYerTrpCYsLeuSerIeuhArgProSerAspArgProSer	280
QY	841	TTTGAAGAAATCCCGAACAATCCGTGGATGACAGGGTACCTCTCCGCCAGGACGTTCT	900
Dd	281	PheGIuGIuIleArgAsnshIAsProTYrMetGIuArgLeuPheLeuProGIuAlaIAsSer	300
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RESULT 4
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; Sequence 10, Application US/10377268
; Publication No. US20040171062A1
; GENERAL INFORMATION:
; APPLICANT: HIRTH, KLAUS-PETER
; APPLICANT: MILBURN, MICHAEL VANCE
; TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
; FILE REFERENCE: 039363/0303
; CURRENT APPLICATION NUMBER: US/10/377,268
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: 60/437,929
; PRIOR FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 60/360,651
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
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NUMBER OF SEQ ID NOS: 38
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 10
 LENGTH: 313
 TYPE: PRT
 ORGANISM: Mus musculus
 US-10-377-268-10

Alignment Scores:

Pred. No.:	2,67e-117	Length:	313
Score:	1668.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.37%	Indels:	0
DB:	16	Gaps:	0

US-10-705-757-5 (1-942) x US-10-377-268-10 (1-313)

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QY 121 GGCCTCGTGTGGAGCGGCTTGGCTCGGCTCTGACTCTGAGATCCGCTGCGCGAG 180
    |||
Db 41 GlyProLeuLeuGlySerGlyLybGlyPheGlySerValTySerGlyIleArgValAlaAsp 60

QY 181 AACTTGCCTGCGCATTAAGACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
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Db 61 AsnLeuProValAlaIleLybHisValGluLybAspArgIleSerAspTrpGlyGluLeu 80

QY 241 CCCAATGGCAACCGGAGTGGCCCAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
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QY 301 TCGGCGCTGATTGACTTCTTGAGCTGGATTGAGAGCGCGATGTTTCGCTGATCTTG 360
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Db 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleuLeu 120

QY 361 GAGAGCGCCGAGACCGGAGTGAAGACCTTCTGACTTTATACCGAGAGAGAGAGAGAGAGAG 420
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Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140

QY 421 GAGAGACTGCGCGGAGATTTCTTGCGAGGTGCTGGAGCGCGCTGCGCGAGAGAGAGAG 480
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Db 141 GluAspLeuAlaArgGlyPhePheTrpGlnValIleuGlnAlaValArgHisCybHisAsn 160

QY 481 TGGCGGCTTCTCGACCGGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
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Db 161 CybGlyValIleuHisArgAspIleLybAspGluAsnIleuLeuIleAspLeuSerAspGly 180

QY 541 GAAATCAAACTCATCGACTTCGAGGTGCGGCGCGCTGCAAGAGACAGACTCTACAGAGAC 600
    |||
Db 181 GluIleLybLeuIleAspPheGlySerGlyAlaLeuLeuLybAspThrValTyThrAsp 200

QY 601 TTTGATGGAGCCGAGTGTACAGTCTTCCAGAGTGGATTGCTACCATCGCTACAGAGAG 660
    |||
Db 201 PheAspGlyThraArgValIleTySerProGluTrpIleArgTyHisAspGlyrHisGly 220

QY 661 AGGTGCGGAGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
    |||
Db 221 ArgSerAlaAlaValIlePheSerLeuGlyIleLeuLeuTyraPheValCybGlyAspIle 240

QY 721 CCGTTTGAGCAGATGAAGAGATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
    |||
Db 241 ProPheGluHisAspGluGluIleIleLybGluValIlePhePheArgGlnThrValSer 260

QY 781 TCGAGAGTGTACGACCTTATTTAAATGGTGGCTGTCTGCTGAGAGAGAGAGAGAGAGAGAG 840
    |||
Db 261 SerGluGlySerGlnHisLeuIleLybTrpCybLeuSerLeuArgProSerAspArgProSer 280
  
```

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QY 841 TTTGAAGAAATCCGGAACCATCGGTGAGATGACGAGTGAACCTTCTGCGCCGAGAGCTTCT 900
    |||
Db 281 PheGluGluIleArgAsnHisProTrpMetGlnGlyAspLeuLeuProGlnAlaAsp 300

QY 901 GAGATTCATCTGCACAGTGTGTACCGGAGATCCAGCAAG 939
    |||
Db 301 GluIleHisLeuHisSerLeuSerProGlySerSerLyS 313
  
```

RESULT 5

US-10-705-757-6

Sequence 6, Application US/10705757
 Publication No. US20040146942A1

GENERAL INFORMATION:

APPLICANT: GRUBENTHAL GMBH
 TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
 FILE REFERENCE: 029310.528180S
 CURRENT APPLICATION NUMBER: US/10/705,757
 CURRENT FILING DATE: 2003-11-12
 PRIOR APPLICATION NUMBER: PCT/EP02/05234
 PRIOR FILING DATE: 2002-05-13
 PRIOR APPLICATION NUMBER: DE 101 23 055.9
 PRIOR FILING DATE: 2001-05-11
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 313
 TYPE: PRT
 ORGANISM: Mus musculus
 US-10-705-757-6

Alignment Scores:

Pred. No.:	2,67e-117	Length:	313
Score:	1668.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.37%	Indels:	0
DB:	18	Gaps:	0

US-10-705-757-5 (1-942) x US-10-705-757-6 (1-313)

```

QY 1 ATGCTCTGTCCAAAGATCAACTCCCTGCGCCACCTGCGCGCCGCCCTTGCAACGACTTG 60
    |||
Db 1 MetLeuLeuSerIySILeAsnSerIeuaLahIbLeuAArgProCySaAsnApleu 20

QY 61 CACGCCCAACAGCTGCGCGCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
    |||
Db 21 HisAlaThrLybLeuAlaProGlyLybGluLybProLeuGluSerGlnTyrgInVal 40

QY 121 GGCCTCGTGTGGAGCGGCTTGGCTCGGCTCTGACTCTGAGATCCGCTGCGCGAG 180
    |||
Db 41 GlyProLeuLeuGlySerGlyLybGlyPheGlySerValTySerGlyIleArgValAlaAsp 60

QY 181 AACTTGCCTGCGCATTAAGACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
    |||
Db 61 AsnLeuProValAlaIleLybHisValGluLybAspArgIleSerAspTrpGlyGluLeu 80

QY 241 CCCAATGGCAACCGGAGTGGCCCAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
    |||
Db 81 ProAsnGlyThraArgValIlePheMetGluValIleuLeuLybValSerSerAspPhe 100

QY 301 TCGGCGCTGATTGACTTCTTGAGCTGGATTGAGAGCGCGATGTTTCGCTGATCTTG 360
    |||
Db 101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValIleuLeu 120

QY 361 GAGAGCGCCGAGACCGGAGTGAAGACCTTCTGACTTTATACCGAGAGAGAGAGAGAGAGAG 420
    |||
Db 121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140

QY 421 GAGAGACTGCGCGGAGATTTCTTGCGAGGTGCTGGAGCGCGCTGCGCGAGAGAGAGAG 480
    |||
Db 141 GluAspLeuAlaArgGlyPhePheTrpGlnValIleuGlnAlaValArgHisCybHisAsn 160
  
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; PRIOR FILING DATE: 1999-01-26
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 313
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-09-971-791-8

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	5,86e-111	313	295	8	10	0
Percent Similarity:	1584.00					
Best Local Similarity:	96.81%					
Query Match:	94.25%					
	90.57%					

US-10-705-757-5 (1-942) x US-09-971-791-8 (1-313)

```

QY 1 ATGCTCTGTCGAAGATCAACTCCCTGGCCCACTGCGGCCGCCCTGCAACGACTTG 60
   |||||
Db 1 MetleuLeuSerIylleahnserrleuAlahlsleuArgAlaIaProCyshanspleu 20
   |||||
QY 61 CAGGCCAACAGCTGGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
   |||||
Db 21 HlsAlaAsnlyleuAlaProGlylsGlylsGlylsGlylsGlylsGlylsGlylsGlyls 40
   |||||
QY 121 GGGCCGCTGTGGGCGAGCGGCTTCCGCTGCTTACTCTGCGGCTCCGCGCGCGAG 180
   |||||
Db 41 GlyProleuLeuIylserGlylsGlylsGlylsGlylsGlylsGlylsGlylsGlyls 60
   |||||
QY 181 AACTGCCGCTGTCATTAAGACGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
   |||||
Db 61 AsnleuProValAlaIlelyshlsValGlylsAspArgIleSerAspTrpGlylsleu 80
   |||||
QY 241 CCCAATGGCAACCGAGTCCCATGGAAGTGTCTGTGAAGAGTGAAGTTCGACTTC 300
   |||||
Db 81 ProAsnGlyThrArgValProMetGlyValIleuLeuIylserSerGlyPhe 100
   |||||
QY 301 TGGGGGCTGATTAAGCTTCTGAGCTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
   |||||
Db 101 SerGlyValIleArgleuLeuAspTrpPheGlyAspProAspSerPheValIleuLeu 120
   |||||
QY 361 GAGAGCGCCGAACCGGTGCAAGACTTTCGACTTATCAACGAGAGAGAGAGAGAGAGAGAGAG 420
   |||||
Db 121 GluArgProGlylsProValGlnAspLeuPheAspPheIleThrGlylsArgIylAlaLeuGln 140
   |||||
QY 421 GAGAGCTGGCCCGAGAGATTCTTCTGGCAGTGTCTGAGAGCGCGCGGCAATTGCCAAG 480
   |||||
Db 141 GluGlyLeuAlaIaArgSerPhePheTrpGlnValIleuGlyValAlaValArgIshlsAsn 160
   |||||
QY 481 TGGGGGGTCTCCACCGCGCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
   |||||
Db 161 CysGlyValIleuIleArgAspIlelyAspGlyAsnIleuIleAspLeuAsnArgGly 180
   |||||
QY 541 GAATCAAACTCATGCACTTCGGGTGGGGCGCTCTCAAGAGACAGTCTACAGAG 600
   |||||
Db 181 GluLeuIylleuIleAspPheGlylsSerGlylsIleuLeuIylAspThrValIylTrpThrAsp 200
   |||||
QY 601 TTTGATGGAGCCGAGGTGACAGTCTCCAGAGTGAATTGCTACCAATGCTACCAAGCG 660
   |||||
Db 201 PheAspGlyThrArgValIylSerProProGlylsTrpIleArgTrpIshlsArgIyl 220
   |||||
QY 661 AGGTGGAGCTGTCTGTCCTCCCTGGAGTCTGCTATGACATGAGTCTGGAGAGATT 720
   |||||
Db 221 ArgSerAlaIaValIylPheSerleuGlylsIleuLeuIylAspPheValCysGlyAspIle 240
   |||||
QY 721 CCCTTGAGCAGCATGAAGATCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
   |||||
Db 241 ProPheGlyIshlsAspGlylsGlylsGlylsGlylsGlylsGlylsGlylsGlyls 260
   |||||
QY 781 TCAGAGTGTGAGACCTTATTAATGGTGTCTGTCCCTGAGAGCGGTCAAGTGGCGCTTC 840
   |||||

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Db 261 SerGlyCysGlnIshlsleuIleArgTrpCysleuSerleuAspProSerAspArgProSer 280
   |||||
QY 841 TTTGAAGAAATCCGGAACCATCGGTGATGAGAGGAGTCTGTCGCCAGAGCTTCT 900
   |||||
Db 281 PheGlyGlyIleGlnAspIshlsProTrpPheGlnAspValIleuProGlnAlaThrAla 300
   |||||
QY 901 GAGATCATCTGCAACAGTCTGTCAACGGGATCCAGCAAG 939
   |||||
Db 301 GluIleHlsleuHlsSerleuSerProSerProSerIyls 313
   |||||

```

RESULT 8

US-10-348-081-12
 ; Sequence 12, Application US/10348081
 ; Publication No. US20040038246A1
 ; GENERAL INFORMATION:

; APPLICANT: KORN, Marcus
 ; APPLICANT: MUELLER, Guenter
 ; APPLICANT: SCHNEIDER, Rudolf
 ; APPLICANT: TSCHANX, Georg
 ; TITLE OF INVENTION: P1W-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
 ; FILE REFERENCE: DE4V2002/0004 US NP
 ; CURRENT APPLICATION NUMBER: US/10/348,081
 ; CURRENT FILING DATE: 2003-01-21
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 12
 ; LENGTH: 313
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-10-348-081-12

Alignment Scores:
 Pred. No.: 5,86e-111 Length: 313
 Score: 1584.00 Matches: 295
 Percent Similarity: 96.81% Conservative: 8
 Best Local Similarity: 94.25% Mismatches: 10
 Query Match: 90.57% Indels: 0
 DB: 15 Gaps: 0

US-10-705-757-5 (1-942) x US-10-348-081-12 (1-313)

```

QY 1 ATGCTCTGTCGAAGATCAACTCCCTGGCCCACTGCGGCCGCCCTGCAACGACTTG 60
   |||||
Db 1 MetleuLeuSerIylleahnserrleuAlahlsleuArgAlaIaProCyshanspleu 20
   |||||
QY 61 CAGGCCAACAGCTGGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
   |||||
Db 21 HlsAlaAsnlyleuAlaProGlylsGlylsGlylsGlylsGlylsGlylsGlylsGlyls 40
   |||||
QY 121 GGGCCGCTGTGGGCGAGCGGCTTCCGCTGCTTACTCTGCGGCTCCGCGCGCGAG 180
   |||||
Db 41 GlyProleuLeuGlylsSerGlylsGlylsGlylsGlylsGlylsGlylsGlyls 60
   |||||
QY 181 AACTGCCGCTGTCATTAAGACGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
   |||||
Db 61 AsnleuProValAlaIlelyshlsValGlylsAspArgIleSerAspTrpGlylsleu 80
   |||||
QY 241 CCCAATGGCAACCGGTGCAAGACTTTCGACTTATCAACGAGAGAGAGAGAGAGAGAGAGAGAG 300
   |||||
Db 81 ProAsnGlyThrArgValIylSerProProGlylsTrpIleArgTrpIshlsArgIyl 100
   |||||
QY 301 TGGGGGCTGATTAAGCTTCTGAGCTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
   |||||
Db 101 SerGlyValIleArgleuLeuAspTrpPheGlyAspProAspSerPheValIleuLeu 120
   |||||
QY 361 GAGAGCGCCGAACCGGTGCAAGACTTTCGACTTATCAACGAGAGAGAGAGAGAGAGAGAGAGAG 420
   |||||
Db 121 GluArgProGlylsProValGlnAspLeuPheAspPheIleThrGlylsArgIylAlaLeuGln 140
   |||||
QY 421 GAGAGCTGGCCCGAGAGATTCTTCTGGCAGTGTCTGAGAGCGCGCGGCAATTGCCAAG 480
   |||||
Db 141 GluGlyLeuAlaIaArgSerPhePheTrpGlnValIleuGlyValAlaValArgIshlsAsn 160
   |||||

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QY	481	TCGCGGGGTTCTCCACCGCGACATCAAGAGAAATCTTAAATCGACCTGACGGCGG	540
Db	161	CvGgYvAlLeuNhiLeaTgaNpIeUyNvBgiLnaNIlLeuNIlLeaPvLeaMaNvAgLy	1800
QY	541	GAATTCMAATCATCGACTTCGGGTCGGGGGCGCTGCTCAAGGACACAGTCTACCGAC	600
Db	161	GtUeUyLeuNIlLeaPvBhegiUeYvAlLeuNLeuUyNvPvNvAlYvTThAsp	2000
QY	601	TTGATGGGACCCGAGATGACAGTCCCTCCAGATGGAATTGGCTACCATCGCTACCGG	660
Db	201	PvhaBvGtYvThvArGvAlYvSvPvPvPvGvIvTtPvLeTgYvNvIvAgtYvNvIgLy	2200
QY	661	AGGTGGGACGCTGTCTGGTCCTCTTGGAGATCTGCTATGACATAGTCTTCGAGATATT	720
Db	221	ArgSvErAlLeaVAlvTvrSvLeUgUyIvLeUeUeUyTvKvBvEtvAlCyvGvUyNpIe	2400
QY	721	CCGTTTGAACGACGATGAAGATCATCAAGGGCGAAGTCTTTCAGGCAATCTGTCT	780
Db	241	PrOpvBgiUvNvIvAaPvIvGvUvIvAlvUyVgUvIvGvIvNvAlvYvPvKvArGvIvNaVvAlSv	2600
QY	781	TCAGAGTGCAGACCTTATTAATGATGCTGCTGCTGAGACCGTCAAGATCGGCGCTTC	840
Db	261	SvrgUvCyvGvIvNvIvLeuNIlLeaGtTPrCyvUeNvSvEtvNvArGvPvPvSvArPvAgtPvSv	2800
QY	841	TTTGAAGAAATCCGAACCATCCGAGGATGCAAGGATGACCTCTGCCCCAGGACGTTCT	900
Db	281	PvhegiUvGvUvIvIvGvIvNaNvNvIvPvTPrMvEgIvNaPvAlvUeUeUvPvGvIvAlvIvNaVvAl	3000
QY	901	GAGATCCATCTGCACAGTCTGTACACGGGATCCAGAC 939	
Db	301	GvUvIvEtvIvLeuNvIvSvEtvUeUvPvSvPvSvPvSvEtvUy 313	

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RESULT 9
US-10-705-757-4
; Sequence 4, Application US/10705757
; Publication No. US20040146942A1
; GENERAL INFORMATION:
; APPLICANT: GRUENTENTIAL GMBH
; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
; FILE REFERENCE: 029310-52818US
; CURRENT APPLICATION NUMBER: US/10/705,757
; PRIOR APPLICATION NUMBER: PCT/EP02/05234
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: DE 101 23 055.9
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 313
; TYPE: prt
; ORGANISM: Rattus norvegicus
US-10-705-757-4

Alignment Scores:
Pred. No.:          5,86e-111      Length:           313
Score:              1584.00         Matches:           295
Percent Similarity: 96.81%         Conservative:       8
Best Local Similarity: 94.25%        Mismatches:        10
Query Match:        90.57%          Indels:             0
DB:                  18              Gaps:               0

US-10-705-757-5 (1-942) x US-10-705-757-4 (1-313)

QY      1 ATGTCCTCTGTCCAGATTCACACTCCTCGGCCCACTGGCGCCCGCCCTTGACAAGACTTG 60
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MetLeuLeuSerIylleAenSerIeuAlAHlSlenAlgAlAlaprocysAenApLeu 20

QY      61 CACGCACCAACACTGTCGCGCGGGGCAAGAAGAGACCCTTGAAGTCGACGTAACAGATTG 120
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      21 HtEAlAAenHyIsenAlapProgllyySGulHySGluProlendunberglntyrGlval 40

QY      121 GGCCCGCTTTGGGCGACGCGTGGCTTCGCGTCGCTCACTTGACATCGCGTGGCCGAC 180

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Db	41	GIYPRoleuLeuGIYserGIYleuPheGlySerValTYrSerGIYIleArgValAlaIAsp	60
OY	181	AACTTGCCTGGTGGCAATTAAAGCAGCTGGAGAAGACCGGAATTTCCGATTGGAGAACTG	240
Db	61	AsnLeuProValAlaIleLeuHisValGIuYrAspArgIleSerAspTrpGIuLeu	80
OY	241	CCCAATGGCACCCGAGTGGCCATGGAGTGGTCCCTGTGAAGAAAGGTGAGTGGACTTC	300
Db	81	ProAsnGIYThrArgValPrometGIuValIleuLeuYIlyValSerSerGIYPhe	100
OY	301	TCCGGAGCTAATGACTTTCGTGACTGGTGTTCGAGAGGCCCGGATAGTTTCGTACTGCTG	360
Db	101	SerGIYValIleArgLeuLeuAspTrpPheGIuArgProAspSerPheValIleu	120
OY	361	GAGAGCCCGGAACCGGTGGACAGCTTTCGACTTATACCGAAGAGAGCCCTACAG	420
Db	121	GIuArgProGIuProValGIuIAspLeuPheAspPheIleThrGIuArgValAlaLeuGIu	140
OY	421	GAGACCTTGCCCGAGAGATTCTTCTGGACAGTGTCTGAGGCCCGGTGGCATTGGCAGAC	480
Db	141	GIuGIuIleuAlaArgSerPhePheThrGIuValIleuGIuAlaValArgHisGlyAsn	160
OY	481	TGGGGGGTTCGACCGGAGCATCAAGAGACAGAAACATTAAATCGACTGAGCCGGGC	540
Db	161	CysGIYValLeuHisValArgAspIleYrAspArgIuAsnIleuIleAspLeuAsnArgGIY	180
OY	541	GAATGAAACTCATCGACTTTCGGTGGGGGGCGCTGTCAGAGACAGAGTCTACACGAC	600
Db	181	GIuIleuYrLeuIleAspPheGIYserGIYAlaIleuLeuYrAspThrValTYrThrAsp	200
OY	601	TTTGATGGACCCGAGTGTACAGTCTTCCGAAGTGGATTGCTACATCGCTACACGAC	660
Db	201	PheAspGIYThrArgValTYrSerProProGIuTrpIleArgTYrHisArgTYrHisGIY	220
OY	661	AGGTCCGACAGCTGTCTGGTCCCTTGGGATCCTGCTCTATGACATGGTGTGGGAGATAT	720
Db	221	ArgSerAlaValATrSerLeuGIYIleLeuLeuTYrAspMetValCysGIYAspIle	240
OY	721	CCGTTTGAGACAGATGAGATCATCAAGGGCCGAGTGTCTTCAGGCAAACTGTCT	780
Db	241	ProPheGIuIleAspGIuIleValIleValIleValIleValIleValTYrPheArgGIuArgValSer	260
OY	781	TCAGAGTTCAGACACTTATTAATGATGCTGTCTCCGTAGACCCGTACAGATCCGACCTCC	840
Db	261	SerGIuCysGIuHisIleuIleArgTYrCysLeuSerIleuArgProSerAspArgProSer	280
OY	841	TTTGAAGAAATCCGAGACCATCCGTGATGCAAGGTGACCTCTGCCCCAGGACGTTCT	900
Db	281	PheGIuGIuIleGIuAsnHisProTrpMetGIuAspValIleuLeuProGIuAlaThrAla	300
OY	901	GAGATCCATGCAGACGTGTGCACCGGAGATCCAGCAG	939
Db	301	GIuIleHisIleuHisSerIleuSerProSerProSerTYrS	313

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RESULT 10
US-09-971-791-9
; Sequence 9, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
; APPLICANT: Kosana Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle Macbeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971,791
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0

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Db      161  CysglYvalLeuHIsarGAspIleLyabpGluLeuHleLeuHleAspLeuAsnArgGly 180
Qy      541  GAATCAAACTCATGCACTTCGGGTCGGGGCGCTGCTCAAGACACAGTCTACACGAC 600
Db      181  GluLeuYsLeuHleAspPheGlySerGlyAlaLeuLeuYsAspThrValTyThrAsp 200
Qy      601  TTGATGGAGCCCGAGGTACAGTCCTCCAGAGTGGATTGGCTACCTCCCTACCAAGGC 660
Db      201  PheAspGlyThrArgValTyThrSerProGluTrpIleArgGlyAlaValPhePheArgGlnArgValSer 220
Qy      661  AGGTGGCAGCTGTCTGTGCTTCCTGGATCCCTGCTATGACATGATGCTGCGAGATATT 720
Db      221  ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyThrAspMetValCysGlyAspIle 240
Qy      721  CCGTTGAGACACGATGAAGATCATCAAGGCGCAAGTGTCTTCAGGCAAACTGTCTT 780
Db      241  ProPheGluHIsarGpGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
Qy      781  TCAGAGTGCAGCACCTTAATAATGGTGCCTGTCCCTGAGACCTGACATCGGCTCC 840
Db      261  SerGluYsGlnHIsarGpIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280
Qy      841  TTGAGAAATCCGGAACCATCCGTCGATGACAGGTCGACCTCTCCCGACGAGCTTCT 900
Db      281  PheGluGluIleGlnHIsarGpIleArgTrpMetGlnAspValLeuLeuProGlnGluThrAla 300
Qy      901  GAGATCCATCTGCACAGTCTGTCAACGGGATCCAGCAAG 939
Db      301  GluIleHIsarGpIleSerLeuSerProGlyProSerTys 313

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RESULT 12

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US-10-394-322A-52
/ Sequence 52, Application US/10394322A
/ Publication No. US2003023391A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNESIS PHARMACEUTICALS, INC.
/ APPLICANT: Prescott, John C.
/ TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
/ FILE REFERENCE: 39750-0006 US
/ CURRENT APPLICATION NUMBER: US/10/394,322A
/ PRIOR FILING DATE: 2003-03-20
/ PRIOR APPLICATION NUMBER: US 60/366,892
/ PRIOR FILING DATE: 2002-03-21
/ NUMBER OF SEQ ID NOS: 70
/ SOFTWARE: PatSeq for Windows Version 4.0
/ SEQ ID NO 52
/ LENGTH: 313
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-10-394-322A-52

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Alignment Scores:

```

Pred. No.:      8,3e-111      Length:      313
Score:          1582.00      Matches:      294
Percent Similarity: 97.12%      Conservative: 10
Best Local Similarity: 93.93%      Mismatches: 9
Query Match:     90.45%      Indels:      0
DB:              15          Gaps:          0

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US-10-705-757-5 (1-942) x US-10-394-322A-52 (1-313)

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Qy      1  ATGCTCTGTGCAAGATCACTCCCTGCGCCACCTGCGCGCCCTTCGAACGACTG 60
Db      1  MetLeuLeuSerTysIleAsnSerLeuAlaHIsarGpIleAlaProCysAsnAspLeu 20
Qy      61  CACGSCCAAGCTGGCGCGCGGCAAGAGAGAGGAGGCGCTGAGTGCAGTCCAGGTG 120
Db      21  HIsarThrYsLeuAlaProGlyLybGluYsGluProLeuGluSerGlnTyGlnVal 40
Qy      121  GGGCCGCTGTGGCAGCGGTGCTTCGCTCGCTACTCTGCAATCCGCTCGCGCAC 180
Db      41  GlyProLeuLeuGlySerGlyGlyPheGlySerValTySerGlyIleArgValSerAsp 60

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Qy      181  AACTTGGCGGTGGCCATTAAAGCATGTGAGAGAACGACCCGATTTCCGATTGGGGAAC 240
Db      61  AsnLeuProValAlaIleYsHIsarGluYsAlaAspArgIleSerAspTrpGlyGluLeu 80
Qy      241  CCCAATGACCCCGAGTGGCCATGAGAGTGGTCTCTGTTGAAGAAAGTGAAGTCTG 300
Db      81  ProAsnGlyThrArgValProMetGluValValLeuLeuYsValSerSerGlyPhe 100
Qy      301  TCGGGCGCTCAATTAGACTTTCGACTGTGAGCTGGTTCGAGAGGCCGATAGTTTCTG 360
Db      101  SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleu 120
Qy      361  GAGAGGCCCGAACCCTGTCGAAGACCTTTCGACTTTATATCCAGACGAGAGCCCTT 420
Db      121  GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140
Qy      421  GAGACCTGGCCCGAGAGATTCTTCTGAGAGGTCTGAGAGCCGTCGGCGCATTCGACA 480
Db      141  GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHIsarGpAsn 160
Qy      481  TCGGGGTTCTCCACCGGACATCAAGACGAGAGACATCTTAATGCACTGAGCCGGCG 540
Db      161  CysglYvalLeuHIsarGAspIleLyabpGluAsnIleLeuHleAspLeuAsnArgGly 180
Qy      541  GAATCAAACTCATGCACTTCGGGTCGGGGCGCTGCTCAAGACACAGTCTACACGAC 600
Db      181  GluLeuYsLeuHIsarGpGlySerGlyAlaLeuLeuYsAspThrValTyThrAsp 200
Qy      601  TTGATGGAGCCCGAGGTACAGTCCTCCAGAGTGGATTGGCTACCTCCCTACCAAGGC 660
Db      201  PheAspGlyThrArgValTyThrSerProGluTrpIleArgGlyAlaValPhePheArgGlnArgValSer 220
Qy      661  AGGTGGCAGCTGTCTGTGCTTCCTGGATCCCTGCTATGACATGATGCTGCGAGATATT 720
Db      221  ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyThrAspMetValCysGlyAspIle 240
Qy      721  CCGTTGAGACACGATGAAGATCATCAAGGCGCAAGTGTCTTCAGGCAAACTGTCTT 780
Db      241  ProPheGluHIsarGpGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260
Qy      781  TCAGAGTGCAGCACCTTAATAATGGTGCCTGTCCCTGAGACCTGACATCGGCTCC 840
Db      261  SerGluYsGlnHIsarGpIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280
Qy      841  TTGAGAAATCCGGAACCATCCGTCGATGACAGGTCGACCTCTCCCGACGAGCTTCT 900
Db      281  PheGluGluIleGlnHIsarGpIleArgTrpMetGlnAspValLeuLeuProGlnGluThrAla 300
Qy      901  GAGATCCATCTGCACAGTCTGTCAACGGGATCCAGCAAG 939
Db      301  GluIleHIsarGpIleSerLeuSerProGlyProSerTys 313

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RESULT 13

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US-10-348-081-13
/ Sequence 13, Application US/10348081
/ Publication No. US20040038246A1
/ GENERAL INFORMATION:
/ APPLICANT: KORN, Marcus
/ APPLICANT: SCHNEIDER, Rudolf
/ APPLICANT: TSCHAN, Georg
/ TITLE OF INVENTION: P1M-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
/ FILE REFERENCE: DE4V2002/0004 US NP
/ CURRENT APPLICATION NUMBER: US/10/348,081
/ CURRENT FILING DATE: 2003-01-21
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 13
/ LENGTH: 313
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-10-348-081-13

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Alignment Scores:

Pred. No.:	8,3e-111	Length:	313
Score:	1582.00	Matches:	294
Percent Similarity:	97.12%	Conservative:	10
Best Local Similarity:	93.93%	Mismatches:	9
Query Match:	90.45%	Indels:	0
DB:	15	Gaps:	0

US-10-705-757-5 (1-942) x US-10-348-081-13 (1-313)

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QY 1 ATGCTCTGTCCAAGATCAATCCCTGGCCACCTGGCCGCCGCCCTTGCAAGACTTG 60
   1 MetLeuLeuSerLysrIleAenSerLeuAlaHleuHrghAlaIaProCyAanAapLeu 20
Db
QY 61 CAGGCCCAAGCTGGGGCCGGGCAAGAGAAGAGCCCTTGAGTGGCACTGACAGTG 120
   21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGluSerGlnTyrglnVal 40
Db
QY 121 GGCCTGCTGTGGGCAAGCGGTGGCTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTG 180
   41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTySerGlyIleArgValSerAap 60
Db
QY 181 AACTTGGCGGTGGCCATTAAAGCAGTGGAGAAGACCGGATTTCCGATTGGGAGAACTG 240
   61 AsnLeuProValAlaIleLysHleValGluLysAapArgIleSerAapTrpGlyGluLeu 80
Db
QY 241 CCGAATGGGCAACCGGATGGCCATGGAAGTGTCTCTGTTGAAGAAGTGAAGTCTG 300
   81 ProAenGlyThrArgValAlaProMetGluValValLeuLeuLysValSerSerGlyPhe 100
Db
QY 301 TCGGGCGCTGATTAGACTTCTGCACTGGTGGAGAGCCCGATAGTTTCGTGATCTTG 360
   101 SerGlyValIleArgLeuLeuAapTrpPheGlyLysArgProAapSerPheValLeuIleLeu 120
Db
QY 361 GAGAGGCCCAACCGGTGGCAAGCCTTCTGACTTTATCAACGAACGAGGAGCCCTTAC 420
   121 GluArgProGluProValGlnAapLeuPheAapPheIleThrGluArgGlyAlaLeuGln 140
Db
QY 421 GAGGACTGGCCCGGAGATTTCTTGGCAGTGTCTGGAGGCCGTGGCGGCTTTCACCAAC 480
   141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValAlaArgHleCySHleAap 160
Db
QY 481 TGGCGGGTCTTCCACCGCAGATCAAGAGAGAGAACTTTAATCGACTGAGCCGGCG 540
   161 CySGlyValLeuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleu 180
Db
QY 541 GAAATCAAACTCATCGACTTCGAGTTCGAGGCGCGCTGCAAGAGACAGTCTTACAGGAC 600
   181 GluLeuLysLeuIleAapPheGlySerGlyAlaLeuLeuLysAapTrpValTyTrpAap 200
Db
QY 601 TTTGATGGGACCGGAGTGTACAGTCTTCCAGAGTGGATTGGCTACCTCGCTACAGGCG 660
   201 PheAapGlyThrArgValTyTrpSerProGluTrpIleArgTyTrpHleAapGlyTrpHle 220
Db
QY 661 AGGTCCGACAGTGTGCTGCTTGGAGTCTGCTGATGACATGAGTCTGCGAGATATT 720
   221 ArgSerAlaIleAlaValTrpSerLeuGlyIleLeuLeuTyTrpAapMetValCySGlyAapIle 240
Db
QY 721 CCGTTGAGCAGATGAAGAGATCATCAAGAGGCGCAAGTGTCTTCCAGCAAACTGTCTT 780
   241 ProPheGluHleuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleu 260
Db
QY 781 TCAAGAGTGAAGACCTTATTAATGAGTGTGCTGCTGAGACCGTCAAGTTCGAGCTTCC 840
   261 SerGluLysGlnHleuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleu 280
Db
QY 841 TTTGAAGAAATCCGGAACCATCCGCTGATGACAGGAGTGAACCTCTGCGCCAGGAGCTTCT 900
   281 PheGluGluIleGlnAenHleuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleu 300
Db
QY 901 GAGATTCATTCGACAGTCTGTCAACCGGAGATTCAGCAAG 939
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Db 301 GluIleHleuHleuSerLeuSerProGlyProSerLys 313

RESULT 14

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US-10-664-421-1
/ Sequence 1, Application US/10664421
/ Publication No. US20040142864A1
/ GENERAL INFORMATION:
/ APPLICANT: BREMER, RYAN
/ APPLICANT: IBRAHIM, PRABHA
/ APPLICANT: KUMAR, ABHINAV
/ APPLICANT: MANDIYAN, VALSAN
/ APPLICANT: MILBURN, MICHAEL V.
/ TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
/ FILE REFERENCE: 039363/0703
/ CURRENT APPLICATION NUMBER: US/10/664,421
/ PRIOR FILING DATE: 2003-09-16
/ PRIOR APPLICATION NUMBER: 60/412,341
/ PRIOR FILING DATE: 2002-09-20
/ PRIOR APPLICATION NUMBER: 60/411,398
/ PRIOR FILING DATE: 2002-09-16
/ NUMBER OF SEQ ID NOS: 169
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 1
/ LENGTH: 313
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-664-421-1

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Alignment Scores:

Pred. No.:	8,3e-111	Length:	313
Score:	1582.00	Matches:	294
Percent Similarity:	97.12%	Conservative:	10
Best Local Similarity:	93.93%	Mismatches:	9
Query Match:	90.45%	Indels:	0
DB:	16	Gaps:	0

US-10-705-757-5 (1-942) x US-10-664-421-1 (1-313)

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QY 1 ATGCTCTGTCCAAGATCAATCCCTGGCCACCTGGCCGCCGCCCTTGCAAGACTTG 60
   1 MetLeuLeuSerLysrIleAenSerLeuAlaHleuHrghAlaIaProCyAanAapLeu 20
Db
QY 61 CAGGCCCAAGCTGGGGCCGGGCAAGAGAAGAGCCCTTGAGTGGCACTGACAGTG 120
   21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGluSerGlnTyrglnVal 40
Db
QY 121 GGCCTGCTGTGGGCAAGCGGTGGCTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTG 180
   41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTySerGlyIleArgValSerAap 60
Db
QY 181 AACTTGGCGGTGGCCATTAAAGCAGTGGAGAAGACCGGATTTCCGATTGGGAGAACTG 240
   61 AsnLeuProValAlaIleLysHleValGluLysAapArgIleSerAapTrpGlyGluLeu 80
Db
QY 241 CCGAATGGGCAACCGGATGGCCATGGAAGTGTCTCTGTTGAAGAAGTGAAGTCTG 300
   81 ProAenGlyThrArgValAlaProMetGluValValLeuLeuLysValSerSerGlyPhe 100
Db
QY 301 TCGGGCGCTGATTAGACTTCTGCACTGGTGGAGAGCCCGGATAGTTTCGTGATCTTG 360
   101 SerGlyValIleArgLeuLeuAapTrpPheGlyLysArgProAapSerPheValLeuIleLeu 120
Db
QY 361 GAGAGGCCCAACCGGTGGCAAGCCTTCTGACTTTATCAACGAACGAGGAGCCCTTAC 420
   121 GluArgProGluProValGlnAapLeuPheAapPheIleThrGluArgGlyAlaLeuGln 140
Db
QY 421 GAGGACTGGCCCGGAGATTTCTTGGCAGTGTCTGGAGGCCCGGATAGTTTCGTGATCTTG 480
   141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGlnAlaValAlaArgHleCySHleAap 160
Db
QY 481 TGGCGGGTCTTCCACCGGAGATCATCAAGAGAGAGAACTTTAATCGACTGAGCCGGCG 540
   161 CySGlyValLeuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleuHleu 180
Db

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